

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7283	21184	A	7343	306	164	IYMLYFTIYITLIYIHTHTHTHLYLDKYI YL*CVHCFL**AYMICQR
7284	21185	A	7344	442	8	SQMSKLTWFRVAHAHWPSTLGGQGR IT*VREFETSLGNTARPNLYWN
7285	21186	A	7345	3	248	HELSSLSSLPFFFKNEKGSR*VAHAGL KLLTSSDPPT*ASQSARITGISHCARPL LSHFLAYLALPCHQNRLCTGHLPT
7286	21187	A	7346	2	246	HELYQSTILLSPLFFKNDIGSR*IAHAGL QLLT*SDPPT*ASQSARITGISHCARPL LSHCLAYLALTCHQNRLCTGHLPT
7287	21188	A	7347	1	130	GTRLLKRLTQETRLNPGRGCREPSLHY CTPTWARQSQTVAHN*KRLTQETRLNPG RGCREPSLHYCTPTWARQSQTVAHN
7288	21189	A	7348	516	288	FFETESRFITQTGVQWCDLGPLQLPPG FKGFSCSLSS*DYRCLPPHPANCFIF SRDGVSPC*LGWSQTPDLK
7289	21190	A	7349	417	148	STSVVQAGVQWHDHGLLPGPRLK*S SHLSLPHG*DYRHILSCLANF*NIFVEA GFRHTAHGLEPLGSSDLPASASQSAGIT GMSHLA
7290	21191	A	7350	143	2	TQKFKTSLSWDYRRVSAHVANFCIFSK DRVSPY*PGWSRTPDPA
7291	21192	A	7351	189	37	EAIIVRRII*NLFFFFFF*RWGLTVLPK LVSNSWAQAILSPQPSKVLRLQA
7292	21193	A	7352	131	2	KSRLGTVAHACNPSTLGGRHGWIT*SRE FKTSRANMVKPRPA
7293	21194	A	7353	1	106	GTRGQCLTMLPRLVLNYAQMILPPWPP *VLGLQV
7294	21195	A	7354	939	653	KGNFIFLRQSFTLVAQAGVQWRDLGSPQ PPPPGSK*FSCSLRSSWDYRHGPPHPA NFAFLVEMGFLHVGQAGLELPT*GDPPT SASQSAGITGR
7295	21196	A	7355	270	26	EARFLGLLRDIAQLCPGWSAAV*S*LT AASTSWAQVKASTHLSLNN*D*ARATM PG*LKKYVFF*RQGLAILPRLRVF
7296	21197	A	7356	329	206	HHLANF*TFCDRGLTMLARLNSWQAI LLPQPPKVLGLQM
7297	21198	A	7357	128	253	MRPDTVAHTCNPSTLGGQGGGRIT*THEF ETSLGDMMKPYLYK
7298	21199	A	7358	2	108	AREGSGGQCSEP*WRHCTAAWVTEQDP VSKTIKK
7299	21200	A	7359	1	340	GTRERNWHLA*ALHTHTHTHTRHTHTH THFSFPANS*RDTFVIF*QSLLEIMTS FSPSLGLKCSFSQQPSGLLSSIAGERDS RIHAGENTVSMCLHNRLKAELRSVISLR V
7300	21201	A	7360	385	1	SVGPSKPCAGYNLLVCHLLRPLEKRSIR VGVT*FSRCHLSPLSLTRKANSLTPCTS WMRRCLILLRLTLGVPHPMSCTHCPTLP SEMNLGPQLEMQKSPIFCVAHAGSPRLE LFLFGHLGSTPNLPSC
7301	21202	A	7361	234	29	LSTEPKGSKALKFNVTLLNIAF*CNCSG CNSNL*S*QY*RVIQSHHLSQTLWLTP VIPALWEAEAGG
7302	21203	A	7362	68	339	DRDIANKPAWQLCQSRILYLAQLQFIDQ GELLPDFRIHYKVI*TCTAWH*RRNRLI DQWNRADIPDLNPCQAWRLTPVILVLE ADVGG

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						FF*INSLFIQNSFLT
7322	21223	A	7382	163	160	PQTSNDEIQRRNSRNRTSPIAER*GLSL LPRLEWMGSSNEAHSNLELQGSNNPPASA SKSTMITGVSHCA*PRLEWMGSSNEAHSN LELQGSNNPPASASKSTMITGVSHCA
7323	21224	A	7383	1	183	VCVCVCVCVCVCIKWDSYSAIKKNELVA FVVTWKRLETIILSEVSQE*NTIYHMS LICGS
7324	21225	A	7384	2	196	KIQMWPGVVAHACYPNTLGGQDGRTA*G QEFQTSLSGNIARPCLYQQQQQQQPRCS LTYDGDKS
7325	21226	A	7385	3	192	RNLSSLQPPPPGLK*WSCSLPSSWDYR RPPPCPANCFMLCEFFRTNGVFPCSPGV YFEPRN
7326	21227	A	7386	266	198	TMLSGFLRSAGLTMTIS*PHDPPASASQS AGITGVSHRARPLVFLRDSLYSGTQAG VPWRDLSSLQSRLEAQMRFCEP
7327	21228	A	7387	164	311	SKQQKGLSGVAHPCNPSTLGGGRGRWIN* GQEFETSMASMVKPCLSLLKL
7328	21229	A	7388	3	218	EIMSFATWMQLEANILSTLSHE*IAKY CMLSLLSGAKHWVLMNIEVGTGDTRDYL GCTYPSSTEQLGYY
7329	21230	A	7389	521	58	SDCGLTPIAQTGVHWHHLLSLQP*LPWL G*FSLSLPSSWDYKYVPPCPASFLYF LVETGFCHVAQDGLELLDSNNPPSSASQ SAGITGMSGCAGLRRF*KLRSWRYLVLL AMQVNEQGTQAGEAVSEADAGQGCCCG LCLHRLLSQQYALP
7330	21231	A	7390	169	322	APGNFKTN*RNKGFWAGNTLGVSVKNMK NGAWWLTSPVIALWEAEAGGSP
7331	21232	A	7391	1	353	GTSPHYGSFHHGQKDVTKGSGSQRPRER VLGSHARKNSLPVHEVKAYLL*KYLSIL RATHILISPDGCWVPFIAQSYIFLSSC GFFLLFFLLLLLTLFCSWHLIISFLALF VIPLY
7332	21233	A	7392	372	3	IQAGACCAECIPSKGIRWNPSIVEGLHS DMSWSLCLFLSGAISVLCNFRLSGSSDS PMSA*QAARTAVIRHHTRLIFCIFSRRD ETGFHHVGQENLLMLLQLFSGLGFSIS ATLLTMLLV
7333	21234	A	7393	362	176	ARMECSGAI*AGLRGSSDSLASAS*EAG YTGKCGHAQ*TFVFLVEVRFHHVGQNAI NIRTS
7334	21235	A	7394	2	304	ARADCCARNE*GSVGMGPSEPGVGYNLL VFRFLRPLEKHSIRVGETRFSRCCLSQL CLARTGNSLTPTCTSWVRQCLALLRLMLG ALHPLSCTQRPTSHSE
7335	21236	A	7395	256	3	MYAARYWNKAKITTESLRHWAGHGGSH PYNPSTLGG*GGQIS*AHKPETSLGNMV KPHLSKNKQTNKQTNQTNISWSWCTCL
7336	21237	A	7396	346	2	RDHFYRESHSLITYICLENVKSNLKCGE GPLNFTFHLQRKNCNLGHTRSPGGVYHV GRTEATGPIKRRNGLGAVAHTSNPSNL GGQGGWIT*GQEFKTSLSLPRWLTPVIP LV
7337	21238	A	7397	2	242	RRYSYDPDAYTT*NILSSVGSFISLTAV ILIIIFMT*EA*KKKKKKKKKKKKGGPF KKTLLGGPKFNRRMEGNKNSLKGGR

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7338	21239	A	7398	1	289	TKLLGLYYTLLQASNDKSPFSIFDGIY GSTFFVTTGFHGLHVIIGSTILTI*FIR QLIFHFTSKHHFGLEADA*YWHLADARR HSESIHQCCSL
7339	21240	A	7399	346	40	IIIFTNKIYIKINKRLKLFIIKILDLYI I*IFFFRK*FTFKQ*KFIININKIYN NIK**IFIYLF*FFFFFFFFFFFFLFFFF FFFFFFFFFFFFFFFFFFFFLKK
7340	21241	A	7400	1	334	NSCRRQRLDLLLLPITL*LPQLIGYIE KSTRYECGFHPISPARVPSIKFFLVAI TFLFLDLQIALLLPLP*ALQTTNLPPLIV MSSLLLIILALNLAYE*LPKGLD*AE
7341	21242	A	7401	2	302	HTINLLGERYVLATTY**STMTLLLTGL TVLHTGLYSVYLMTTTQWG*LTPLINM KP*FTR*DTLVFIHLSPIILLSLNPDI TGVVLVLLSYELYLLT
7342	21243	A	7402	57	338	TTHNVIGYIEASTAYESGCDPISPARVP FSIKFFLVAITFLFLDLBIAILLPLP*A LQTTNLPPLIGMSSLLLIILALSLAYE* LQKGLD*AE
7343	21244	A	7403	407	68	QEELVDPLTTVREQCEQLENCVKAR*RL *LCDERVSSRSHSEEDCEDLDFDLHAR DHCVFLLIYLINLKYMCALT
7344	21245	A	7404	494	154	SLFIFYLYLIFLF**FFHYFFYFLLSI FSEKLLFFFLHFFHMFLLFFSPENK IFFPKIPRFFLPLF**KFFFLPFPKF LSPLGFFF*SPPFFFFFFFFFFFFFFFFF F
7345	21246	A	7405	1	400	NPGRFLSTSNSSLYERTREIRPTSQSAF PRK*YHLKKKKKKKKKKKKKKKKKKK KKGGLPKKKPRGGQK*TGGEKKK*PKR GGKKKPPGKF*KKTFFWGGKKMGKTPQK KINPLGKKKIFKGKRGKTPPL
7346	21247	A	7406	2	257	RASLCHPGWSAVV*SWLIAALTSWLKQF SHLNSLKCWDYRHEPHLA*LRFEHRHS GSSICTLNR*ILLSFPILSIRYKNGLIL Y
7347	21248	A	7407	259	47	YVFFFLFLFFIRLQSVSPFFFFFFFFF FFFFFFFFFFFFFFFVK*SPIEMFSFVV LYLLRQVSI SIAYTLFG
7348	21249	A	7408	3	248	VTFL*CDVEIAVLIP*ALPTTNLALI DMSSLLLIILALRLAYE*LRGGLD*AE EHQATHSAYERAPPL
7349	21250	A	7409	2	350	RSGMPRRYSYDPDAYTT*NILGSVGAFT CLTAGILIIFMI*EAFASKRKVLIVEQP SINLE*LYGCPPPYHTFEEPVIKSRHI RKESNPPLVSSQPHGLHDFKKKLGTI TEKN
7350	21251	A	7410	2	232	LDQTYAKIHFTIVFIGVDLTLLPQHFLG LSGMPRRYSYDPDAYTT*NILSSVGSFI ALTAAILIIFMI*EAFAKKF
7351	21252	A	7411	2	321	TSLLAVALLIIMTL*LPQLNRYIEKSTPY ECGFDPICPRVPFSIKFFLVAITFLLF DLETALLPLP*SLQTTNLPPLIAMSSLL LIILDLNLAYE*LQKGLD*AE
7352	21253	A	7412	2	194	SIECFVLPITLLCDLEIALLLPLP*AL QTSNLPPLIVMSSLLLIILALNLAYE*L QKGLD*AD

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7353	21254	A	7413	1	197	LYTTYFVTKTLLLTSLFL*GRTAYPRLR YDQLIHLL*KNFLPLTLALLI*HVSIPIT TISSIPPQT
7354	21255	A	7414	1	185	STPLP*ALQTTNLPLIVMSSLLLIIL LSLAYE*LQKGLD*AEKKKKGA AVLKDP SGGPS
7355	21256	A	7415	347	228	LE*LYGCPPPYHTFEPPVYIKSRKKE SNPPKLVSSQPHGLHDFFKHIKNYRKNK RKEGLASVKENDRGP
7356	21257	A	7416	1	296	HAYDHASQNLNGYIEQSTPYECGFDPIS RARVPFCIKVFLVAITFLLFDLEIALLL PLP*ALQATANLPLIGMSSLLLIILALS LAYE*LHKGLD*AE
7357	21258	A	7417	3	202	TCSI*HVLVRMT*LIYDLEIALL*PVP* ALQSTNLPLISMTSLLLIILALSMAYE *LQTGLD*AE
7358	21259	A	7418	1	321	SNTLLALVLTITTS*LPQLSGCVGECTP YECGICRILNARALCCMQIFLKAITFLL FDLEIALLLPLP*ALQTTNLPLIDMSSL LLIIILALS LAYE*LQKGLD*AE
7359	21260	A	7419	1	212	RTRGIIIFRPLSQSLY*LLAANLVILT*I GGQPVSYPTIIGQVAVLYFTTILILI PTICLIENKILKWA
7360	21261	A	7420	2	257	GRVGRVGYSTIAFFLQAITVLVLDLESA LLLALP*SLQTTNLSLIVMSSLLLIIL ALS LAYE*LPLGLD*AEYWGEMMTTLD A
7361	21262	A	7421	367	269	HCDLKLKGSSDPPASAS*VAWITGTCHH TKLS
7362	21263	A	7422	2	116	ALQTTNLPLIVMSSLLLIILALRLAYE *LQKGLD*AE
7363	21264	A	7423	2	336	KPECGREGILPCCSSSAWPEGSFRPFQM NLGSFLSFFLFFFEKGLFLCPPV*S PYGKSNLLEPSASRFQFFCLGPLNWD YRLFPPFPNGFVFKNRVFPFWPSLV
7364	21265	A	7424	3	154	LFL*IRTAYPRFRYDQLIHLL*ENFLPL TVALLI*HVSIPITISSIPPQT
7365	21266	A	7425	3	154	LFL*IRTAYPRFRYDQLIHLL*ENFLPL TLALLI*HVSIPITISSIPPQT
7366	21267	A	7426	1	314	INTLLTLLLIITL*LPQLNGYIN*STP YECGFDPISPARVPFSIKFFLIATFLL FDLEIALLLPLP*ALQATNLPLIDMPSL LLIIILALS LAYE*LHQGLY
7367	21268	A	7427	1	331	ILIINTLLALLLIITF*LPQLNGYIEK STPYECGFDPISPARVPFSIKFFLVAIT FLLFDLEIALLLPLP*ALQTTNLPLIVM TSLLLIILALRLDYE*LQPGLD*AD
7368	21269	A	7428	2	373	SDRNHIIHALVITILLGLYFTLLQASEY FESAFTISDGIYGSTFFVATGFHGLHV IGSTFLTICFIRQLIFHFTSKHHFGFEA AA*YWHIVDVAGLFLHVSIRGGSYNHQ IIPSVAQESTPA
7369	21270	A	7429	378	63	PSFFPPFP*NEFFPPRDLFSPGGFPDF FPPQKGPFPKIPPGFFSPFWEKFFF PPPPLILPPRFFFNPPPPFFFFFFFFFF FFFFFFFFFFFFFDFLGS GC
7370	21271	A	7430	1	109	QTTNLPLIVMSSLLLIILALS LAYE*L QKGLD*AE

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7371	21272	A	7431	358	290	FLLVIPNLFHFLIYIISIVPNVSFFH LIYILSIFFPFIIFILLSSNFILFFF FITSFPFFVFFFFFFFFFFFFFFFFF FFFFSFFFFFFFF*FFFTN
7372	21273	A	7432	1	95	PTRPTRPHNSLQL*TPGLKQSYPRLP SWD*RHMPSPANFRKFF*RWHLCPGW S*TPGLKQSYPRLPSSWD
7373	21274	A	7433	1202	870	HNIFKIRPHCRLTHRGKFFYWGLLVTPV FSPSLRPSFLPSFLPSFLPS*LPSPFLPS FLFLSYSFCPLSFLCLRCIPHSAFFWG NPROVQENCIVITTIYRYSFTALHQL
7374	21275	A	7434	163	1	SVYVKRIGLGRVAYTCNPSTVGGQDG*I T*GQEFETILAKRREPLFLACFLFLI
7375	21276	A	7435	148	362	NDDNSVEFGIRLHKGLGTVAHTYKPSL GGQGGHIA*AQEFMTSLGHMT*SSLYHK LTEYGWRDTASLLMC
7376	21277	A	7436	61	233	GGDLRHWPSDSFFLSLSFFF*KNKGGG LALLPRLDLNSWSQAILPLKPPNALGLQ A
7377	21278	A	7437	44	242	FVCLFLFFFKEKESTFQHDLSLQPPLP RFKRFSCLSLPSTWDYRLAPQCLANF*I F**KSGFTFG
7378	21279	A	7438	119	300	YCVSLLIFFIFIYIFILLIFKFLFITL NYISFLFFYF*H*FYF*KNFIFVFPFGY FPRP
7379	21280	A	7439	1	221	LKLQHHDPPTISLVITRNWKQPKCPNVQ QIVH*SAIKRNELLIHAKTWMNLRGIML SEICQPQKILYLEIPFI
7380	21281	A	7440	35	345	FSFCCVCVCVCVSLPKHAIIEMLNQTHP YVPKGVAYLPEREPFIVPMDPELTA*YE DYRTHESAQEPSEPHQLSRRSLPH*PGH ATRDHSPPTDSWGRRTSH
7381	21282	A	7441	3	384	VIHL*AGAVIIGSRSKSTNALAHFLRQG TPTPVILVLGIIETMNLIIQPVALAERL TDNITAGHLLMHLIVSATLAILTINLTS TLIMFTVLILLTILQIAVALMHAYVFAL LVCLYLHDDAYDHGG
7382	21283	A	7442	15	277	GLAILPRLVPNSWPKVILQVWPPKMLG* QA
7383	21284	A	7443	21	694	NGGLNAHLASASEFDHSGVQLIEREEI CIFYEKINIQEKMKLNGEIEIHLLEEKI QFLKMKIAEKQRQICVTQKLLPAKRSLD ADLAVLQIQFSQCTDRIKDLEKQFVKPD GENRARFLPGKDLTEKEMIQKLDKLELQ LAKKEEKLEKDFIYEQVSRLTDRLCSE TSGCKQDTLLFTKKMNGYSRRIKNATEK MMALCA*LSMKQAPTIELQKEVQGERRP
7384	21285	A	7444	141	428	DRSLLEAGDGRIAGDFFFF*TGTFVAQ AKVQWGIHSSLHP*PPGLKQSSYLNLG SYHHWLRPHALFFFLKNRGSFLCPGWFG TGFRGTFWGAK
7385	21286	A	7445	35	343	GYSIIGCPKFLDEKIFDSGHEKERKINS LLF*KKKKKKKKKKKKKKRGLLKK TSGGPKIKRGGGIKNFPIKGGVKTSGE FFGKKPFFGGEKFWELP
7386	21287	A	7446	403	193	EYIKQGAE*NNQPKLHAHRKRLTWKETP RCIHEGIAPAIMNSDCLVFDTSIAQLFA ENGNLGINVTISM

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7387	21288	A	7447	411	110	LTDSLINIVYR*KMSYIS*TNSA*VYLY IFCIYIYIYIYIRRIYSIYRC*YIYYG PAHIVLVYSSSYILVYVESHKYGYIMGL NILSYIFIYSYFSACS
7388	21289	A	7448	1	380	PTRPQKLKKNCNGVSNGLCFFGGGQFL IWGFFFFFCILIEGGLNSKNYELKSLIK TYGAKKAEIEHTEN*KNRETLLEAAQL AIKVTNPANMLRTVEHDYAMYMHNFWLN KLNNCHKVAISCKQ
7389	21290	A	7449	200	437	VQSNNNKNFKRRRL*PGVVAHTCNPSTL GGQARRIS*AQELTGLNNLMRPNYNYK FINVLDDVHGVTSPPVSQYKKVC
7390	21291	A	7450	405	3	PPRFFGFFFPYPLKFFFPKGFNFEGG FFPIFFPPKKKFFFKNSPGGFFLPPFLG KIFFFLPPFKFGPPRGFF*RAPLFFFFF FFFFFFFFFFFFFFFFFFFFLQRINF ARPGTPLSRVPLRGALPPSA
7391	21292	A	7451	2	348	PRVRPRVRYKLQTKRCDLTLP*GHSHV SLRNTTFDALKS*DTDSLSPKLECHGV NTPNCNLRPLSLSDYPASLSREAWIAST RLRAWEIFVFLAQMRQDYCMNPGGGGCN ELK
7392	21293	A	7452	1	168	LVHDGHAGLKLSTSGDRPA*AYQSAGIT GVRPLGPPTYYYFRTASFMTFICEFATV
7393	21294	A	7453	184	260	SSRGGSLASRSSR*STLLGLPKCWDYRC MPPSLANFFFFNF*I*NFCFW*RRSLGM LPLRLVNS*MQAILPLRIRLQGIHFAQT QTFSL
7394	21295	A	7454	405	64	FFFFFFNF*KKKI*DVFAKIFFKIFFFF SGLKIFWGGGFQNAAPPQKKFFF*KIKSF FELNFFF*KNIFFFVAGVFFLLNFFER GAPLFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFF
7395	21296	A	7455	368	2	SQSFGPRPRWENRLGPEQHIKISRYRPAQ VHACHPSTLGGGRGWIT*QGEFKGSTHL GLPKYWDYMEPLLLVYIQCFFHRTFCN KAAIHCFKPEQLLYNKTSYFKESYKVK ALVACKPTRP
7396	21297	A	7456	2	183	TERDSVSKNKYIYIHTHTHTHTYICVHG VIYVYI*SLLLIYNIAYILYHVFIYLL IFKA
7397	21298	A	7457	281	127	YNFCIFM*RCGFNNVVGQSGLKVLLRGYS PASASQIAGITGVSQCAQPVAYS
7398	21299	A	7458	2	194	TSVRKYF*YPFTITDRYGSTWVATGL HGLHVIIGSTFLTICLIRQLIFHFTSYH HFGSEAAG*YWHFVEPARLFLYVCIY** GSTWVATGLHGLHVIIGSTFLTICLIR QLIFHFTSYHHFGSEAAG
7399	21300	A	7459	22	319	GGSVTGAYHRILDHNRNQIFLA*GGSVT GAYHRILDHNRNQIFLALLISMLGLYF TLLQASKYFECPTICDGIYGSTFFVAT GFHGLHVIIGSTFLTICWIRQLILHFTS RHHFGLEAAA*YWHFVDVV*LFLVSIY **GSVTGAYHRILDHNRNQIFLALLISM LLGLYFTLLQASKYFECPTICDGIYGS TFFVATGFHGLHVIIGSTFLTICWIRQL ILHFTSRHHFGLEAAA
7400	21301	A	7460	1	222	TILLGLYXTLLQA*EYFKATFTTYDGIY

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						GSTFFAATGFHGLHDIIGSAFLTICFIRQLIFHFTSEHHFGFEAAA*YWHFVDAT*LCMVYSIY**GSTFFAATGFHGLHDIIGSAFLTICFIRQLIFHFTSEHHFGFEAAA
7401	21302	A	7461	3	246	LNYSLFFHGEANLGTQTQVLTHPSTTAMYFVHYCQPP*ILYGTINT*PPVVHKNPIK KKKKKKKKKKKKKKKKKKKRGGGF
7402	21303	A	7462	2	155	SRRAALLPLP*ALQTTNLPLIVMSSL LLIILALSLAYE*LQKGLD*AE
7403	21304	A	7463	1	136	PTRPAPSHLLYCKNIKKLFPSGTANEAL I IADI FLRCKKKKFKVK**VLKASEE*N GCKHLHGMH*NSAVCTVFWLKQIMNSD* **KVNTQ*KKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKGGENNK*KNIKKLF PSGTANEAL I IADI FLRCKKKKFKVK
7404	21305	A	7464	166	192	NIN*MWYMHTVECYSDFKRKEILIHATT WMNLEDIMVSEISQSQDKCYCMILHIEY KLYIHM
7405	21306	A	7465	416	55	LFFRLRGYFFLPNIRVFFFLSTLFFFFFF VWGFFFFGRFFFFPPQVECVFFFI*G IFFFFLEK*KNMFFFFFFFFLWGPPPPFFF SGAPLFFFFFFFFFFFFFFFFFFFFFLR KANTKKMF
7406	21307	A	7466	295	84	IWGNVTLQLVSLCFLCFFLH*GFFCCC CCLFLFLFVCLFVCWFLNLKPSIKCLLP FLSLGLCAEIPSSF
7407	21308	A	7467	142	258	PGTVAHTCNPSTAGGQGGRIIP*GHEFKT NLANMVKLHLY
7408	21309	A	7468	3	192	PSEYFESPFTISDGIYGSTFFVATGFHG LHVIIGSTFLTICFIRQLIFHTSKHHF GFEEAA*YWHFVDVV*LFLYVSIY**GS TFFVATGFHGLHVIIGSTFLTICFIRQL IFHTSKHHFGFEAAA
7409	21310	A	7469	2	110	GRVGKHHFGFEAAA*YWHFVDVV*LFLY VSIY**GS
7410	21311	A	7470	380	8	TPQKRKKLKKAGEGVFP PPPKTT PPPP PIFIYFIFFFFFIYFFFFFFFFFQYMSF FYSHIMIQRHFLNF*ESFYSCISILQ*L FKFFSFLGGLIKL
7411	21312	A	7471	1	107	PTRPHHFGFEAAA*YWHFVDVV*LFLYV SIY**GS
7412	21313	A	7472	2	360	VNTLLALLLIMITF*LPQLNGYIEKSTP YECGLDPISPARVPFSIKFLVAITFLLL DLLEIALLLPLP*ALQTTNLPLRAMSSL LVVIILALGLAYE*LQRGLD*AEWLHSL TQPTNNN
7413	21314	A	7473	423	167	VKVHKCFLPGVAPHAFNPSTLGGRGGRI A*AQEFKTSLGNIVRPPSDTCNP IVLGL QA
7414	21315	A	7474	1	73	IKPE*YFLFAYTILRVPNKLGGV
7415	21316	A	7475	131	3	ISWGAEWLTVIPAL*EAESGVSRGQE IETILANTVKPDW
7416	21317	A	7476	2	103	PRVSTGFSSIAHITRDVNYG*IIRYLH ANGAK
7417	21318	A	7477	2	325	NTLLALLLIITF*LPQLIGYIEKSTPY ECGFDPIPARVPFSIKFLVAITFLLL DLLEIALLLPLP*ALQTTNLPLIVMSSL L I I I L A L S L A Y E * L Q K G L T E R D T

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7418	21319	A	7478	423	170	FFSFFFFFFFFFFFFEIDKNVYLIM*CTNPQEKRNLLFCFLVMVSPVCITPHTYICVCVCVIYIYIYIYIYIYIYIPFIFSCCD
7419	21320	A	7479	433	50	RVFFFFFFFFTPEKKTFFPQEIYLFSPFPL*NNFFSPKPLFFLGGFAPNFPKKVFFLKFPFPGFFSPFPKKKFFFPFFFA PPRFFF*GPPSFFFFFFFFFFFFFFFFFLTVKFTTRGFRGFCGQI
7420	21321	A	7480	401	337	FFFFFGKFFFPQEFVFFPPFPKIFFFSLRLFFFWGGFAQFFFPQK*VFFSKFPRWFFFPPLFRKFFFPFG*FLAPQGFFLKGPPPPFFFPFFFPFFFRPI*VGGRVGNNPNPNTNYLPN
7421	21322	A	7481	1	84	KNFLPLTLALLI*HVSIPITISSIPPQT
7422	21323	A	7482	562	412	LFSFHVSGTMAHTCNPSTLTG*GRIT*GLEFKTSLGNTVRSRHYRKKKIA
7423	21324	A	7483	12	233	DIFHFTSKHYFGFEAAA*YWHFVDVRLFLYASIY**GSL
7424	21325	A	7484	385	56	GNEFTPKKFNFFYPFYLSIFFFPKKLKF*EIFIIFPPPKFLFLPNFPVLFFFFLFWEFFFSFLFWFFFPFFFPFFFPFFFPFFFPFF*KTTEFYFVNSNFQHTK
7425	21326	A	7485	424	6	FFFFFSEGSGLIREDPGAGALYDGR*LVVVTG*TLFVGVIYVIEIARGNRLCD
7426	21327	A	7486	16	129	FXXRXRLXKEPSINLE*LYGCPPPYHTFEFPVYIKS
7427	21328	A	7487	183	387	IASGLDIFLLLLLETGSHSVTQAGVQWHNHDSLQPRLTGLK*SSRRSPRGSWDYRVLLCHPGWSAEA
7428	21329	A	7488	351	169	EKKIFFFSRPGYGGPPFFFLKAPPHIFFFFFFFFFFFFFFRGGGDHKNFFFWGELKNFLPLFFFPV*I*IFFFPFFFPFFFPFFLGGGGTIKIFFFPFGF
7429	21330	A	7489	47	212	THASALFL*IRTAYPRFRYDQLIHLL*KNFLPLTLALLI*HVSIPITISSIPPQT
7430	21331	A	7490	98	273	TSGSCSAHILAFKP*AGMATFITKSL*CHTHTHTHTHTHTHTMYIYTHMHTYIF
7431	21332	A	7491	70	405	LYGCPPPYHTFEFPVYI*EAFASKRKVLIVEEPSINLE*LYGCPPPYHTFEFPVYIKSRQKRKESNPPKLVSSQPHGLHDFKCKKKKKKKKKKGGGPLKKPRGGPNLTGGGKKNFPPFRGGKKPPGGFWKKTFLGGLGLGTPPPRRF
7432	21333	A	7492	22	208	RSSLPARPTRAVILIIFMI*EAFASKRLVLIVEEPSINLE*LYGCPPPYHTFEFPVYIKSYV
7433	21334	A	7493	2	204	KLPEVKKKKKKKFYSFRSIVMLLLYLS*SLSFLLYSLLFFLLSFYIYSFLCFPLCKTATTEH
7434	21335	A	7494	2	104	TTLLLSRT*NKLT*LTPLIPSTLLSLGGLPPLTG
7435	21336	A	7495	291	160	PRHF*IFVEMGSHYVAQAGLKLVAASNLLAWASQSAGVTGVSHGSLITSC
7436	21337	A	7496	422	180	LGAPQGVF*KGPPFSPSSSSSYSSSSSSPS*QNIFNKIFLVCFVLETESVTQVGVQWRDLGSLQPLPPGFKRFFTIITH
7437	21338	A	7497	244	296	FFFFFFFFFFFFFFFFFFFFFFFFFFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFFFFFFFFFFFFFFFFFFFFFFFFG GNF*FYK*LLGNRDGVCPLPPSSYL
7438	21339	A	7498	1	410	PTRPDQLIHL*KNFLPLTLALLI*HVS IPITISSIPPYT
7439	21340	A	7499	51	478	PQKYTLIMKICITPPGKGRFPVEMLAGG NENTRCLIEERSYKYHYSLIKGLQQQC IFSSLLYKYNMIYCLMLCYIYIFIFY DMYYRQYSVLYYKLYNYVMLI*YIILYL FMCI*KYIYFIFM*YKYIFIYLYLY*YK YIFYIYLCVYKNIYTLNININILYTY IYININIIY
7440	21341	A	7500	3	110	FTSKHHFGFEAAA*YWHFVDEV*LFLYV SIY**GS
7441	21342	A	7501	168	327	APCYKATVIKTI*Y*YKHRYTEQWSRTK NPDINPYICGQMIIFLQLKSLHKI
7442	21343	A	7502	400	159	NNFSPLRNLCQFFGGLKFFPMGFQAGPPG *GFSSFFLRNFFLDVFRGKY*TFGF*DF FYCPSPNEVLGEPPLMGKNKPGFP
7443	21344	A	7503	401	257	TSQKKKKKKKTPKKKKKNREKPPKKKR GTRGEPFKTGGGKEKKKFKKKKKKGKG PP*PQLVKRGGREKKKNLWKKKGAF*K KKKKKKKNPKKKKKKPGKTPKKKKGDPG GTF
7444	21345	A	7504	44	344	LLASLANLALPPTINLLGELSVLVTTFS *SNITLLLTGLNIVTALYSLYIFTTQ WGLTHHINNIKPSFTRENTLMFIHLSP ILLLSLNPDIITGFSS
7445	21346	A	7505	286	252	I*FAFHVHGQAGLEFLTSDLPASASQSA RITSVSQHAWPVHNIFYSL
7446	21347	A	7506	3	213	RELPLGKRFFLLSLLSSWD*WRMPHSPA TFCIFCRDEVLPCCPAGLLILLVWNLKN CCCYHHHRYYYCY
7447	21348	A	7507	400	20	SLPQKKVSLKLKSAVQLVMF*DRFSLC HPGWRA*GQSGVTTASSLRAR*SSCLTW EYRPSPLPLADFLFW*RRGLPI*PRVVS NS*GQVGLLHQPSKMLKFSSLSPCARPL FFFFNRSTNLRVQS
7448	21349	A	7508	349	227	SDFLTSANPPASASKSFGITGVSHHTRP *PRFLKVNLIYSEMEVYN*ASFRHVD*G GLELLTL*FTHLGLPKLWDYRREPPHPA LTKIFKGKPYIQ
7449	21350	A	7509	371	21	FLVETGFHHVG*AGLEPLASSNLPASAS QTAGITGMSHCAQPNPGLLNKTMMLAVA TEQWVGVMWPSVFGHITARPEGKRLSDC LHSDTNVCVVCVCSGLIFVCFETGCRFA LQPG
7450	21351	A	7510	330	14	DKVCSVTQARVQWHDHGSLLFLSSGLRQ SSHLSLLSSWDHRHMPPGMAFFFYF**R LRSHYVAQAGLKLASSNPPTLTCSAG ITGVSHNTWPKALFSVTDLKH
7451	21352	A	7511	417	33	APPCGGGPPKRIFGSPSRKRGKGPFPKR FF*KNKPPKGGGKKSPPPKNFFPKKN LGPKKKSGFWGRFAPPRAPGGGVFNFP FKAGGEKFFSRGEINPRGAGKKKGFFL GKKNTKKKT*PKKKDL
7452	21353	A	7512	81	296	CLREGASHSAAQAGLHWDHSSSLHP*NP GLRGSSRLNLLSIWDYRCVPPSLANFES CLLKIILGSPFPKKNL

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7453	21354	A	7513	412	279	KKYTQGLGVVAHAYNPSTLGSQGRRTIP* AQFETSLGNTGRPCLH
7454	21355	A	7514	74	126	KI*DWVPKGAPLQGPVF*NSTFRPRVRN RGPPWP RP GPPTVWKG*NKKN*PAPRGSN PPFFFPGNPGPFKLRGWPGSS*GSFQNC KKAQAG*APT*KPGPPPPQNKV
7455	21356	A	7515	332	20	GERQVGSYFFMNTERLFGMTKKF*KWIV SMVAQHSSSISGVWVFRGQELAFPLSPD WQVDYESYTWKRLDPGSEETQTLVREYF SWEGAFQHVKGAFNQGKIFK
7456	21357	A	7516	1	167	RTRGQRFTVLARIVLIS*HCDLPASASQ SAGITGVSHCTRPGLSFLYTPTAKHST
7457	21358	A	7517	2	223	GRMEEMGSHYVA*AGLEFLGASDLPA*A PQRAKILLLLGGHKPGLTILPRLSSNSW PHVKWPRWPLKALGLRG
7458	21359	A	7518	151	476	SLGKFAVSFSFSFLK*RRALAVLPR LCS NSWP*AVLLPWLP RVGIAGMSYHTQPDY HFQARAVAEILGLVSTQHSSVTGLPVEN SFRAGHGGPRLQSQHFGRLRWADC
7459	21360	A	7519	3	134	CSFRLGAVAHCNVITLGGRRGRIA*AQ EFETCLDNIA RPCLY
7460	21361	A	7520	14	219	APSIHGFGFLYTYIHTHTHTHVYMI*V YIHTHIESIKCOPLTQLQSNKKANRIVF RTQFMLTCYFMR
7461	21362	A	7521	134	334	RKHSC*IFFNFCFYLSLETRSHYVASTG LDLLASSNPALASQRARITGMSHAPP VLT RFKKS LF
7462	21363	A	7522	406	145	FLKTGFSPFGPFVF*TPPPGFPPPPPPP IFGVPGGGPFAPPLFFFFPQTKHFPFPL NPSPPPQRGFFRGFFLPFAFFLKTPP FFF
7463	21364	A	7523	3	382	HPQEGGRLTSLE*NTSLRLKKKKKKKK KRGGPFKKNPWGAQI*PGKKKNFFLKR GAKKNHLGNFGKKPYFWGGKKLAKPPKK N*TFKGGKKFLRGKGKKT PKPWLLKIF FSGFYLLKIFPPGP
7464	21365	A	7524	319	106	GTRSCSVT*AGVQWHDHSSLQP*TPWLK RSSWLRNRWDYKHEPPCLNNFYFFCRDG GLLCHPGWSQSP ELK
7465	21366	A	7525	433	228	MQPYNWEVNSSS QLSLSARQRVTHVLT GNFFIK*ERWDLPLVLPRLVSKSWPQVIF PPWPSKVLKLQV
7466	21367	A	7526	26	351	CRSLVFSLPKPGLRFVSILHIQVFSHFD FFFLTGNTOK*RK*TPFIFPA*LFKTPA PKPGMVAHTCSPSYSGGLDGR IA*AQEF RTSLGNKTNP SLEGGRRKKKKPSGS
7467	21368	A	7527	438	62	QLSKIHRPPAGGRFFKSGGGFKFPCVVG LPPFGKKANQPTPKNP PPKQKPSGGGLS PMGKPP*FPCSMPSDSPGSVSFSRGVA PAPKDYCP IV*AALIPSKKKKKSKPG*V KKGKPNLYSIYNK
7468	21369	A	7528	3	132	FYYL*RRGFVLPRLVLNSWLQVILLPW PPKVLN*AAHHPHG
7469	21370	A	7529	2	628	FFFLPGVVNRVLLMGRGLGEANSREGRG PSQPRGMHGQLEVRGGRSQGDGWHGTLS PPWGR IYRGAPPTFAAPQAPKPFRLLP M*LPGRPSSCLLPETPALSPLPSAEWGG FKLLTGTSETPGPSGSPSVGSANAQAAG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ATTIVARGHTPCTRGPLDTHAHSRLRWH AHTRPPPRPLAHEHGTHHAHPHTPGAW VGEQPFQGWGRA
7470	21371	A	7530	63	205	GRPTRPRTRGVKIL*QFEHTKPTPGLPT LIALTTLLLPISPFIIL
7471	21372	A	7531	390	56	KTFFFFNLIAFTEAKSVLLFLLFFETG SRSSAQPGVQWHHQSLLQPQL*LGSS CLSLLSN*DYRCAPPCQ*SPCLSLKWC DYKREPPHPAKESHMQQSYLIYSLYIA
7472	21373	A	7532	543	335	LAAYGGTCLQS*LFSRLRWEDHLSPGVQ GCNELQLQHCPAWATE*DPVFKEGKKE RVLVKVFS
7473	21374	A	7533	3	145	WCDHGSLEPRSPGLKQSSCLSLPSNWDH SSEPLHTTSMWNF*IFKFLNLK
7474	21375	A	7534	386	106	SWVTDEITMEI*ECVLNDSNTPYQNLW DTEKVVLRKFTALNACMKKSERAIQRH TCVHTHTHTHTHTHTGSKCLLRKYLTLT IQQNIRIN
7475	21376	A	7535	398	2	SLQPLPPRVKCFSSPSPRRWDYRGAPP RGGKFFFGKKEFPVQGQGF*FLPPGV LAPPPQKGRISGGSPRRPFFFFFKIR ISYPILAKQLKLCFLKKKKKSIQAIKLY HHQKNPITKSSVFWESQRA
7476	21377	A	7536	2	344	HSKCVPAEVTMAYYIRYLSISSLLHIL ENIVHFFHFHLY*GPNLFFFYFAGTRL IQRSWK*PMII*VHVQIKREGQIFNK* IFCMIGRGG*ITCGQEFETSLVNMVKPC LY
7477	21378	A	7537	116	224	LHTHTHTHTHTHTHTHTQFNKLP*LFIP CGHIPRRY
7478	21379	A	7538	1	383	WHERTHSRITILFQGLETLPLIATF**L LASLANLVLPPTINLLGELFVLVTTF* SNITLLLTGLNLTALYSLYIFTTQ* GSLTHHINNIKPLFTRENTLMFIHLSPI LLLSLNPDIITGFSS
7479	21380	A	7539	31	332	DNYLSSYSSSGSWMRELILASQIRWEP IVDRTPSHHRTHTHTHTHTHTHTHTV LFRIGPWTHAREPRGHICGN*IRNQSP* KNPRTRGKNLRTPHGW
7480	21381	A	7540	199	15	NNVQIK*QFEHTKPTPFLPTLIALTTLL LPISPFIIL
7481	21382	A	7541	337	157	AEIVPLNSSLGNRVRLH*MESYSVAQAG VQWHDLSVQPLPPGFKRFSCFSLSSW DSRLYFRCHD
7482	21383	A	7542	28	313	RARIGSDQCLSAGTQVVENKSQISGDFM WNDFRS*SVTRVGVRWRNHGSL*PWIPG LR*SSGFLPNCWDYDRNEVWGGKKEV TCPTVNLQKSQ
7483	21384	A	7543	493	180	GGFRGSWLVRDGGQGVGFCSLPPPSR VKQFFCLRFPRRWGGREGSPRPSYFFFP *EKPRFFFLGRVVLNFLGQGVGPWPSPQ RVGFPGLTGPGRASFFFNLI
7484	21385	A	7544	403	426	FF*KFFITFHTLFFFTFFFTFFFTFFFT FFFTFFFTLAPPPGGGFFFSFFYQKIFL KFPQGPEKFALPFGGGFF*GKFPQFFF CFLVFFFTFFFLFLENGVSLYCPGRSRT GLKLSRLLASLRAGITGVSH
7485	21386	A	7545	3	335	RHYSDYPDGYST*NILSSDSLISLTAA

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						LLMVFMI*EAFAYRRTGLIA*EPSMNL *LYGCPPPYHTFEPPGYIKSRLKRKESN PPKLVSSQPHGLHDFFKKKKNRGGPF
7486	21387	A	7546	424	140	RRVKFVGGGAPQGGPPPKRGVLPKIPREK VFPPPPG*NGPPGPAFKTPPKKKNISS PPPGNWAPPGLLKGPPIFFFFFFF FFFFFFLNPLK
7487	21388	A	7547	2	348	FCHVAQSGKLKLASSDPPTLASQSARIT GMSHHGGLK*GEFLGPSSNKGALLWEA TWLQSFMSASLFLVKRPPTFVFVFAFV GYRDIYFTASSLIKVIQEGLYTKMCA LTL
7488	21389	A	7548	2	90	RKQAYTHNTHTHTHTHTHT*KKTGIIHAH KHTHTHTHTHTLKAQKQIRGGK
7489	21390	A	7549	256	405	CELYSGKEMELVFGLFIETGVTRLET FYKKECSSFFHSQSRGHLQPSILNEWHI RNPLGLTHFLL*KTGVAEYKNSLNVVH HPFFLSYAVSFLLQGWSEFAMLSKLGSNS *VQARCLPQSPKVLGLKESPOERTVNVS SIRGKKWSWYLDYLFSSQGLQGLKLFIRK SVHSSIPRAEGINCNHQY
7490	21391	A	7550	2	362	ILIMNTLLALLLIITTF*LPQLNGYVEK STPYECGFDPISPARVPLCIKFFLA AITFLLYELEIALLLPLP*ALQTTNPL LIGMSSLLLIILALSLAYE*LQKGLD* AELKEQKTLC
7491	21392	A	7551	1	317	TFDNSALLFFWDGGEIEFHSVSQAGVQ WHNLCSL*PQPPGFKQKLILPQIVKENV SKISSQLFSRVNINISPSQCITPESL QLARIGIFYAAKIHLTKGLRG
7492	21393	A	7552	479	183	YLFHVHTTASHSNGACTGPTVGDII VSSL*SMTEQVTMPLASAVSDGTVP SVRTASRGSEQAESMVSSHEIILEHAGEL VIASPEGQLEVQTVIV
7493	21394	A	7553	454	105	KPPWGNKIRPPLFPGRKVPVPRF*NP VRGSPPKK*FVFPVGRVLGTGVTPLSP PFLKTTPLLLDWPLSQPPGGVKPENSL YPGKKRFR*PKFPPCPPANGTKRKPPL QKKKKQVL
7494	21395	A	7554	439	1	LLKRCVRKDSPPPPQNKIFFFILKKFV FFFAPY*VRKFYFLTAHFGKRPPQIYI FGPPVFLIFCFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFNKQVFI ERLLCARHCFRPPPEEKTKNKIEANPN SEGEER
7495	21396	A	7555	323	82	FFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFR*AYL VRSPLLFLFVFSYF*LI*HVIHRYSVYI ELDVLLTGSKIILI
7496	21397	A	7556	194	412	KMYRTSLGHLVEAKKKKKKKKKKKKK KKKKKKKKKKKKKDSRGGVV*KKFGG GHNTRGVKIIFFFSLG
7497	21398	A	7557	414	219	KGFKKLFPVPV*FFLCPPPIFLKGFP* GRKPPPKNPQGGPPFFFTTPPLFFF FFFFFFF
7498	21399	A	7558	377	25	THVGGVFWGKFFFSRRVFFFFHYHLIQIL SPPPKRPPPKGTPEG*IFPLFKEINFF FF*DDFFAPPPFFFFFLFFFFFFFFF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PPPGYFVFLVNGVFPVGPFGFELSPSPS *VAPPASQKGGVSGVSPCPRVWVPFFKK KKKLRGVEQRCCTMHLLVYSKNVPVKPQK KSSIGSL
7514	21415	A	7574	2	383	PRVRSTAFSSIAHITRDVNYG*IIRYLH ANGAKKKKKKKKKKKKKRGGALKKKPG GGQKKGGGEEKKNFFFKGGEEKKKPGGIFE KKTFFGGGNGAHPPQKKKTPGGKKKIL RGKGGKKPLYPWGEK
7515	21416	A	7575	402	69	KIFFKNSPLWKISHPPTYRGFFPPFPF* NFFFLPGPYFFLGGCSHLGPPPKKGGFFQ KIPPGFLFLSPFFKKKIYLFPPRIFLAPP GVFLKAPPPFFFFFFFFFFFFFFFFFFFF
7516	21417	A	7576	1	119	LIFHFTSKHHFGFEAAA*YWHFVN*V*L FLYVSIY**GS
7517	21418	A	7577	219	69	NDISANTAKKFWKLPKCPTTEGWLNT* LYIHLVEYYATLKVCGLDYVR
7518	21419	A	7578	3	287	HASAQNLNGYIEKSTPYERGFDPISPARV PFFIKFLVAITFLLLEIALLLPLP* ALQTTNPLIVMPSLLLSIILALRLAYE *LQKGLE*AE
7519	21420	A	7579	10	125	ALQTTNPLIVMMSLLLIITLT*ALQTT NLPLVMSLLLIITLTILAYEGLQKGLN*AE
7520	21421	A	7580	3	299	DAVVRLLDFDF*VELPTEARIRIITTSQ DVLHS*ADPTLGLKTDAPGRNLNQTFTT ATRPGVYQGQCEICGANHSFMPIALLEL VELKIFEIGPVFTL
7521	21422	A	7581	3	116	AFASKRTGLGVEEPSLTLE*LGGGPPP* HTLEEPVNI
7522	21423	A	7582	398	2	RVFPAPKNSLQIFPPLFFFWGSPWKFFF TFPPHFVFWGNFKFNPFPAFLERLFPF GEKIPLVFFFFFFD*NFVENFFFLSLL FFFGFFFFNM*S*LF*SPANFNV*VTH LFI FMVFFHDPFWSFGPILW
7523	21424	A	7583	288	9	RGSKNLEKNSFPYKVNHNHNGSPLFPHL FFSPRGVGPFFFFFFETRSRSVIQAGVQW HDLSSPPGLK*SSHLSIQSSWDY*RAPP HPANFVYF
7524	21425	A	7584	1	124	RDGGFTMLPRPILLTGLKQSSCISLPK* WDYRCEPLHLASC
7525	21426	A	7585	339	76	THPGHNGISVSPKKKKIPRGGGPPPLFP PLPRVGGGDSL*PRKGGFN*TKPAPFPS SWGKKKELPFSKKKKKKRKKGSISTPFS SRIE
7526	21427	A	7586	205	87	SISLSLSLSHTHTHTHTHTLTHSHPRCV PQPIGLPISKWAKVKELIT*R
7527	21428	A	7587	353	256	PHPSVTTLVTSQQYQDPPPAKRL*LAEG SDDC
7528	21429	A	7588	159	195	QICRHRVVHINFLMSMGSIMITPPSFLF LNFL*SYVAQAGLKHLSQSDPPASASQS AEIRGMSHNAWPHF*YFVELVHFYINK FVGIELFILTS
7529	21430	A	7589	76	205	RKKPEPEKTCFDNITGNTYPCLSYEH SD*YVVRNT*LCAER
7530	21431	A	7590	218	20	LSLYLASHLWLPKPPHLEWAPSKSSLRL GTVASPCNPSTLGGRGWVT*GQSESETS LANMAKPCFY

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7531	21432	A	7591	142	12	QIDYYYLFT*RKGLTLMRLVSNWLH IILLPWPPKVLGLQM
7532	21433	A	7592	2	224	QIIEALLITILLGHYFTLLQA*EYSKAP FTISDGIYGSTFFVTTGFHGLHGIIGST FLTICYNPQLIFHFTSEHKFGLQAAP*Y WLFVDVARLFVPASIY**GSLFYPTSL RVLQGSLLHHFRRDLRLNIFCNHRLPRT RHYWLNVPHYLLQPPTNISLYLRT
7533	21434	A	7593	1	323	HAYGNTLVA*LVVTMTF*LPLVDGYIKK FTPYEGGFEPKSAARVLFSEIKVFLVAIT FLLSDLQSALLPLP*AVQTTNPLIVM AALLLDIILALSLAYA*LLKGLE
7534	21435	A	7594	1	104	RACVCVCVCVCVCLCLLMKMCVCVCVCV CVFCAC*KMCVCVCVCVCVCVCVC
7535	21436	A	7595	383	43	VFISETLCEHVAWSQTTIESLGLGTVAH TLNASTLRG*GRMIA*GQ*SKTRRGND SISHSQTIASPHLLGRHQPKWCMCVQ AAEAVLKQGQVETDASFQIQKIPINSLIN L
7536	21437	A	7596	2	331	WPPTGITPLNPLEGPLENTGGLLA*GVS MT*AHHSLGENNRNQVIALVITILLGL YFTLLRASEYFESPFTISDGVDRSTFFV TTGFHGLHVIIGSTLLSIWFIRQLICNF TSKHHFGFKAVA*YWLNFTKYLVPPTN M
7537	21438	A	7597	384	23	LFKTKQYRFLPPFPPLKIFFFPLKA*IF LGGFSHYFPPPKKGFPPKSPWF*IPPP YRKKHFCSTPKNLAPRWF*KRPPHFF IFFF**RWGLAMLPRLFSNS*AQAVLLL QSPEVLGL
7538	21439	A	7598	401	189	RVLPFCFAGWS*TPGLKCTCLGL*KCWD YRREPPCLIRFYLFVYFLRQGLAMLPSL VLNSWP*VILLP*SP
7539	21440	A	7599	81	368	KCVIYPFLSITLGKAKYDFFFFLEKELA FFPQGEHQGNL*G*LPPLR*RDPSCL ALPRGGNGRGAPPSPTNFGFLGGNGVYP SGPGGFETPDLK
7540	21441	A	7600	264	25	AVEHPQLRLFCSHY*NNIVEERLGLAR TCNCPLEDKAAWIT*RHEFETSLANMV IFCLDIGSKSFLSMRFSRCLLWKL
7541	21442	A	7601	1	196	WEPVLGETNVNSFNQKYINWPGAVAHT YNAGTLGGQGGWIT*GQLEITLSKKVK PSTYFTNTR
7542	21443	A	7602	315	82	TCTQVFIALFITAKKFKLICPLTDNWIS RVWYVHTMKHISAIKRKAVIHATMWVKL ENIILSEIKQSQKATGCMISFI
7543	21444	A	7603	334	118	PKIKTEGGPPPKKNAGGMYK*KKFILVL AAPHPFPFVFSVFSYFSWFFRFFFFF FFFFFFFFFFFFFLR
7544	21445	A	7604	3	288	DAYTT*NILSSVGSFISLTAVILIFMI *EASSSSSSPPGGLRPRAFPVRPPGAGL VF*VSVPDLQCSLAGLQVLRFMELAR LAPHIRWIIQ
7545	21446	A	7605	354	33	EGRARYTRVPQRPRFHLGLGIFAPQLGK KKKFSFSSKKKKKNQLWLGAVSHANNLS TKGG*GRGRSFT*A*EFRTSQKLGTGKN MVKPISTNTFKNERGGAELSOL
7546	21447	A	7606	401	161	YLVSHLLQIILPPALFVVIFFF*DRVLL

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						CGPGWSAVVWSYCSLCLGSSNSPPCQSL PSSWDYRHLWRFLMPRGILCVYV
7547	21448	A	7607	354	50	SGAQDPAGQHGTTPFSQKVPKKVYPAWW CMVVPATQEA*LKKSLEPWRRRFLRLREA FFVYLGWVLSNGEPPPLGGGGSVFLEAL EKSVGFSSLGFGWVFFF
7548	21449	A	7608	370	115	TIKNICNSWEVKIPRFTGVWKKLIPATL MDDLEGFKTLVEEPTEDVV*ITGELEVE PENVIEFLQSHDQTSTDEGLLLMDEQRR W
7549	21450	A	7609	120	358	TTAVYLGHYCQSP*ILNGTVNT*PPVVH KDPILFLTPFPFCFHASSAMNQLSHISC NSKATPHPLGYQQTYPPLTVHMT
7550	21451	A	7610	3	164	HE*ASIP*NTHTHTHTHTHTHTHTFYK EENLSHLWNISCIFLGAHKGKKMMN
7551	21452	A	7611	85	324	FRFFAFFFF*KKISFCQAGGQGGLPS LDPPPPGLKKFSGLTPPRSWN*GPCPPP GLIGVFLKKRGFPLVGREPNLWT
7552	21453	A	7612	268	317	FLENCNPGGGGCSQPKLGPCPPAWGAK *ASLSKKKKNNKN*LSYKAPSYGYKKG
7553	21454	A	7613	101	339	AVPLTMVKIHALWKRVRFRHNSKL*LP CDPAISLVSMYPKEMKSVCLKDVCSPRL ITGPLTIAGMWNPPNRSMDYSG
7554	21455	A	7614	366	208	LELLTSGDLPASASQSAGITGISHRRAP GTLFF*AVNGGGNQVFLFLRVNLGL
7555	21456	A	7615	30	328	NYCLDFHGETELGTTHFLTHPSTRAMVF EPYCQAL*IL*GVINT*PTVLHRNRSHI KAACLCLQARTVVNLQISHINWKY*TPP HPL*YQQTPALEYI
7556	21457	A	7616	39	159	TPGLKQFFHLGLPRCWDRHEPPRCPN MYLI*ISF*CV
7557	21458	A	7617	290	91	KMSFLIFFRDMASLCCPGWT*TPGLKQS SCFHLPRSWDHRCTSLHLAVKTFLYYFL KMFYQNVWH
7558	21459	A	7618	37	246	TQQLVYIYRYIDTHTHTHTHTHTHTHS HTHYWIYTWKHTLKGPKLF*EKTMGST PIISWKERLSLYRS
7559	21460	A	7619	23	190	IPPQPCPFLLSLFC*IDMSCNMCAVC VCVCVYVCVICDMVLLPFCCKLECSK
7560	21461	A	7620	367	2	FFSPKALIFLGGGGPIFPKKSKFFSKI PPGGFFPLPGFLKPPPPPLF*NPPLKKK NFFFFPPENWAPPRVFFKGPPPPFFFFF FFFFFFFWSSRFILFPQFFFLNNKIGKK KIFRHLGAG
7561	21462	A	7621	6	25	SVILQSTIIIFIATTNLLGLLPHSLTPPT QLSINLAMAIP*AGAEIIGFRSKIKNAL LAHFLPQGTPTPLIPILVVIETISLLIQ PIALAERLTANITAGHLLMHLIGSTTLA ISTI*LLYNNP
7562	21463	A	7622	383	67	AFLNPGKKPFPFGFKRFFCPPPCKWGWK NRGPPPRGKIFFFVFVKTKFFHVGPFG F*ILTSGDPPGQGGGLGGFFFFQIGGT GDLNLSHKSPMPFTINTHNG
7563	21464	A	7623	372	35	TGGFWGVFFFFFFFKQGFPPKSTGGLGP KNPCPKGPRVSPPPPPF*NRGPQGPPPP PGKKPFFFFFFFIETGFPHVALAGLEL PGSGNLPTSVSQSAGIPGISTWPNGVFQ
7564	21465	A	7624	287	6	LSGVEWVDHMINICLFFKKLPCCV*KWL

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						YQPVAVAHACNPSTLGGDRWIPGGQEF KTTCLSLPKRWHRREPLYLAFCPFYNG IGCLLIIGF
7565	21466	A	7625	271	277	NRGKGKGTGSLGILEKNPFFGGGPFWANP PP*GLKFWGVGPKRPPPKRVFFQNSQ GTSFPLPPVLKSGPGLVLKAPQKEKNI TFQPPGKFGPPRGSLKRAPPFFFFFFFS LRKSSVIEK
7566	21467	A	7626	2	269	LLGELSVLVC*FPPKHTTFLTGLSLILF TGLYSLYILTTFQWGSLSLTHIINLKPLF TPKNTLMFIHLYPILLLSLNPDIKKKK KGGAF
7567	21468	A	7627	397	164	FPPPKKVFFQKNPKKKFSPPRVF*TPPP PFFFLPPPKKKKFFFSPP*IWPPPGIF *KPPPLFFFFFFFFFFFFFFF
7568	21469	A	7628	3	324	DGMNVSTLYGATGSHGLHIDMSALLTI WYIRQLILHFTSKHHFGFEAAA*YWHFV DVD*LFLCGSIY**GSPGGPKFSRGKG IAPHWGDD
7569	21470	A	7629	2	246	SGLGTTLS*KNISVLLTGLKILVTGLYS VYIFTATQWGSLSLTHINKIKP*LTRENT LMFIHLCPILLLSLNPDISYPGFTS
7570	21471	A	7630	112	290	LISGKGQWTQMRPLPVLVTLFTDSFSK*K NPSTLGEQCGRIT*GQELTSLGNIVRP HLY
7571	21472	A	7631	248	2	KVPASGKRPEPHWYPYHAVPGCGRIPAT AIWTQKWYQGFPPALSPRLCSGAISAH CYFGFPGPSDSPAAPS*LAGTTGTRP
7572	21473	A	7632	383	106	GWGQCFKPATPALERPNOECFRPGVLN QP*PQNKSPFFFFFFFFKKKYIYICMVV HAYNPSYSG*GGRIT*AQFKTSLNNT VRPHLYKK
7573	21474	A	7633	435	133	YACLGLPKCWDSDRHEPPGLANFCIFSKN RGFPISDRVINSWPRVFG*PKPPKMG FQTLVQGASLGFLILFKTGFPFFSQHE EQGWDTSFQHRFFRGK
7574	21475	A	7634	1	209	NAYRIVILCQKLFPLLSGKMNFKKTRCW LGMVAHACSPSTLGG*GGRIA*AQEFGT SLGSILRPCHCKK
7575	21476	A	7635	117	495	STSFIDKVQLRHSFLFFSLFFETKSCSL TQTGVQWHDGSL*PPPPRFK*FSLGLP LSSWDYRHAPRPASFFVFLVEMRFHHV GQAGLELLTSGDPPASASQSAGITGMSH HALAHLVFSSGKS
7576	21477	A	7636	1	241	LPGSSDSPTSASQVAGITGMCHHAQLFF FLAF*LIFNF*FFFGNSFFVFPQAGGHW GIGG*LNPPPPGLKRFSCLTWGG
7577	21478	A	7637	3	93	EAEAGESLEPGDRGCSKLRSCHYTPAWQ QSVTLVSKKETKNTKTSEVPFGVLNLLY KVSINILIFKEIFYQAPLILV*DNPDS TLSSALQPGQQSKTVSNKTKQKTVS*PG NRV
7578	21479	A	7638	46	228	GTPHIQPSKSVFNNVHGPGTVAHTRNPN TLEY*GGSIT*GHEFETSLGNIVRLPPP SLQSI
7579	21480	A	7639	1212	1023	KNHSNEWIKKM*YICTMEY*AIRRNEIM AFAAT*MKLETIILSEVTQEWKTKYCMF SLVSGS

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7580	21481	A	7640	479	318	AEFLNLGDGGCSEPR*HHCTPAWATRAK FHLKRKKK
7581	21482	A	7641	470	172	RNIRPRENQYPVFMVAFFLIANKW*QPK CPSSEAMNKLRCIHTTAVLHSSEEEQP TDTNNSDLRSIAPSWRSQTRAAHRMI PWHSGKGKTPSTENA
7582	21483	A	7642	2	201	AGAPPPAWLPCCRLISDC*ASNQRDSVG VGPSEPYATVRKYLELLLCQMHHDMCTY RFSIRIVLNL
7583	21484	A	7643	521	385	GGSPLETH*YTSQGGGIPYTDLTGHHPS OGRIQEAPKLTHL
7584	21485	A	7644	331	3	DLVPPKGGGGKKTTPRIKKFPPKGEDFF FFTPHYFVVVFFVFWGGAFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFT*DYIIS F*EERFNKFYRCQSTLVQIGHTSNL
7585	21486	A	7645	88	367	HCSFLLLGKKKKKKKKKKKKKKKKKK KKKKTKKNEYKNLLGGAPP*KPPSGALY KYRRENFIPFSFERVSKYPPRDLCKKNL FWGGLNIPS
7586	21487	A	7646	378	37	FFFPXFFFFFFSPPPXFFFLXFFFXPFF XSFFSLPPLPLXXPPPPPLFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFNI*TI VL
7587	21488	A	7647	34	293	TGIPGVISAIFMI*EAFVSKRKVLIGKK PSINLE*LYGCPPPYHTFEFPVYIKSTQ KRKESNPPKLGSSQPHGLHDFFEKKKI IK
7588	21489	A	7648	22	106	KNFLPLTLTL*KNFLPLTLTLI*YGS IPITISSIPPQT
7589	21490	A	7649	1	231	PDRTISKDISK*MVLVSKKKKKKQKKK KKKKKKKKKKKGGGPFKKTGGGAPKNP GEEKIIFFLGGGKKNWGGFF
7590	21491	A	7650	79	286	VVSRLVSLRNPCI IKTCS*AKKKKKK KKKKKKKKKKKWGAFLKIPWGGPIFPG GGKFFFFFFGGGY
7591	21492	A	7651	57	375	SGKSEFHRVPQWPGTGADACNPSTLGGR GRWIT*QGEFETSPQGDPISTKKKKKKR GALLKDSLGGPNLPGFNLKVFSFRGGI LKPTWEFWEFTFILGGEKIGPN
7592	21493	A	7652	3	357	LAFLALSKITHASIPVSSPSKSPRS KGTKKKKKKKKKKKRGGLKKTLLGGPK INGKKKKIIFFFKGGEKTPGGILEKKL FLGGGKMGNPPKKIKPLGEKKNF*GEK GEKKP
7593	21494	A	7653	113	378	MQAFNLGPFLMGGGNPSGPNHGWVLA GSYLGPGLTPPKKSQKGGPPDL*GRGG QCSPGTKPGGGGEKTGLAPPFTKSLGFL LQKK
7594	21495	A	7654	341	147	NFFFSCLKPFIFFGGFCPIFPPPKSFFS KIPPVVFSPPF*EKIFFPPPLNFAPP RVFFKGPP
7595	21496	A	7655	395	3	FFFFFFFFFFFFFRGKSE*FVLFPVSPAP SLRG
7596	21497	A	7656	2	162	ESKGYTHTHTHTHIYTHIYTHYTPREH *PKKADVAMLILNKLFFKPRCVALL
7597	21498	A	7657	333	28	LEFFNFNFFSYFLFFS*RVWGPERRPPP LKKAV*KFFLFDIFLFFFFFFIFGLGFFF

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						FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFLEHIRLLMFVTFSSHR
7598	21499	A	7658	1	137	HSSIGDRVRPCLKKKKKKKKKKKKKKK KKKKKKKKKKKKGGGLF*EKKKKKKKKK KKKKKKKKKKKKGGGLF
7599	21500	A	7659	236	32	IIFLIKFLYF*FIFI*F*FFLTFFYPKR LKILFFFFFFFFFFFFFFFFFFFF*KNFIK NIIYFFIFYLFYLLKFFIYIKTFLFLKI
7600	21501	A	7660	301	65	KAPPKIFWFFFFVFFVFSFYIFFFFF FLFFFFFFFFFFFFFFFFFFFFFWKS LAAT*FLRGFETF*LAYILKTT
7601	21502	A	7661	70	273	KHSPPHKPSD*NTELTIKKKKKKKKKK KKKKKKKKKKKKKKGGGALIKNPWG GPIHRGGEKFFFSFLRRD
7602	21503	A	7662	1	353	ILIIINTLLALLIIITFGLPQLSGCLQK STPYEGGSDPISPARGRFSKGLPLQAMT FLL*ELEIALL*PLP*ALQTTNLPLIDM GCLLLNIIILCLSLAYE*LP*GLDCSRYH SQRIQ
7603	21504	A	7663	1	131	FIRQLIFHFTSKHHFGFEAAA*YWHFVD VA*LFLYVSIY**GS
7604	21505	A	7664	2	192	PLSQSLY*LLAADLLILT*IGGQPVSY FTIIGQVASVLYFTTILILIPTISLIEN KILKWAY
7605	21506	A	7665	356	2	TFFFLSSPGSGSGSP*PARPKKNPPWG GGLPLFSRRGALFPKNFFWGGYPFFFLF *KKPPFFPPGPQSPVTSKDVVPLRM PPPRPHVRPLGLPKKSFSSPRWEKQVKK TKKRAA
7606	21507	A	7666	312	2	GFFFFFFFFFFFFL*DRVLLLLPRLECNG VISAH
7607	21508	A	7667	1	233	FWLSSNAEFDSANSCECLEVQRMQDQD SFPTYHYFDMYVCIYV**RSLAVSPGLV SNSWPQAILQPQPQSLGLQE
7608	21509	A	7668	174	295	IFFLPFCGEHSLAVLPRVLNWSQTAIL PPLPP*ILGLQA
7609	21510	A	7669	183	330	NKFKLYWSPVAMAHACNPRTHRGWIT* CEEFETTLANMVNMVVKPLY
7610	21511	A	7670	3	319	TSNTLLALLIIITF*LPQLNGYIEKST PYESGFDPISPARVPFYIKFFLVAITFL LFDLEIALLLPLP*AVQTTNLPLIVMSS LLLIIILPLALAYE*LQKGLD
7611	21512	A	7671	1	313	ARGERERERERERERERERESGGGGP TQTDCKGGRNT*RGREIYRESE*DDRPP FLPTYRVNLQRPVGLRRLKGAGDKTFCL ILTLDYVWPDYRMKRAHDM
7612	21513	A	7672	3	91	TRRERERDR*REREREREREIIFREKNSQ S
7613	21514	A	7673	1	115	DELANLFII*KAGFPVLPRVLNWSLQV ILLPWPRLN
7614	21515	A	7674	3	232	TRRERERERERERERERERERERE RYRE*DRERERERERDCVWGGVISLSR AVALSGAPAVGRQTRERISR
7615	21516	A	7675	1	234	ARGERERERERERERERERERERE REIERERERLTQRERERERGRGVHAPL AIERG*KPQGGFWWKEERVKKEPLGKLL
7616	21517	A	7676	1	262	ARGERERERERERERERERERERE RERERERERERERARAPQNL*ERWAH

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						TPPAPGVSLSWREHTRGGPPWGKKEGGW GRLGHPPPSILRAKGG
7617	21518	A	7677	214	2	QQASVAQAGVKWPDLCSLQSMPPRFK*F SCLSLSSWDYGPPPPCAGLHIWRRNVT LALQGLPTTSLALV
7618	21519	A	7678	3	341	HERHELEELIKTLFFFFFRKKNHLCKP GGKKRGPIWFLKKFFSPQKKPPPPPPF LRBIGAMAPQPGGGLLI*NKTPFRPRGQ GGPKPPTPGKPNPPPPKGNFPL*GNP QPPGSPTPPPPQKVIFPFEHQA
7619	21520	A	7679	1	357	GTRINTLLALLLIITTF*LPQLTGYIKK STPYECGFDPISPARVPSIKFFLVAIT FLLLDLEIALLLPLP*ALQTTNLPIDM SSLLLIILTLSLAYE*LQKGLD*TDFY SVGGEAN
7620	21521	A	7680	365	1	PDASQ*HCTNGQSNRLNLLIKALLTTA KIWIQPKCPPVDARIKKMQ*IPRMEHPS AIKKEILPSVATWMSLEDTPVSRISQAQ KDKYHTVSCMWNLRMLNAEPEGRPVPR GVQGWGAARA
7621	21522	A	7681	387	3	FFFKKEFCPRKKAKK*NWGPNGLGRG* KNFPPPPQKRGKKGGPPQGGEILGFL* KKGFPMPGRGSKLWPLGFSPLNPPKRG GKKGEPPPPQRGKPGGPPPKGLFFFFF FFLRQSLTLSPRLLV
7622	21523	A	7682	107	290	ELNKRWGLGAVAHACNPST*ELNKRWG LGAVAHACNPSTLGG*GRWIT*ALEFKI NLDNKRSHLKIKKQHQQQKNSGLDA
7623	21524	A	7683	1	348	GTRERKPTWLWYHRERGMERDCSCVPGS SGISESRVWVQVGMEVYPAIIYLCLEPK YLVISEFSPAFAFIWFLGSLVVAHTCNPS NLGGQGGRIT*SQEFKTNLANIVRPHLF FFLF
7624	21525	A	7684	364	77	GGPSIFPRLLALLGGGGPGGPPLPRGNFS FFNFFVKKGVFFPPGVFPLPPGVLPFP PPFWAPG*PRPPNFFLGAPGFFPFFFLG GGFFPVAPGGV
7625	21526	A	7685	3	24	HEETIIQVKREPVE*KKIFANPTFNKGL TSEIYKKQLNRKKPNPI*KQSSK
7626	21527	A	7686	1	125	GTRPGMPGTYSNYPDTYTA*KIISIGS FISKTAQPGPWE
7627	21528	A	7687	459	298	LSLPSSWNHMCALPHPASFFL*RQGLAL LPRLVSKSWAQVMLLPWPSKVLGLQV
7628	21529	A	7688	374	248	FPHHNVEVIVRPLSPRYPIISHVTCTY RSRWP*ASEGSQKK
7629	21530	A	7689	284	163	GTVAHTCNLSTLRGRGWIT*GQEBIDS PAWPPKVLGLQA
7630	21531	A	7690	83	255	KVDYVSIKSEFF*DRVSLYHPS*GTVAR S*LTTTPNPGIKQSTCTVPSSWDYRHV LPLPTRTIFSVPTQSLATILI*ITNLNY INLGKIHFL
7631	21532	A	7691	3	193	HERLDPADFSFNFFSVDVGLAMFPRVL NS*HQVILLWPLTVLDYRHELLRPAWG FYVLNFT
7632	21533	A	7692	1	364	NFKSFFP*LFYLYHLLFFGFGLFLFFLI KLGSSLFINFSKSVL*FTNWIYFSVLV FTDFCFIFIISFFGFSLIYFIIAVFPLK FIGFILSFI*ITVFYQQAQWLTVPVIL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						WVAEVRGSL
7633	21534	A	7693	370	151	GKKYSVASPGKLWPPQGFFKTAPPPFFFF FFLK*RCGFTMLPRLVLNPWPQGILPPQ PPKVLGLQVLRHHIWL
7634	21535	A	7694	3	373	WPGYTLNQAYAKIHFTIIFIGANLTFFP QHFLGLSGMPRRYSYDPDAYTT*NILSS AGSFISITAVILIIIFMI*EAFASKRKVL IVEEPSQSAGITGVSHCARAEYLFIDRR DGLSLCWPGWT
7635	21536	A	7695	406	394	KFF*KKFLFPPTPTFLLEACLFFFLPPI KGFLFKYIAPGIKTPPPKKEKFSSSLKV LFSPPYFFFIPPPPIFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFRRFEG ECWRL*W*FYFYFFKESPHCIP
7636	21537	A	7696	2	334	ILINNTFLALLLLIITFWVPQLKGYIKK STPYECGFDPISPARVPFSIKFFLAIT FLFDLEIALLLPLP*ALQTTNLPLIVM ASLLLIILALSLAYE*LQKGLD*AE
7637	21538	A	7697	2	95	LNLTIIYIILTTAFLLLNLNSSTTTLL SRT*NKLT*LTIIYIILTTAFLLLNLNS STTTLLSRT
7638	21539	A	7698	423	326	RQCLTMLPRLVSN*SQVILLPWPLKVL GSQA
7639	21540	A	7699	400	32	FHKEYESYFFSPNQPFPPPPH*NFY VGVLKKQPPKKKFFLLFTPERFFPFEL *KKNIFFP*YFFPLVIFFL*PPPLFF FFFFFFFFFFFFFFFFFFFFFFFFF FFSSNSFPFY
7640	21541	A	7700	125	407	FINTSSTFVVKPTTCNMQKHTPIARTKD LCITIFFFFLEKNFLFVQVGGQGILG *LKILLRG*KQFSCFTLPGRWTNGGIPP PPKNFLKFF
7641	21542	A	7701	50	225	PWNMVKMSCWLKVAHVCPNSTLGRGR RIA*AQEFETS*VTQ*DPVSVIKRKN FK
7642	21543	A	7702	2	146	EIALLLPLP*ALQTTNLPLIVMSSLLLI IILALSLAYE*LQKGLD*AE
7643	21544	A	7703	1	93	ILIINTLLALLLLIMTMGLPQPKGYIKK STP*ECGFDPISPARVPFSIKIFLIAIT FLFDLEIALLLPLP*ALQTTNLPLIVM ASLLLIILSLSLAYE*LQKGLD*ALLL LIMTMGLPQPKGYIKKSTP
7644	21545	A	7704	2	112	GRVGKHHFGFEAAA*YHVFVDVG*LFLY VSIY**GS
7645	21546	A	7705	1	325	TAGQFLPKLSILLSYNPAITFLGIYPKI LKTIVYMKCTCTWMFIAALFIVVQTKQQ SKLWYIQTIKYYSVLK*NELSSYENTSK KLRCILLRERSQYKPPYFLIPTM
7646	21547	A	7706	2	169	SRSRAGTLAT*LINLPCTLMIFTLIVL TILEIAGALIQAYVFTLVVSLYLHDST
7647	21548	A	7707	263	346	MLINVPLGLLFVGVLSKESPSVDQGGV QWINLFSMQPPPTGFK*FSCLKA*ASDN LSPHEQYRLALSFLKLT
7648	21549	A	7708	343	163	PKEF**RQGFHVGQAGFKLLRSGNPPP SASQNGKITGVNPLAWQTNNIPMAP
7649	21550	A	7709	459	144	FWPGASSHAFDPTTLGGRGGRIA*AHF KTSLGNIVRPPSDTCNPKVLGLLA
7650	21551	A	7710	2	83	NFLPLTLALLI*YVSIPTISSIPPQT

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7651	21552	A	7711	19	181	KVHTKACT*MFISLSFIITKNWKQPIF SSIGE*VNKT*YIHTMEYLLFRNKRK
7652	21553	A	7712	392	49	SDIFNSDIFSHY*CSVF*SYLAYNRYLS FL*LFLEFIYSYP*IDHAFHCFLHPVSS FWLDFFLFIFSFLLFSYFYSFYF*FYF *FIFNFIFNLFFILFYF*FSFFSKCLKF PC
7653	21554	A	7713	334	208	FFF*EWVLTTLPRRLVLPQAPAILLPWP PKVLGFTGVSHIKI
7654	21555	A	7714	2	408	WNGMEWNGLKWNRLERYGMQWNGLEWNR TE*TRMVWNAMEWTRIELNGLEWNGMEC NGMHLNGLEWNGMERNGTDPWNGTDP WNGTDPWNGTEWNGMEWNEVDSNGMEW NGIDSNEMGWTRMEWNGMESTRV
7655	21556	A	7715	362	223	VWFMPIIPTLWEAEVGG*LEPRSSKPA WATWQDAIFKKKFQHP
7656	21557	A	7716	2	335	LIVIINTLLALLLIITF*LPQLNGYIE KSTPYECGFDPISPARVPFSIKIFLVAI TFLFDLEIALLLPLP*ALQTTNLP MSSLLLIILALSIAVE*LQKGLD*AE
7657	21558	A	7717	2	142	SITL*LPQLNGYIEKTPPYECGFEPICP ARVPLSIKFFLEAITFLFDLEIALLLP LP*ALQTDLDPLIVMTSLLLIILTL SLAYE*LQKGS*AYMPRPRPFVHKILLRS YLLII
7658	21559	A	7718	6	92	FFEAAA*YWHFVNVV*LFYVSIY**GS
7659	21560	A	7719	417	164	PLEPLISGRGLPQIAPPPKKSPPKSPR WFFFP*KKKNYFPPPKILPPPGFF* NPPPPFFFFFFFFFFFIFFYFFKTALPL
7660	21561	A	7720	25	401	THNS*DPNWD*IPHYA*P*TSTVKKKKK KKKKKKKKKKKKKKGGGLIKKFRGGPKY TGGGKIIFFFFMGGKKPLGDFLKKNFF LGGGNLKGHPKKLSLQKKKNFKGRGG KKTPLCRRGKKFS
7661	21562	A	7721	388	2	APPPFFYFFFIFFFYFPLGVGFSGK*N SKVFWISNFKKILRVFICSLEKGINPF LEKCFYMFVVAFIIRLNFSLOAKFFL LNFALLPFPEIFFFFFFFFFFFFQIEDFW HPYIEQVYQLSLSLS
7662	21563	A	7722	389	71	FFLPHQKQVFFPPPPFKIFFFSSRVFFF WCGWAQKPPPPKFFFLKTPPGFFLPPP *KKKFFFSRFFLPPPGFFFKPPPNF FFFFFFFFFFFFFFFFFLN
7663	21564	A	7723	77	220	TPRRGWAYWLMPAYPAILEA*AGGLLEP KSLRSTWPTWRNSISPKRK
7664	21565	A	7724	16	258	ISSFVFKRRSFAMFPRVLNSWPRVLP PRPPE*LGLQACTTTFSFNFFDGIFLRP LKEDVTARDQREILYVFALFYGGGA
7665	21566	A	7725	353	111	IFGAGPRFVFKAGGQGANRSLSKFPFG NKWSFPFSPSKKWEGRG*PPRPPFFFFF FFIREGVSLCCQGSQIPGLKQSS
7666	21567	A	7726	2	185	MSMGHTRLSSAWTGKPPLSVEDDFEKLI WEISGGKLEAIEDLDPKDEDDLLLELS *MIDT
7667	21568	A	7727	346	143	SQAFLYLESFLLLLLL*FLFFEMESH VTQDRVQRHLSSLQPLPPRFQPPSRLT LPSSWEAEVGG
7668	21569	A	7728	411	221	NLRPPGSSYSPASAS*TAGIPGARHHTQ

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						LIFAFLAEILKNLAKLYLIPRKPNIIYYL PNCYINI
7669	21570	A	7729	2	303	AAASTNMLLFFLGRHLVVEWLGHMVGLI FTFFKKLPNQAGRRGSHL*FQHFGRQRWE DHLRSRVQDHPEQHSKTPSSSLQKNKMSI ESNLLNIHKLFFSTGRM
7670	21571	A	7730	67	65	SICEYCFVSSVFVLKRLFSVMQAFSLEG CVSCQS*AFLQHYLFKKLYFLY*WGLTMLSRLVLNTWPPQVIHLPPPKVLGL*APC GNEA
7671	21572	A	7731	354	238	QSILDDVAMVLD*QAEVFIVKMWRLLIY VHEAKKIGLVK
7672	21573	A	7732	33	186	RGALAVLSRLILTPGLKESSCLDLPGKW DYRWEPPRPGCFF*LMVLVLSF
7673	21574	A	7733	1	181	VNAGADCSSIGGVPFLQHKKCHGKDYEP RGITTLERSYVEETTEHLVSKSK*PLRA QINL
7674	21575	A	7734	336	80	HKLKEPPGVFPVFPFKNLEFGPGPPKFF FKAFSPILSFFFGKIFKIPRFRGENFA P*NFGKNS*KPRFSPPPPKKGF F
7675	21576	A	7735	2	163	TPVSTGTPVPTLT*VPSPFIIPVSEKWA GCLHLCLNFTCTELRLTSLLTIRS
7676	21577	A	7736	87	258	KAPSVCLFSALLMLLRMSARTSVCTVRP LSPS*AVISPTCTYTSRWPEATEDSQK
7677	21578	A	7737	1	103	LDSKGIYMTLQPSKLEPKLEANVEIREH MLENSSRF*RDLYDSAAFKARTKARSKC RDKRAHVGEFF
7678	21579	A	7738	193	300	GGLPPPPFFFFFLKKRGFPVWTRGGPN PPPLMGGPTPPKGWNYGGGPPP*FHPF GGVGPPISKGGGLGPPRVTPQKPLFFKK KKKKNGGGKPPYPSPFLGGVKQKGVNP KGGGSKPKFPPPPPPGGKKKKPFLKKK KKKK
7679	21580	A	7739	150	17	GRVAQVWVLMHAIPAL*KAEAGRSLEPR SWTPDWGTWHLPISTK
7680	21581	A	7740	1	358	SPPRPPPPPPPPKKEFKKLENPPPPPK NPQKQNPPPKTKKKSP*TTPKKKPKIGT PPQTPKKINCS*KKKNPPENKKGLNYP NKPNNPHAPPKEPKQREKPLVPTKKKKG PSPKKK
7681	21582	A	7741	235	147	F*FFLGDEISLCCPGWSLTPGLEQASCP GLPRRWNYRCEPPHSVKTIF
7682	21583	A	7742	131	12	AASTYQQ*FKICGAILRLMPIVIEPIPL KILQIGPVFTL
7683	21584	A	7743	1	184	NQYPWCFCNHSMSGKESKTLNRSGMVAH TCNPSTLGGQGGRIT*A*GSKSSLGDKV RPHLY
7684	21585	A	7744	347	202	SLFVETGYHYVD*AYLELLASGSPPASA QSFGISSVSLCTQPMFQFE
7685	21586	A	7745	138	263	KKRKTYIHTKTCM*MFIAALFIRVRKWK QSKCHSADEWINKF*YIKICLSIHQLND IWIATSF
7686	21587	A	7746	358	169	AAAVAERTONTEKTEDLVGLWIKKVIY WPGVVAHVCNPITLGGRGWIT*GQEIE TSLPTRR
7687	21588	A	7747	78	346	AIQMLRNQVKIKLPKSPVEIIPFKIVPQ FOVQKIKSQNNFLLLFQESQIFFATSTG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SVRPLSPS*AIISPVTCTYTSRWPEVTEKSQKK
7688	21589	A	7748	222	98	KKKARHGLGAVAHACNPSTLGGQGGRIT*VQEANIVRTCLY
7689	21590	A	7749	314	52	LNNVDLQFFLGP RKKKRNLDSSFLVSAEEVRLMYCFNKLA ILHYF*FSNKFIVPV*KFGHLLDENMGSKFDNIGMNAMANKDNASK
7690	21591	A	7750	371	216	YHTHTHTHTHTHTQIPSLPLNLEGPVGYLLSCGSLHLKNLW*KCMRKERKK
7691	21592	A	7751	3	238	FLIQTGFGHVSQAGWELLR*GNLPALAFQSAGITGMSYLCVAESLYLLPFLKILCSSLLTSLSPYDTWKVALLCSYTV
7692	21593	A	7752	2	247	NSDIFDIYITQYIFLIYLYIYIYIYIYI*VFLIIFFKFTLK*EFIFISLSISFRLAFIVYRDVILFLFFFS*NFVGDSIS
7693	21594	A	7753	359	2	TLKIRPLLYLPLFFFFF*KKKIFFFFPPGGGKGV*SGFYLMGRGTFSLFFKRFFLFYPFKEGGLRGSPPPPSFFFFFKRGFPFLARGV*KKGPQGTPLPWLPKSLGLRG
7694	21595	A	7754	3	174	CSVIQAGGQWCGHSSSLQ*IPGINQSSYLSFPSSWDYRHATMPS*FLFFIEIKMLQ
7695	21596	A	7755	292	219	IWPLSHVHSNPLTHSPSQVDQGIFFTLPLCLSGYMYVQFPLAEMPFISLLLENACLSLCEGSEAQKPLLWEGLSYLPPLNQLPLCL*LCVCISGGVCRCLMCILGVCVCMHVCVSVCPCTHTLAQETKGC
7696	21597	A	7756	2	195	VALMADGAIDTESNDYGAFMPLGIERGLDRIWEMPELWLRPNEFDCMTD*PCIQHA PSVSCGLA
7697	21598	A	7757	4	280	DHIVDMITPSFTRRTIAVF*DLNLYIVI RGHITSILKPNKLNKLWYIYTI EYYSALKGNEILIHATIWINLENMQDEINQTKQDIYCTISLI
7698	21599	A	7758	352	107	FLTRASRGHNGETIVTSWPGAVAHVCNPSSLGRRRWIT*GQEFKTS LANMVI TFFISKNSNRFLSQFPISLRPTHYKVL S
7699	21600	A	7759	92	4	RPSPRRGGWT A*GQEFKTS LGNMVKPCLY
7700	21601	A	7760	92	4	RPRRRRGGWT A*GQEFKTS LGNMVKPCLY
7701	21602	A	7761	328	124	PLFSFLFPFFFFFFFRRRDGVLPCCPGWS*TPGLKLSSSLCLPKCWN YKHEPLHTAHNHF
7702	21603	A	7762	1	167	VDSTDKRPGAVAHNYPSTVGSQGGQIT*GKFNPSLANTVKLFKKKKRKRKRGALF
7703	21604	A	7763	309	226	RPRRRITLSPLR*CSGALSAHCKLR LPG
7704	21605	A	7764	349	7	QVFCFLFVCFSSIFMTFNE*QGLKVTSGISSNVY*FLLIWILGKIT YQDIGRCFS EYGSPEQHNLGIVRNASSRLGVVAHTCN PITLGG*GGWIT*GEGFETSLANMGKPLLY
7705	21606	A	7765	43	339	FFFFLFFFFFFFIIFLLSFFF*DHFFVSLFISINFVFLFPIFIFTVFQAHLFICLLFFPICMFLNLFFPNFNYYFYFPPLFFYL LFFFFG*FNHLFY L
7706	21607	A	7766	352	102	HTSCLIKSSLSKMNISCVSSSISFFF*FILIEIGSR*VVQAGLQLLGSTDPASA

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						SQSARITGLSHHAQLSSTSLVVENVEW
7707	21608	A	7767	346	90	TPSSFFSFPFPFFSFIPRFFFSNR DRVLVCYLGS*TPCLK*SSQFGLPKCW DFRCGPPCLTSTAFYISITVNFSPSNCY S
7708	21609	A	7768	278	87	AASTGVGPSEPSAGYLLVCRLLRSLEK CSIRVGVT*FSRCHLSPLSLTRKGNLSLT PCASRV
7709	21610	A	7769	5	272	AVYHPINESCVLNIGKDSCLLY*LFEKK KKKKKKKKKKKKKKKKKKHYE*FNTFP G VARKINLFLCIQKVDAGGTLWGGGPP IFFFL
7710	21611	A	7770	198	33	QRQPSRQCRAWLGMVAHAYNPGLTG* D RRTT*GQEFKTSLGNIVRPYLYEKM
7711	21612	A	7771	97	410	A*WLMPIPIIWEVKVRLLEPGSLRPS WATWRKP
7712	21613	A	7772	5	415	ILCVYLHFVGTHTPFVHL*YMHFLPLTLA LLI*YVSIPITISSIPPYT
7713	21614	A	7773	1	342	VVRVTSGHSG*AAAYAT*YILSAEGSFF PLTEELLI*FMKREAF*KR*VLIIEHP SINLD*LYGCPTPYHTFDPVYLSKRR RRDSHPKCLASRLPHVLHDFKKKKGG RR
7714	21615	A	7774	398	122	SPPPPFPSSPSFFLPPSSSFFLFFLFF FFFFFFFFFFFFFFFFFFFFCRD*VSLC CPA*SQTPGLK*YSYHGLPKFWNYWHEP PCLAYFL
7715	21616	A	7775	1	336	FNFLIIIIEMESRSVSAHCKLSLPGSS NSSASASRVAGSRGAHHHTWLFFFFFF F*KKKGAPPGQGGLTLKKKNPPPRAP QRGGINGTTPRPQNGGKFFPWGEKKKF
7716	21617	A	7776	1456	1232	FAIESHCVTQAGVQWCNLSLQSPTEF K*FSCGLPSSWDYRCVPPHPANFYIFS RDRVSPCWPGWSKTPDLK
7717	21618	A	7777	400	2	NTEFPYGPPIISLLGM*P*EMETIYIPRK P CTOMFLEVLFTIAKK*KKPKRS*LING* ILVYPLMEYYSATKRFDMIHNTKNVD AI GNIILSERRQM*KTHIVYSIHRASCTAE VRIKVSYKRAATWIKSILIA
7718	21619	A	7778	360	218	PYLANF*NLL*RWHLNMLPRPDSNSWPQ VILSLWPPRVLG*QRGRVEQRGARGNW MSKCPEGGDCLCWAGA
7719	21620	A	7779	1	372	FEVRSCSVAHAGVQWHDHGFELGSSD DPSVSASCISRTGASHCTQG*L*LLTK VL*VSACLSVNTLRLTSLKSDTFLGS RSKLSLGSLSQTYISPSRHFQILLCFR SLFPRFLVKHKK
7720	21621	A	7780	372	219	ATSLLSYFKKLPPQSSATTTTISQ*S STSRQDLPPAKRLELETSDDP
7721	21622	A	7781	358	145	IKNIHDSWEDVKISTLTRV*KELIPVLT DNSEGLKTS*EVTAEVVEIARELELEV EPKDVLVQFHDITNR
7722	21623	A	7782	317	146	GRVDCCKPFYRFQMLLVRLGMVAHVCNP STLGGRGGWIP*GQEFKASVSRMPRPHL Y
7723	21624	A	7783	13	186	DRVSTQTSWAHPPTSAS*VAWTGMMH HTWLNFFVFFVEMGFHHVQVQVIRLPLLS WK

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7724	21625	A	7784	339	221	KWDLAMLARLVSNNSWLQGSYSLSL*NCW DYGSEPLCPAL
7725	21626	A	7785	355	3	FGNSGRVDLFFFFFFLDRVSLCCPGCSA VTNLEVHHSALQPQTPLKPPSSHLSLS SWDYRRVPPHPS*GLF**GK*YSITQLR FLNLHLESGLRSLLPKPVASTVRIRTQS GLGLK
7726	21627	A	7786	1	201	QQFSHVFRLLFQFSFSCQEPSSHIQPG VCTRNTKVSQAW*CVPVIPANREAETGE SLEPGRRSTRP
7727	21628	A	7787	270	1	RPRRHLPVCVLMGLPKCPGLPHTLTTLTLP YTLTTPSPTRSLGPPECK*SFHLSFPSS WDYRRMPQRLANFCRGRILLCPDWSSS PGLKQS
7728	21629	A	7788	229	2	DGWVRINWAQPGTVAHAYNISNLGGRGR RIT*GQEFKTSLTNMEKPCLYSDHEVRS LRPARPTWRNPISTKNTKM
7729	21630	A	7789	118	263	CSKSYYPDAVVHTCNPSTLGGQDGWIA *AQEFKTSLGNIARPPISVF
7730	21631	A	7790	246	359	TFIFSETRSHSVTQAGV*WHDHGSLLQ* PPWAQVILSC
7731	21632	A	7791	70	102	AA*SRLTATSLSRVQAIPLPQPPEQLGG QGGRIS
7732	21633	A	7792	7	312	FLDFQLRLHSNSYCEDKGVDFSEIYEIC IVLIICKK*RKFLNQKKKKKKKEKPLI* KKKKNSQKKWDFPWLPPNPETKNSLFL PKEFLWLKTKPPFPLTLT
7733	21634	A	7793	1	341	IKPE*YLLFAYTILRSVFNKLGGLALL LSILILAIIPILHISKRRSIIFRPLSR LY*LLAADLLILT*IGGQPARYPFTIIG QVASVLYFTTILILIPTISLSENKVLW A
7734	21635	A	7794	1	143	YGSTFFVATGFHGLHVIIGSTFLTICFI RQLIFHFTSKHHFGFEAAA*YWHFVDV *LFLYVSIY**GSTFFVATGFHGLHVI GSTFLTICFIRQLIFHFTSKHHFGFEAA A
7735	21636	A	7795	2	257	KWAIIEEFTKNNSLIPTIIATITLLNL YFYLRLLIYSTSITLLPISNNVKIK*QFE HTKPTPFLPTLIALTTLLPISPFIIL L
7736	21637	A	7796	22	326	RDASDCSFQNLVPVPLWVEK*MVFLLT KKKKKKKKKKKKKKKKGGGPKKNSWG AKIIPGKKKIIFFFLEGQKKLWGFFKK KPLFWGGKKRPNPPKKN
7737	21638	A	7797	506	281	RGAN*NRSGCGKRHEERERERERERE RERERERERERESRPPKQRERERE TLSLTVSLAPPPTCVF
7738	21639	A	7798	435	336	MRSNIHFFSHTHTHTHTHTF*ILKQH TFSK
7739	21640	A	7799	411	106	RNPPPLFFSPPLQRGGFPPPIYWGPPRFF PPPPL*KTTPPKLKIGAPPKKKPPPPPG EKMVSF*PPPPPPPPFFLRRPPLFSP GGGPWGHFRGPPPPPPGV
7740	21641	A	7800	2	296	FVPSTANWCFFLWSVF*TGGSNYFFVHR SYSQAGVDLIFIRLANTISNLSFI**RG GLAMLRLVLETRAQTIILHSWPPKVLGL QVWATVPSEQFLKN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7741	21642	A	7801	344	105	PGFFFFPPPGKRGFFPKPFFLGTGFFFP PPLF*NPAP*FFFWAPKKKIFSPPPGK KIFLLKGPPLEFFFFFFFFFFF
7742	21643	A	7802	68	216	VHTIAKIWKQPCPSMDD*IKNMRYLTY VE*YSVLKEREILLYWGHIYAM
7743	21644	A	7803	407	3	GFIH*FPLFSGYTLDTYAKIHFTIIFI GVNLAFPPQHFLGLSGMPRRYSYDPDAY PT*NILSSVGSFISLTAVILIIIFI*EA FASKRKVLIVEEPSINLEWLYGCPPPYH TFEEAVYIKSRQKRKESNPPMY
7744	21645	A	7804	2	156	THRRITILSQGL*TLPLIAF**LLASL ANKKKKKKKRGPPFKKFPWAKI
7745	21646	A	7805	2	309	THSRITILSQGLTTLPLIAF**LLASL ANKKKKKKKGGAPLKKIPGGAKIKRGME IKNFSQGGGKKTQRGIFGKKPYLGGGQ NWEKLPKKFKGLKGGKKNF
7746	21647	A	7806	110	362	TLSDLERLLMKAVSHFLMIDLLEKC*CV LKNQSSKKKKKKKKKKKKKKKKKKKK KKKKKGGPLLKNSWGGPNFPGGKIPFF FRRGGF
7747	21648	A	7807	295	108	KQRGVFFFFFEMESRSVVQARVVQCNL SSL*PPPLGFKQFSLRIVYRKDSLFSN KPRLLP
7748	21649	A	7808	2	142	GSTFFVATGFHGLHVIIGSTFLTICFIR QLIFHFTSKHHFGFEAAA*YWHFVDVV* LFLYVSIY*GSTFFVATGFHGLHVIIG STFLTICFIRQLIFHFTSKHHFGFEAAA
7749	21650	A	7809	390	2	PASLLHCG*ISDCCASNE*GSVGLGPSE PGAGYNLLVCHLLRPLEKCSIRVGTRF SRCLSPPLDRKGNLSLTPCTSQRQCL ALLQLTLGALHPVSCHTCPTISGEMNPV SQLEMQKSPICVTHAG
7750	21651	A	7810	1	157	FLHFGQAALLLTSGDPPASAS*SAGIT GVSHRAQLVCTFITIYVFLKNSSY
7751	21652	A	7811	368	44	QNFPKKRLLPPQPLFFFLVPSFKGEG FFFFLGRGFFFSQAQALL*FIYFIFFF FFFSFFFFLYFSISPSDKGDTHTDLLL GVSWWTRSLPLWIARHNMHKVVGW
7752	21653	A	7812	400	80	PQNSFSPPGIGGFFPPL*NFFFSPKA FFFLGGFSPFFPPPKSFFFKIPGFFF SPPLKKIFFFFPPFLAPPRFFFKAPP PFFFFFFFFFFFFFKYFRHI
7753	21654	A	7813	119	230	SEEFETSLRCIVIPSL*KKKKKKKKKK KKKKKKKKKKKK
7754	21655	A	7814	3	412	HEQEH*LLLP**PLAII*VISTLAETN RTPFDLAEGETELDSGFNIEYAAGPFAL LFIGEYTDIIIRNTLTITIFLGTTYDAL SPELYTTYFVTKLLTSLFL*MRTGY RFRYDQLIHL*KNFLPLSLALLI
7755	21656	A	7815	1	183	LRLERLSEFSTRRERERERERERERERD TRIDIYIVSQKRKKYIV*IRRNIIFYHA EFSKR
7756	21657	A	7816	484	97	QPRTPDLK*FACGLPKCWDYRHKPPCL ASDGNHS*SSPGLLVLSASVSPSGHMS PSQQTSPWVSEESLLGRVPGFLYFPV DAPGPGAWLAHVQAVLKLGGSSDPPVL PSQSAGFAGLSNCAWPW
7757	21658	A	7817	2	219	ADRLRNS*EA*EREREREREREREPY

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						PPSHIYTDNRH*MRHEERTLFLWGSGE VRDAAPWVSHIPNTAL
7758	21659	A	7818	190	292	NSHLIFPWTKVFFMS*CTYNLVLPGSEK KFYSHA
7759	21660	A	7819	498	139	RRAATPAPAAAEPPPPPLQRP*PPSEPPD TQRDARGRRRGEDPGNSPFHPNPDRQPS RALCSTPRMHLRWIGPAFFLMTSLSVSG AVIPRNGGPGGVSSGPGCLLQLLCGQAGS STIRKIPS
7760	21661	A	7820	489	330	ELGFLHVPQAGLELLS*SNPPASASLPT SWDYRHDHRTGHHPGIYDSKMCIF
7761	21662	A	7821	490	260	FFLXXNXFXFFFXFXFXFXFXFXFXFXFX FFXXXFFXFFFXFFFXFFFXFFFXFFFX FFFFFFFFFFFFFFFFFFFFFLY
7762	21663	A	7822	493	482	VGQAGLKRLTSGDLPASASQSAVITGVS HRARPIMYFRYVQ*AKGSHV*RWY
7763	21664	A	7823	456	121	ASFFPIQYKGLGGATPPQEGGCG*GIP KWGYKRRPGGPHGGSKRPPTQ*KKSYFI NVLVLFYLRDKGLAIPTLVSNNSWAQVIL PEWPPKVLGLQTRVTVPQONILKENMFF
7764	21665	A	7824	294	457	LCIGFVILISYFNIMENWYCRPGTVAHT CNPSTLGG*GRQITRSRDRDHPGQHG
7765	21666	A	7825	26	235	SVWWSQTGNKVKFTISW*IDKQMRCTH LMEYYSIAKRNEVLINATTTWINLNTIK LSKRSQTLKSNTL
7766	21667	A	7826	30	303	SYVSVEFPSSGPTLPSPWHQTPRTYL NSVASAINLTQCPH*PEKKKKKKKKKKK KKKKKKKKKKKKKKGGAFKKKGP*KTPK KTPGGF
7767	21668	A	7827	464	21	REPPHPAPADILILHFWLEL*ELISVV LNTRCVVICDDTPRKLTCQMPRLLLQT EPL*VLFSNLGSFGSLSKS*MGLVNFFC KGTDSRSFSLFVAVFCLFL*RWGLAMLH RLVLNCWPQVILPPPPPKLLGLQVEATT HEFHGTE
7768	21669	A	7828	372	205	FFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFIKKFI
7769	21670	A	7829	463	313	DIYPERNSKIMSFAATWMKLEATILK* LKNRKPNIVCTHL
7770	21671	A	7830	449	266	VVQMRFLHVQAGL*LLPSGDPRASQVQ SAWITGVSHHAQRSIFFKRNNDCDRPD NTECT
7771	21672	A	7831	480	148	TELRLSHGAEBFHRPREWYGIFKVLKER DFYPRIIYPAKIIILRHEGEMKTFDPKQT LRHFINTRPVLQEMLLKVHQSEIKGC** ATNNHLKVKKKNSLW
7772	21673	A	7832	23	131	QRGNSKGYHLKMIQEEIRKLEEEKNQL EGEIIHFYKMAASEALQTLSTDTKKD KHGKKQ*FL
7773	21674	A	7833	16	339	NTDTLGSMAFCRDGLAMLPRFLNTGL KRSSCPDLPNCWDYRHGPPYLASFVLLK *TLSILLPPYHKMHTCFMVLCTNFCG GVCPGMELLCLKVYGYLSLKHTEH
7774	21675	A	7834	355	70	KKTPRGFSGVFLGPFYKGLPFFFFFFF FFFFFFFFFFFFFFFFFLQFFILCQQFL S*STEKTVHSKYILSFPFHCLIFCPFIL LCSTFCNGAHY
7775	21676	A	7835	494	282	PENGMIQGGACSEPR**HCTPAWAKER

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						DSVSNAKTIQNKKNLGN*HSISTAKAKN IIIS*YKSELRKKM
7776	21677	A	7836	305	185	LVITETCLTVRPLSPS*AIISPVTCTYTF RWFEVTEESQKK
7777	21678	A	7837	179	191	LGCRKYLFLYLNGLKCLYIKVCVCVCICI YIGVYIGMCVYICITYILMAS*NQVTSF LSFYVFLNLYR*IPVKVITVLFNLRLMTG LP
7778	21679	A	7838	466	343	LGRLRQENHLPPEGRGCSEPRSRPCTPA WETEEDAVSKINK*INK
7779	21680	A	7839	451	89	LRDTR*SGVICLPKQAWAMVGAPPPASL PPCSLISDCCASNQRDSVGVGPSQPGGG YNLLVRRFLSLSEKRSIRGVNRFSRCH LSPLSLTRKGNLSLTPCASVRVQCLALLR LAHGARTH
7780	21681	A	7840	442	164	AHTNQFSQCIKKSVPDLMEEYKKAHA AI*ENPVYEKRPKKEVKKNRWNCPKMSL AQKKHQVA*KKASSLRAQEQAAS
7781	21682	A	7841	494	359	ICMLPRLVLNS*PQVILLPWPVKVLGLQ A
7782	21683	A	7842	577	224	IFFFFNKIFLFRPGLNLMGDIWVPSTPP LQG*TNFPPQPSQEVGLKAPPPGLIL VFLSRQGFPLGRVGFHFPPPGDPPPRP FKKIWSHPGGGKSPPKKKKKKEIAEVLG AFRLR
7783	21684	A	7843	404	56	HTLSTNVCSSYLNLDFFSLRGRGLIMLP RLALNSWAQEBILLPQPPE*LQLLRRLRQ ENLLSPGVQGPQGHNETPTS
7784	21685	A	7844	1	323	INTLLALLLIITF*LPQIGYINNSTP YEGGFDPDISTARVPFCIKFFLEAITFLL FDLEIALLLPLP*ALQTNLPLIAMASL LLIITILALSLAYE*LQGLD*AE
7785	21686	A	7845	419	159	FLFFFFFXXYVLSCGIY*YWCNLFSS* QYFFFYVMAFRIFLFTFLHFYNNMF* CTYFYLSC*FEYICSHIIHYFIYFLHL ENF
7786	21687	A	7846	475	124	FFFFFQPPQKEGGPPPPKNNFFFFTRI FFFGVFFFFFPQKNFFFF*KTGVEFFF PFF**KIFFFFPGVFFFPVFFFLSPPP SSSFFFFFFFVFVFVFVFVFVFVFVFVF FFLKRQAS
7787	21688	A	7847	6	189	LIDTVSPSVALAGVQWCNHSSPQP*PPS LKRSSRLALPRFWDYRCAPLCKAHSENS NHEK
7788	21689	A	7848	20	249	KINFIVVELTCSNTVHTFYVYGFDKCIL PTTQLFFFL*ETGFHSHVARLECSGVIMA HCSLDILGSSWRPANFLNFL
7789	21690	A	7849	101	398	LFQKKKKKKKKKKKKGGPLKKKPGGGK NKGGEKKKIFLKGGEKKNPRGNFKKKT FFGGGKKGEKPPKKKKSPEEKKKF*RGK GGKKS LICWVEKNLG
7790	21691	A	7850	87	226	GSLSPIMLVLPFLIHL*KNFLPLTLAL LI*YVSIPITISSIPPQT
7791	21692	A	7851	2	440	GAIIIRLLH*FPLFSGYTLHQTYAKRHF TIIFIGVNLTFPLQHFGLSGMPRRYS YDAYTT*NILSSVGSFISLTAAVLTL MS*EAFASKRKVLLVEEPSIDLERLYGC PPPYHTFEFPVYIISRPRKESNPAKL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SSQPHG
7792	21693	A	7852	1	80	SSLLLLIIILALSLAYE*LQKGLD*AE
7793	21694	A	7853	5	135	ATFLYFS*K*SLSMLPRLVLNSWTQAIL PPWTLKVGLCFFDPL
7794	21695	A	7854	38	419	FVMMPLHSSLGEGVRPYLKKKKKKPPWE GGSPPKNFNQIFA*NQKPPFFFIIPP KKWGSPPGGGASPL*SHPSGGPGGPNNK VKISKPPCPPGGTPVFTKIPTFT*PWGP IPEKEGRKTVCPRTH
7795	21696	A	7855	398	61	FFSPRPRGGGFPPPPKNEFFSPPTIFF GGGVWNFFPPPKMVFLKISPVVFFFP IRKKIFNLSPGSFWSPOGFFF*GPPPKF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFF
7796	21697	A	7856	1	121	LDASGRLPSPKPIKIKYNRP*EPK*T KICSLHSLPPQS
7797	21698	A	7857	1	332	TPPIARPAENSARGAEGRRR*IIALQVC NKKWPPTKLHCICKKKKKKKKKKKKK KKKKKKKKKKLWGGGGGKNFFKKGGKK KLGGGFKKRGRKKKK
7798	21699	A	7858	3	191	SPRHLTRAAGIRHEGTGLKLLTSGNLP ASAS*SAGITGMSHRIGPRMLDLTLVS WKQHGL
7799	21700	A	7859	503	62	FFFFLNCCLSLRHLIKLFEPQFLHL*N GGMVLSIILSIKSPLSLSYSWL**P REKIKWGGQVRWFMPINPRTLGGGGGQ IA*SQEFKSSLDNMVRPYLSEPP
7800	21701	A	7860	355	86	YIKG*QMVGNRGASQAGMTGYGMPRLIL
7801	21702	A	7861	336	225	PQLAGPVKTVRKVKKEKARVPEEKK FKAFASFRKGRANGRVFGIRAKKAKBAA KQDV*KKPPIPLAGGSPTREPPSQAHLF PQNPPRGNNP
7802	21703	A	7862	465	170	GGPPPKTHPFGGERGGKYHRGKKPPGH QRVNPPSPKKKKKNWGRGKNPFTPLIGG GQAKKPPQPRGEC*KKVPPNNSVLGK KNFFFPKKKKKKKK
7803	21704	A	7863	495	275	RSFFFFFFFFFFFFFFFFFLVARK*YVFL ATKKKKKKKKKKKKKKKK
7804	21705	A	7864	493	70	PLTASISLPVNWRYIAPHRVVKIK*KSV Y*KYLA*CLAQSKCPKSVCSHLSSP*LH FVPPPNPAEAMWTARQC*CIRGLGGKGT LCVAHTYNPSCSGG*GRRIV*AQEFKAS LGNSEPLILKKERKKESQAWWLPIIPA F
7805	21706	A	7865	67	385	VARTTGMQHHAWLIFFIFIIFVETGSHY VAQTSLEFLASSDPFTSVQSTWITGVS YSWS*PGIAHTCNPSALGDRGERIT*GQ EFKRS LGNIVRPCLYKNNKNN
7806	21707	A	7866	454	0	LSFFFFPLGDRVTLCCPG*SAVARSQLT VALNSWAQAILLPQLHKHVPPCLANF*N FF*RQRYTMLHRLVLNSWAQVILQPWPT CPTAAQA
7807	21708	A	7867	1619	698	PATSSSSSSSSSSSSAAAVAAAATAASL PPCRPPLRPPQPLAPHEVATLAPWRG*K PSFTSSGKRWLTSEPQTSGSCASCL*SM RASSPSSG*SKKKPPLPAEAAASVAACA VCWRVRAPPYVAATTAYTMVGMWMAFP WEVIWTRWRMMSQAIRPLQTWTNSVTAP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						S
7808	21709	A	7868	52	187	LDFN*RRCLTKLPRLVLNSWAQVILPPW PBKLLGLQV
7809	21710	A	7869	33	373	AGVQWRDLGLLQPPPPGFKRFSCSLPS GWDYRHAPPHLANFVVLVEMGFHHVGOA GLKLPT*GDPPTLAYQSAGITGMSHRAR PGISVFHLKLHSFDPFKIIFRPGAETMP S
7810	21711	A	7870	100	119	VFVEIVFPEGLLFSPSCSFHLGCFRIHLK AEF*FFVETGSMLPRLVSNWAQVILPP WPPVVL*LQA
7811	21712	A	7871	471	446	LLMLPRLVLNSWAQVILPPQPPKVLGL* AYI
7812	21713	A	7872	449	33	FSFFFFFFLGGKDLFFSPRGGGGGANSA FFPPPNFGKKSAPPPPLKSV*NPAAP TGVFFFCCGGGA
7813	21714	A	7873	334	41	PCPSLFFFFFFLRQSLTLWRLECSGVIS AHCNCLPSSWDYK*HCPYLATGAPGLL SQSELSYVTL*LQESRPLCIPVDFMTFL PSLCFQSPNSTTL
7814	21715	A	7874	342	716	STGIFLFVCF*DGVSTLAQAGVQWPDLG SLQSPPPRLK*FSCLSLASSWDCRHVFP LLANYLYF**REGFTVLAMMVFS*PCD PPTSASQSAGITGVSHCAHPGMFFLNWP LKSCPSESGAAV
7815	21716	A	7875	454	215	PPPARCH*PP*TLVHAVEFKSHHYSLI SSTQGHKHCGRPGQPLPRKTRDLCSLVY LLTFPSLLSYDPAKSLSARNTQE
7816	21717	A	7876	492	176	PCGGRGAGGNWGWPPWHLRASASSRWAW ALQPHTRSSQAPGPTGPRQ*GAQHLGQQ LLCSISHQALAAPQGRAQDLQPAMPEP SPRPPLPWAAQ
7817	21718	A	7877	281	439	TWSIDL*HMAYFLFFSFLFFAFLSFSLL SFSLLFFAFLFL*VPSFSLFQRQSL
7818	21719	A	7878	507	338	LLRRLK*EGHLSPGGRGCSKPRLLHCIP HWATE*EPFSKTINK*N*S*MKMKKIN
7819	21720	A	7879	55	298	PPCLANFLKFFL*RQSLPMLSRPFSNSW PQAVPLPRPPKRNQLYLYFGCCSQLCNP QHLCSKQHTFKILFDIEKHFRLEH
7820	21721	A	7880	145	292	YFGGQIYFIFCRDRISLC*PVLLTSLV SNSWPEAILPSQPPKVLGLQA
7821	21722	A	7881	3	203	LSLLPRLECSGTFTAH*SFKLLGSRDSP TSAS*IAKTGMRHHAQLRFFFFVPGGV CVCVCGCVYV
7822	21723	A	7882	324	211	AWWLMPIPTL*EAKMGGSLEARSRLRPV WAHNETPFLF
7823	21724	A	7883	2	124	QHFGRLRQVDHLRLGVHYQRQGHGETPS LLK*INVYIYMT
7824	21725	A	7884	367	141	KCWDYRREPRLAQGLEFLFNFCFEIVT EPPCPALAYF*NFL*RWSLATLRLVLN SWPQAILPRWPPKALGLQE
7825	21726	A	7885	471	215	RGMCVSHIFLCVGARYNISSARESLLKE FTECTERKHTHTRAHTHARATHHTHT HTHTHTRV*NSRSQPYCRVHACSPAYLG G
7826	21727	A	7886	462	204	RHSS*LGLPKCWDYRHEPPLACISSF* RKSDISLSDELGTCKCHKWWPQVVKSRAG SVGRDPCSGHFILAGFGQLGA

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7827	21728	A	7887	409	152	PVFLALERPNDQDFLRPGVLDQPP*QNNKISFFFFFKKKKKYIYICMVVHAYNPSYSGG*GGRIT*AQKFKTSLNNTVRPHLYK
7828	21729	A	7888	1	152	GVHVCCDCKCICVCLCVGVVHECLCVCVSK*VHMCHREGTIFGNISWEGD
7829	21730	A	7889	101	399	EIINIVFFVFYFLLPLFFFWGGRRFKQLNPEFLTNSWKKNHKTIGGKNPMGG*KKAITNPQKKGRKRSFSF*NKAQPTQKGNGQNSQGSKAVGALTAH
7830	21731	A	7890	478	142	KFSKKKKRGVLFNFYKKKAFFSKPPKPVFKKKLLKNPFFKAKKQFFKTPTPLRPFREKFFPGPPKKKKRPPGLFKNN*KGPPWPREKKRVKKKKKKVKSHYNNHMPISVH
7831	21732	A	7891	497	320	PPWKFEFEFWFSP*LHKYPPYVVCVCVCVCVCVDFRFFKPAPSPQSHFGINLSFLL
7832	21733	A	7892	217	23	TPPFKKFF*EMGSHAVT*ARVVQWHNHA SLQPETCGLKGFSHLTLNSWDCRSVPS SSARRQSH
7833	21734	A	7893	652	470	SSSSSSSSSSSSSSSSSSSSSSSSSQFERKTRSA PQVEGKGNFCSLEAPPPGLSLFSCLNF*RSWDPGPPP*PHATPKTRAGDGLCATHHRARHCTPGLRFLFLAL
7834	21735	A	7894	25	178	GILFFWRDGLVILHRLVSNFVPSSDSPISASQSWDYRCDPPCPACPLIFW*LLKHSF*FFWRDGLVILHRLVSNFVPSSDSPISASQSWDYRCDPPCPACPLIFW
7835	21736	A	7895	104	451	ILSFMTTWMEADIMLSISQTQTDTRYCMILLVESKNVNLPGMMAHAYNPSTLGG*GERIS*GQEFETSLVNIARHYFYKRNFKIKSKFKKIVRKSQKKNVRRWLLLEARNKGRYG
7836	21737	A	7896	510	335	SCIVSLHRSWDLWHVPPFLANF*IFRKG GVLPCCPGWQIYTFQLQIPFLSITPVAFSG
7837	21738	A	7897	37	260	AGNSQNQGGGACSEPRWRHCTPA*ATERESVSKNKQTKFLCSVPYFESTHFHCTNEATGAWGVEKVALGHAASW
7838	21739	A	7898	35	466	THTCGGIRKCLTNKRENQK*SQQKPSAPKEPEVKNKQKTKKNPKKKKKTPQIQPTKKPFRNPNLRVFTFFVITQNKTPTRGRKTFQKVLFPPNPCLGNKPQTLLPRGGLQKKKKKIPFFYSHPPPLAQKKKATPWQNGLGFT
7839	21740	A	7899	494	149	PARLLSLHSYEVKSVLPKEEGLLNPFVQSVTAHPTSCIGLEEI*LLD
7840	21741	A	7900	494	114	GAEGGPLSKKKKNLLPDYHTGPMLSLYLWPFSLNGLTLTLMCAHTHTHTHTHN*LSRVGLPVLKPGQYQANGNRWSP*YNIKE*PRKTRVMPVTPQLRNDGPMLTFWCSSRNSFAMHVLGKL
7841	21742	A	7901	19	454	VVCNSSVSIHTHTHTHTHTHTHTHTRSWVGWHMPTVLSTQEAEGRLLGSGSLRIQRAMIVPLHSSLGNAARPCV*HTGCCVVSQAGVQWHNHSSLYPQTPGPKQSSSLSLLSR*DYRHVPPHPASCVCVRVCVCVCVCVCVYGDRTGTPH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7842	21743	A	7902	3	393	DAWDPLNPLVNLVSPKRNSSLDTRKKP CRESKKFNTHSRPKSSHQLRKRSSSTPT T*KIPNI*LNSSTPSRAKKRKKKKPKK KK*KNSQKKKKPMRKTKKKKGGGLKKI LGGAKFFGGRKEKIFFF
7843	21744	A	7903	424	139	LLLLLLLLL*G*GFVIFCVGVGL*LL TSGDLHISASQSAEIRGVSHHAPPLSLI VVFISQCVGILNHTVHLQYIQCSFVHHF LINQEKIDIK
7844	21745	A	7904	1	181	SQ*LY*LLAANLFILT*IGGQPGSYFPT IIGQASGLYLTITLILIPTICLIESKI LKWA
7845	21746	A	7905	3	281	HAYAHASATFFVSTCFHGLHDIMGSAFL TMCFIRQLIFHTSKHHFGFQAAA*YWH FVDV*LFYVSIY*GAULKEPWGGQS
7846	21747	A	7906	1	84	PTRPLTMLPRLVSTPGLQSSQLSLPKC *DYRCEPACTAYSF*LTMPLRLVSTPGL QSSQLSLPKC
7847	21748	A	7907	3	392	DPDNYTLANPLITLPHIKPE*YFLFAYT ILRSVPNKLGGRLALLLSILILAIIPIL HISKQSIIFRPLSQSLY*LLAADLLFL T*IGGPRSYPFILIGQVAFVLYFTTIL ILIPTISLIGDRILKWA
7848	21749	A	7908	2	231	GCVEKGTLSHC*WECKLVQPLWKTWVGF LKEKIDLPDPAIPLGIYPEENKFTL GPLHSVGRSSRKLPGYSRV
7849	21750	A	7909	529	297	KIFIGAPVFCPPPHFFFLIPPF*GVEKI FFSFFVLLPPGFFFLFLGLFFFFFKLFF FFFFFFFFKIPFFSKKVGVGK
7850	21751	A	7910	410	61	FNNQAMQVFPFPLKIFFFP*RV*FLE GGWSNLSPPK*GPSPKPTRVL*GPP* GKN*NFGFPG*NWAPHRFF*RAAPFFFF C*DRVLLPRLVSNS*AQVIHPPWPKVL GLQA
7851	21752	A	7911	512	314	ANFC*LFITGFPFHIGQAGLELLTSNPN PALASQIAGTTGVNLRPQDFSSYSEN PLVYGSLYIA
7852	21753	A	7912	1	264	SSTTTLLSRT*NKLT*LTPLIPSTLLS LRGLPPLTGFLPKWAKKKKKKKKKKKK KRGGGGWKKPKKGGGETSSKDTFFK KGGP
7853	21754	A	7913	416	129	FFFFFFFFFAPPKIKTPPFFFKREVYIY* ALSVFQSVCKALYIHFRIISSQYPC*LG FFFFFFFFFFFFFFFFLKGSLDLLSAYCVP GALHTLSH
7854	21755	A	7914	397	34	IFSNLFFPPQKKMFFPPPLKYFFFSFT ALFFFLVFPFPPPKIFFFNPPKFF FYPS*KKKFFFIPIVYFLAPPEFFF*AP PPPPPPPPPPPPPPPPPPPPPPPPPPPP FSVSKQPLFCLKI
7855	21756	A	7915	396	86	IFLSPRK*GFFSPPPP*KFFFSPPKPLIF FGGFFPKFPPPKKNFFQNPFGVFFYPP FKKKKFFFPPLNFGPPRVFF*RPFF FFFFFFFFFFFFFFFFLWVC
7856	21757	A	7916	351	112	FFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFF*KYVFIYISLSLIPCKFLK GRECDIHFCDIQHSYSKYLGHFKCSTND RQMNK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7857	21758	A	7917	445	2	FFFFFFFFFFFFFFFFLSYF*LIHYAEGIG ASPCYIMLGYNFSSFP CGTISIAPGFNF YRLYFISHASADAWVDP RFLDRYRRGIN
7858	21759	A	7918	2	407	PPPPQVYFNIWRTIFFGEGLLHIFPQK RFCFYKTYTNYIKTLFIKKNI FSLAHI KMVPPRSIY*TPPPLFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFL
7859	21760	A	7919	107	11	KMWYIYTLECYSAKKKKEILLFDTTLI NLKDIMLSKISQHRKHT*FKT
7860	21761	A	7920	1	70	FFFF*AAESCSRIKSGTTIIAQCNPELP GLSDPPTSAT*VAGTKGVCHHTQLRFIF IV*LSGRILLQDQVQWHNHSV
7861	21762	A	7921	123	260	GIQARKEPGAVAHAYKLSTLGG*GGWIT *GQELETSLVNMVKPCL
7862	21763	A	7922	184	399	LHLLMRVLKKKKKMGGLYRSPRGAKVN PALQRLDLSLIGSRILSNLIGFKAPHS WGG*AFFAATGLHGLHVIIGSTFLTIGF IRQLIFHT*SKHHFGFKADD*YWHFVDV A*LFLYDSIY**GSRILSNLIGFKAPH SWGGTKWDNPPPDMS
7863	21764	A	7923	2	407	GRVGM*EAFASKRKVLIVEEPSINLE* LYGCPPLHTSNKKPPHTKKKQKKKKK KKKKKKKKKKKKKKGGGLLKKLWGGPK NTGGKKKNFFFWGGKKKNLGDFLKKNL FWGGGKI GTPPPQKNPLGEKKF
7864	21765	A	7924	1	398	PTRPPTRTSSRSRAPFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFVSAALFFGKKKNFFFFFF*F *GFYFFPPLYFFICGGGGVFFFFFAGW NIFFI PPKNIGIFKTLRGKG
7865	21766	A	7925	2	335	NLTFFPQHFLGLSGMPRRYSYDPDAYTT *NILSSVGSFISLTAGILIIIFI*EAF SKRKVLIVEEPSINLE*LYGCPPIYHTF EEPSIKKKKKKKKKKKKKKKKKKKK
7866	21767	A	7926	1	328	RTRGRTRGESNPSLRIONSPCHLSHPIL KKKKKKKKKKKKKKKKKKGGPLKKNPG GAKI*PGPKKNLFFKGGLKKTPLGNFE KKPFFGGGKKRKKPPQKKKTLEKKKF
7867	21768	A	7927	27	226	LSR*KM*NKSHIYSFEKKKKKKKKKKK KKKKKKKKKKKKKKQKENRPKNGDSEN GHPKSKIFWL
7868	21769	A	7928	398	2	GGGGGPGGRGP**NPHKKEGRDPPHPK KKFFPRRKNRGGGGRKSPQKKKAPQ KKPGRGFKRAPQKKKTTPPPRKGPPP KNFKKGAPPPPPPPPPPPPPPPPPPP FFLGILARTTTTNDMKNHR
7869	21770	A	7929	3	156	HASAHASAPV*SVLMTAVLLLLSLPV LAAGVTILLADRILNTTFDPA
7870	21771	A	7930	405	249	ASAHASAPLV*SVLITAVLLVLSLPVL AAGITILLTDRNLNTTFDPA
7871	21772	A	7931	921	699	DHPGQHSEILSLQMKMTMSQCGAHL*S QVLRRLRREDCLSPGSQSCSEL*SHHCT LACETE*DLVFQKKKF
7872	21773	A	7932	423	259	HDLGSLQPLPPGFR*SSYLCLPSSWDYR CEPLRPAQRGILMAATSRILTRSKGW
7873	21774	A	7933	395	35	PRVKRFSCFWLPSKWGPRPAPWPGYFC FFC*NGGSPFLPGGSWTLAPNYSPPAP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QNGLVQALREPPGPPTFFFLIFPTKAPWS WPFPGGKKKKLSPKGHSERHLHHKYIR LLSQHGGM
7874	21775	A	7934	1	118	NF*IFCRDWGLALSPRQLSNSWPQVILP POPPKVLGLQA
7875	21776	A	7935	322	383	KKKTGLIKISTLCFVKNTFFKTKWQAPE RKKKVPIFLSYKRPVFKIYKKLFPFCRK KIKKKIPPPGFTSFSCSLSPSSWDYRHP PPCPVNFFCIYNKNGVSPG*PG
7876	21777	A	7936	3	131	GFHRVGQVGL*LLTLGDPPASASQSAGI AGLSHRSQPLTWSL
7877	21778	A	7937	334	146	HPQGLNI*NMVSSSGAKHSRSLSPKW WDCRQEPVPCPVIMFLKRGINHALYSPSR KLLHFL
7878	21779	A	7938	2	371	SEPGAGYNLLVGRF*SPSEKCSIGVGV RFSRCCLSPSLTGKNSLTPCASRVRO CLALLWLQGVVHPLSCTHCLALPSEM NVPQMEMQKSPICADAGSCRPELFLF GHLGSSPQSKL
7879	21780	A	7939	2	95	RLNLGGGGCCCEP*SCHCTPAWVTKRNSI SKK
7880	21781	A	7940	1	191	PTRPSQTPGLK*FSHLSLPKSWDYRCEP PCLAVILSIPQNSSMPNIFAASYSS*F GLYSSRW
7881	21782	A	7941	127	383	SKDCVRIVLLRAQAKAGSYRTVNWCRPG AVAHTCNHSTLGSRGGR*GHEFKTSL GNIVILPLYKKNKKKKRGARLKEPNLT P
7882	21783	A	7942	235	3	KNILPGYFCFFLREKPPPPGLESLFSKK KKKKKLARHGVAPLLGRMR*EDRLRPGV QGCNELWWCHCTPAWATEQNP
7883	21784	A	7943	3	225	EHGSLYPPTPGLKQSSYLSLSL*DYR* AAPCPANFFIFNFI*REDLTMLRLVSN SWTQAVLLPPKVLGLLV
7884	21785	A	7944	2	232	TLLPDNLSTIYPNKKKKKKKKKKKKKK KRGGPFKKKKF*TRGGGKKNFFFRAPKI FFGGRVLKKGKKKPGPEPTN
7885	21786	A	7945	394	41	WCRWLETWGAGGSGAVPPPPPPPHSSS WDLALQGGSGASSPFGAVAHACNPSTL GGQGGWIT*VQEFETSLANMMKPHLFSK KGPVTAVAHAPAKAHAMWCTPTMHMTOH VLHVL
7886	21787	A	7946	405	100	FFFSPRFSSSLFLFLSSFFFFFFFFFFFF FFFFFFFFSTGLFVYWSPTH*SLPVPRIFFF SYLWQTEVETMLGTE
7887	21788	A	7947	391	212	KEMQIMPAMR*HLPVRMVITKKS KAKC WQGCBEKGTLAHSWWKCKGTAETGKLAG F
7888	21789	A	7948	106	301	LQLPITQLVWHSTIYFMKKIRYRLGVVAH TYPNSTLGGQGGRIA*QGVFKTSLSNTA RQKKKKKKG
7889	21790	A	7949	342	208	GLGAGHTYPNPSTLDN*GGWITSGQEF DTS LANMVKHHVVQTGQF
7890	21791	A	7950	391	21	RQGFPMPLRLISNS*PKGSAHLSLPKWC EYRSEPPSLATWYVTLSRHFCSTLLLGQ GRSKFHMKWESRLEGLLAKVSSLRSSYC SSLRILGLEILLSPLLFLETGSGSVSQ AGVQPLCPGLK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7891	21792	A	7951	146	355	ENIRQTQNEDEVVTKSSNETVFCNKNIITSLGVVAHACNPSP*LGQGRIT*AMEF*TSLDNIRPCLYQK
7892	21793	A	7952	289	327	KGIPPLPRLKDKGPPFFFFFLKRESLFLP*FWKNGCRGPPLFFFFFLRDSVSLPLRLVSNWP*VILLPQPPKVLRLQA
7893	21794	A	7953	861	586	DRVRSVAQARLQWHDLGSLQPPPPGF*QFSCLSLLSSWDYRRMHTWPFVF*WRWGFTCVAQAAGLDLLSSDNPPALASQSARIIGESCCVLLK
7894	21795	A	7954	402	52	PRKVSIS*PHDLPASASQNAIGITGVSHRTRPSFNFSYIETAITETRKSLQSPGMN*SLPSGMVGFKPHSFHISANFCEALAVQQTILGEVPGHAPLSPPRQEPVCPKVKCLKTALK
7895	21796	A	7955	259	3	YNTKVLSPFILL*TFLKHLWLGAVARAFNPSTLGGGGGRIA*GQEFKTSLGNIERCRLYKNLKLFLSGLFLMAWRGAKRVTRTG
7896	21797	A	7956	171	386	LPIRLFSLVFTTIEKSRPGMVAHTCNLSLLEG*SGWIT*AQEFETSLGNMAKLSLPKIQESASLITRSQNK
7897	21798	A	7957	397	283	PQPLPPGLKQFSCLSLPC*DYRRDSARPAKKNPTFNK
7898	21799	A	7958	169	324	GTHRVEMCQWLGVVAHACDPSPLGGQVRKIT*AQEFETSLGNIGRPCLYIK
7899	21800	A	7959	290	397	DCSSCCSPLKGR*RG*AQWLTVPVIALWEAEAGGS
7900	21801	A	7960	496	298	LSKTGSLYVAQSVVYWLFTGTIMVHDSLKLLCSSSPVVSAS*VAGTTGAHRCCCVLTTFQPDVYRL
7901	21802	A	7961	404	174	PGPQKGSFF*KKKKKKKEIDHILSHKANLNKC*RIKII*TMUSDQNEIKLEIIIKRQLLKETLFLEMKKYTIRKLS
7902	21803	A	7962	25	99	PGLFLSS*HQVILLPWPVKVLGLQL
7903	21804	A	7963	436	106	GGGKSPPPGNWAPPNGPPLFF*KKKKKNPGGGGGRFFPPPPGGRKKKGVPYGGGGFYLTNFP PPPPWGKKKNFFFKKKKKKKKKGRIAICYIILFITSINFKKAIFI
7904	21805	A	7964	212	395	ERERKERDRGEREREREEREGRKKHGR*GGREGERHRPRGAEDPDGRATDKRTGAL
7905	21806	A	7965	344	345	FSDCYKRSSCASWTWYTRLAHHQPPARPAAAPSPKRWVDFAVNRNFPSSRRHPCATPRPAPGATGRPSRVPKSTAFTQMLTQPRDPHLPLPIPLSQPPSP*PAPLVMR
7906	21807	A	7966	397	298	RGFTMLPRLVLNSRTQVI*LPWPPTVLGSLSIF
7907	21808	A	7967	92	268	IKMSLCPNFFFFFFKKQNVGPRAGAYPCNPITILGGQGRKIT*GQDLKTTLVNMGKPHYFY
7908	21809	A	7968	257	107	RTHTHTHTHTHTHTHTHTHTHTCENSKTKNIANNCS*LESQRNNGKCTYAKF
7909	21810	A	7969	413	12	PPPPPLTPWPCFFPQIL*PVGHSAPPLFK*LKIPRPFFFPKIGAPPPKIFFPPGFSLPPFVKLPPGEKILFPKPKKKYPPPPQS*SF*PPPPPPFFFFFSTSAKSKKNFLFIFSPFFNPKYYNT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7910	21811	A	7970	399	212	TGVQWSNHSSLQSQTPGLKRLFLLLILLS IWDYGCMPYPYLSFKN*FCTKGGSCYVAE ADVNIL
7911	21812	A	7971	584	424	RPRRENRLNPGGGGCSEPRSRCTPAWV TE*NSVSNRNKTNQNPIFFSCKQFD
7912	21813	A	7972	105	1	PSMPQLSHL*NGILGRVRWLTPVIPALW EAETGRS
7913	21814	A	7973	363	28	SSSLGGHPQLWFHTLKLRLPVTVSYA*NK LCDKIEKKLFFTIALHNKFLRKKLTRDV KILFNKK*IKKEGPNEF*NILCLWIERI NINKVPYPYPSKVMYRSNTLP IEVAVFKSQ
7914	21815	A	7974	404	250	FFFFW*R*GFTMLPRLVLNSWTQAIHPP ALASQSAGITGMSHHAQPLSIIF
7915	21816	A	7975	2	60	FSCGLGLPFCWDYRHAPPHLANFCRDGVL NY*PQVIHLPLQPKVLGL*ACTTTTPG
7916	21817	A	7976	325	81	KTIHSLFLGQFFLLQPLLSPPIPHAAPP TPHLIFLLLLFCF*FFK*RQGKQGLTTL PKLISNSYSQVTLPLQPKVLGFQA
7917	21818	A	7977	406	282	QWRDLGSLQPPTPWFK*FSSLSLPNSWE TKAGRSREPGGD
7918	21819	A	7978	382	221	DCIISASYLQKNFFFFLGDVKLLCHPGW SAVA*S*LTVTSKRWHFYSSEISLY
7919	21820	A	7979	423	29	FLW*RRGFTSLPRLVSNFWAQGICLPWL PKVLGLQA
7920	21821	A	7980	3	238	SLAFFVETGSHFVA*AGLELLSSSNSPA LASQSAEITGVSHHTQPE*GYSHM*PQY PYQLRFNSDTIILSNVLFVNF
7921	21822	A	7981	324	128	WLSVSPYTFELSLLVGYEFVIHVDI*TL IFVVVVVSLFCFLWFFLVCMFVVFVFC CCFLSVFCI
7922	21823	A	7982	1	86	NLTMLPRLVSNWSAQAICLSWPPKVLGL *AQAICLSWPPKVLGL
7923	21824	A	7983	1	137	RPAFCIFFVETEFCHVAQAGLELLGSG DPPTSASQAGATTGMSH*D*PANFCIFF VETEFCHVAQAGLELLGSGDPPTSASQ AGTTGMSH
7924	21825	A	7984	2	277	PRVRSVQRVIYQYV*NLQIHVPFDSTNL GIYLTDLPHVWNDNMVYVFAAVSFVIA KY*NPCLTRRQCCKLWPIHAMEYVVTIK KNEDGRA
7925	21826	A	7985	211	42	GPQKWPRGPGENLGGFFFFFRCRDDGL TMLPRLALNS*VHAILPPQPRKVPGLWV
7926	21827	A	7986	409	183	LLRLK*SSHLSLPKWWDYRCEPPCPAIF FKRKQILKESFPGENTCCHLNFNSLEVLK NKRRTCYNFENTLAVLKNM
7927	21828	A	7987	2	194	RFFETQSRLQLPPPPQLK*SSHLSLQSS WDYRHVPPCLANFFLFWYFLQGQGFAL LKLKFLFK
7928	21829	A	7988	483	209	SSPSLGNFCIPSSGGVSPCWPGWFQTPD LVIWPPGPPSLVFFFFFFFRDEGLSMLLR LTLNF*AQVILLPLQLPB*LGLQADRQVP LYPAEVF
7929	21830	A	7989	164	29	KFWFWLGTVAHACNPISILGSQGRRIA*A QELEPSLGNENRCPCLYK
7930	21831	A	7990	3	474	PTRAPLRAPFETIVQEEFSSKHHPGFEA AA*YWHFVDVV*LFLYVSIY**GSPPPP PKILIKNGAETKKFFF
7931	21832	A	7991	469	323	VETGLHHVAQDGLLELPTSGDSPASASQN

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						IGITGVSHHA*PDFTFLEQF
7932	21833	A	7992	469	13	KGDTVSSSDSSPSCGGLFPVGAS*LLCL FTQALAMVGARRPFSMLPCSLISDCCAS NERGSGVMGPKSPKPGVGYSLVCRWLRLPL EKRTIKVGVTRFSRCRLSQLPLARKGNS LTPCVFWVRHCFGSHSVGCTHCPAPAVR QAPVK
7933	21834	A	7993	15	439	IASGRPFSIKFFLVAITFLFDLEIALL LPLP*ALQTNLPLIVMSLLLIILAL SLAYE*LQKGLD*TEPNKKKNKKKQKE KKKKKKKTKTKGGGLLKKILGGAPILW GGKNMFFFFWGGEKKTGPGFLGENLFLG GGK
7934	21835	A	7994	392	186	YFYIINNFFFKKIFI**IFFFLKKFL *YSPKKVFFLFF*IFFFFPSSSLFLFF SSSSPFFFFFFFFFFFFFFFFFLRG
7935	21836	A	7995	11	386	TWEVEVAVS*DHAIALQPGQE*NAISK KKMTGRMFIEVSFIASSWKQLKCS*TG E*MKSLWYIHIIEYYLTIKENKVLEHEV SRLTLIDTGRERSKTKEYTLYNPIYTNL RIAKLSGCGGSHL
7936	21837	A	7996	3	186	DSFCF*RQSCSITQAGVQWGDGRSL*PQ SPGLKRSSCFSLPKHWDHRDEPLHPAGV AVLN
7937	21838	A	7997	316	649	RDHSFFFEMESRSVAQAGVQWHDLSLQ ALSSGFMPFSCSLSPSSWDYRHPPPCPA NFLYFLVEMGFQHVQNGLDLLTS*STR LGLPKWLGITGVSHWHPAQDGGFHHVG
7938	21839	A	7998	468	336	RRGFTMLARMVIS*PSDMPASASQSAG TTGVNHHIRIHRSL
7939	21840	A	7999	464	283	TLCGGIRPTNIMKGNLLYSKISGLNVSL LPKNPRRNQNNV*PNTWALQPSHVDI
7940	21841	A	8000	46	487	RQRLSLQKFLLPFVQLCPAHRGGVYRG RQASLSCGGLHPVRVSPQLCLPT*VSAM AAAPHPASLLPCSLISDCCASSEQSSVG VGPSKPGAGYNLLVCHLLRLLEKRSIRV GVSQFSRCHLSWLP LARKGNSRTPCTFR VRRCLAL
7941	21842	A	8001	295	1	TQPWGTRKRLPLKKKKKNSGDREWRWLC NSVTILNATMYTSEWLRPGTVTHCNP KTSGG*GGEIA*TQEFKASLG NIA*SWL YKKILKISPLWWQT
7942	21843	A	8002	144	317	ELFYLKEMV*RPGPVAYACFPSTLGDGRG GRIT*AQEFRTDLGNIRPCVYLKKKK RG
7943	21844	A	8003	69	291	HCVWTMIFIVIKYFYLNPNQNSMRYYS HFMDKETDVQSD*MTC*RLGAVAHACNP STLGRIA*QGEFKTSL
7944	21845	A	8004	3	176	IVAHSSLTPLGLKQFSCSLPSS*VYRNM LPRLANY*FFGTNRVSLSCQGS*TLAS LLGSSSSPASACQVAKSTGTCTYHAWLII DFLVQTGSRCLAKAGHELCSCL
7945	21846	A	8005	419	178	NPPPKKFLSSSSSSPLHLNWGTPGFF PPPPF*NPPPEFNFGAPKKKKLSPRA EKLVPFKGPPPPPPPPPP
7946	21847	A	8006	429	225	QPLPPRFK*FFCLSLPRR*GHRHRPPHP FNFFFF*YFLRWSFVLVAQAGVQCMDLS IYLNFEFWLLDF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7947	21848	A	8007	756	224	PERHQPOHVPEPPLLHFSTPSPAPPKSHA AAPNSNPQAHAPPAPPAPRAHSPSPPP RGATPPFPFPFSSFLAAVGRAPIFPREP LLPSSSSPPPPP*IGPEPPGFSPPPLKKT RPPK*N*GPPKKKNFFPPRPKNWFL*K GPPPPFFFFFLLRQSFLLVAQAGVHKT RLHLKKKSN
7948	21849	A	8008	170	559	SSHLSPQSSWDYRSGMVAHTCNPSMLGG QDGRIT*AQKFQTSGLNIVRCHFVFKKY FKNKIFFYSPFINTNPKKKKKGGAVLK NQSLRPRAGKVLVFLWGHLIQFRGPRFK NGGTGKPGGLEPNLLAPR
7949	21850	A	8009	1	662	RTRRTSRWWYMPVLPPLSHYGEAGESLGP *KWMVD*APIAPLHSTLGDKMTLPDIKK KNGETVANTSPLSTTAKPAKLFLKAKKD QLMRDLFLPKTPKKPQMTGLDARSKRW LKIIWRRHGIWPLKNIGPTEDVQASAHG GVEENMTSDIEIPEAKHHRPTEDVQVS AHGGVEENITSDIEISEAKHDDLVEDL SESLSVCLDEFMTIGSQWKPICLS
7950	21851	A	8010	377	2	NFFFFFFPFWGFFFLGPGFFKVF*IF PFFFPNPPFF*FFLGVLFFKK*IFFF PFSIRFCFFPKKFFFLILFFFF*FFFF FFFVYVDFEFSFILIYIFFVYFSLPFT VLIISLIYHFAPA
7951	21852	A	8011	1	363	PTRPLF**RGCFMTLPRILNSWPQVIC PFRPPKVLGLQT
7952	21853	A	8012	278	39	FXXXFFLSPPXFLIFFFFFFFFFFNFFF FFFFFFF FH*DQ*FSNFDFTPFTLISNII
7953	21854	A	8013	79	412	MNECILGKGKDGFFEQCENLGLC*FL KVP*DSDIWLGAHAHAYNPSTLEGQGER ST*AQEFKTRLGNMTRPCLYQKHTHKKK TKKKPHPGLGWANGPTYLGGVGTKIT
7954	21855	A	8014	277	19	FGNIHNFFLIGSRSVTQAGQWCNHSLS *PQTPVLKQSSHLSPSSWEIEAAVSQV RITALQGRQSKTLPGNSGPVLRADARR SI
7955	21856	A	8015	1	130	ARIVSIS*PCDLPASASQSAGITGISHH TQLAHNTLKASPTLF
7956	21857	A	8016	4	417	RLMPPHLANFLFF*RHGFTYVAQVGLKL LGSNDPSASTSQSTGTTDVSHCTQPHLL KSSHSTFPLKTLDSMATNCSDWKVHYLP TACRALLPCPLPSACFPPLSQVPSVFTC CVPATLTITLLPLLRAFEHVTLCPLE
7957	21858	A	8017	388	158	CVTWASNCINWICFPLS*INSHLCNEIT VLI*GEIYNVCISIYLCIYMCVCYIYISV CVCVCYIYH*TPYLIHKCLI
7958	21859	A	8018	154	382	GIKRPGAVAHNCNPSTLGG*GKWIG*AQ EFKTSFGNMVVKPQIYLLKKKKKKGAVLK DPSLRPRAGKVIIVFFWGPLI
7959	21860	A	8019	396	237	FFFFFFW*G*GFTMLPRLVSNWAQVIH LPWPPKALGLQVRTMVPGRLRANF
7960	21861	A	8020	412	168	GNLLGSPLPGNVCKNKPFI*KKK*SL AVLPKLVSNFWP*MILPPWPPKI*GVQA RAPPPSQILKKKKSSHFYNSHVNSL
7961	21862	A	8021	1	124	TRFLHVSQAGL*LLTSGDLPASASQSAD YIFIISPAKIIFL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7962	21863	A	8022	3	200	HLSPYFYFFKDRVALCHPGWSAVVQ*PI VTSIFWSSC*KLTSVVRWRPSWLTR*N PVSTKNTKN
7963	21864	A	8023	3	132	FLFFFQF*FMRLGLAMLPMLGMNSWA*V ILLPQPPEWLGQA
7964	21865	A	8024	3	187	VGQAGLEPPTSGDLPASASQSAEITRMS HRAQTK*DFIGSFSEEF
7965	21866	A	8025	405	231	SDKWIKKMRYIHTTEYY*ALKRKEILTH ATTWLNLENILLSEISQSPKHRYVVIPL T
7966	21867	A	8026	175	382	GKRIFPPYPYPQEGGKTGPPQTPGLFFFF LKKK*PGGLGGARFSPPLGGVGRKNSFT LKGGGAINLKGPPLPPGGKRWAPPQKK KKKGQAWWLMPIPALWEAEAGRS
7967	21868	A	8027	83	374	GDQVWVLMHACNPSTLGGQCGRITWDRE FETSLANIFFPISTKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKASSGGGVS*K KNFSPRAGKEIFF
7968	21869	A	8028	382	148	SPHCSLDLVGLKQSSHLSPST*DHRCV PPRLAIFSFAFLFFWEATTTTKATMLP RLVLNS*AQAILLPQPLVLR
7969	21870	A	8029	88	208	SGSV*ENNPLSWAWWLQSIIPATQEA EV GRILLEPRSSRSA
7970	21871	A	8030	1	283	NKSRIKKAIKMTEKMKKEIEMMKLMNQL PNGEHAMIQMMMKIEMKGRMKIKE*DK ESDKDDRKDEREDRDETDEPTPERRTS RDDSDDDEDREDEGKNEDEKDDSKDDDE ADEDTDQDDYDPMDAHKADEDDDEDED EVAEQMTKKKKKKKKKKKKKK**KDDR KDEREDRDETDEPTPERRTSRDDSDDDE DRDEGKNEDEKDDSKDDDEADEDTDQD DYDPMDAHKADEDDDEDEDEVAE
7971	21872	A	8031	2	139	LQTLPLIAP*LLASLANLALPPTINL LGELSAQFAVIGMYILY
7972	21873	A	8032	80	324	YLHFFYFVR*KLMGLDTVAHTYNPSTLG DPERRIA*A*EFKTSLGNMVKPCIYKK KKKKKKKKKKKKKKKKKKKKKKKKK
7973	21874	A	8033	299	158	GNQPGASAHTCNPSTLVGQGGRII*AQE FKASLGNMVKHYLYQKHKN
7974	21875	A	8034	416	60	AQWLTSIIPPL*EAEVGGFFEPRLSPA WATE
7975	21876	A	8035	398	271	FYFL*DEVSLPRLVSNWTPAILPPWP PKVPGLRHEPPRA
7976	21877	A	8036	385	151	FLYFL*RLGLTLLPQLVSNISSDPPT* ASESAGITGVSNHAHLRICILTRLPGNS SH*NVRAGLGDTQSSALIPPG
7977	21878	A	8037	3	406	PASAS*VAGITGTHHHAQLIFVFLVETG FLFFFVAVFLFFKTKNGPPGGQLFFFA APPALGGDFGGQGFSPKGLGVLGET RGGAPAPKKLGAKKEPSHLLGGGAQNLP KPRGQKGFYFYFLARDFFLG
7978	21879	A	8038	428	20	LANQ*WKPPSNPWETKISPKKKKGPPGQ GPPPLTPPLWEAPKARKLGSPWLPR*NP LFPQPKKKFFGFGGPPYSPLPQKLSPK NGVTPEVGPSHKPKFPSPPLGQK*TP FFPQKKPKRLKRGMFHGSTFQSL
7979	21880	A	8039	3	194	QNKISQVWWYTPVILATWEAEGGESVEP GRQLW*AKTAPLHYSQDEKYLKASVDS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						YCLISCH
7980	21881	A	8040	415	96	LEPL*KYFPILDAIKNICDSWEEVKIST LTGV*KKLIPMLMDNFPAFKTSMEKVTA DVVEIGELELEVEPADVTELLQSCAKLE GMRSCFLWMSKESGFLRWIYSW
7981	21882	A	8041	413	254	PGFKQFSCLGFPKR*DYRHKPPCPASKY FKINYLRNTYRSLILKN
7982	21883	A	8042	409	102	GFFPFGPFFF*PPPPGVFPPPPPPNFWF *GFGPPPPPLF*FFFRGCPKKIWFPPFF LWPPPLFFFFFPWPCKTTPPKKARSLKIF FFLGPKKIPNPPPPPPFF
7983	21884	A	8043	414	153	GRGWATNFYFFLIILK*FFFIFKKFFFF HLFFFFFFFPPPPPPPPPPPPPPPPPPPP LFTLVLTCPQTSCEABPFDDHKVCSVLK ML
7984	21885	A	8044	401	292	NYLPPQ*KKKYYPQGPFRKPIKKSPPPC FFFFFFFFFSPFPFPLNIPPPQKGFPPK KYFFNPPLFPPLFFLKPPPLFFF*GPKK KNLIFHPPSKKICPFKRGPP*FFFFFFFF F
7985	21886	A	8045	370	14	TPPPTKTFFFLYPPPWREKREGFF*K NMSPPVWKKKIPPLPPYIYL*KGGSRYL AKLSLNLKGSYLSFCFPPLPPSLPLSL FERWGLTILPKLVLSWAQMILLPWLPK VLGLKV
7986	21887	A	8046	395	268	PPFFF*ETGSCSIVQGVQWLTGTILV LISVGVLTCISIDL
7987	21888	A	8047	379	98	GPAHNSPPLGGESETPLGYPGKPRFF*K NKKINPARGPGPVVPPPPQG*AGKRPLP PRRGFQLTQNGPPPPPPGKKKPPFQKK KKKREPAIC
7988	21889	A	8048	369	177	RNTRGGPTFFFFFFFFFK*NLARLSRLEC HGTISAHCNFRLLGSSDSLPLTSNDIGQ INKSLFA
7989	21890	A	8049	1	128	ALGLVAHAYNPSTLGSQRGKIA*GREFG TSLGHRARPCLYKK
7990	21891	A	8050	166	163	PVHQGEQT*QDKCLR*STHLGLPKC*DY RREPPCQASKLVPTGILADSKHSCQTM DSCFSNQLYKQR
7991	21892	A	8051	402	245	YFKSVCQAQWLNTYNPSTLGG*DGWITC GQEFRLPWPSGITGASHHAQPHFF
7992	21893	A	8052	404	268	QQLWRLRQRDCLNLGCGGCSEPRSCYCT PA*ATEPDPVSNKQINK
7993	21894	A	8053	1	154	GFLRVGQAGLELLTLRLDPTSASHSAGI AGVIYRAWPGEAYLFSG*WLRFT
7994	21895	A	8054	406	150	PKKKKNPCPPPEVKFDSLKRAPLFFFFL EESCFVTQAGLECSGAILAHCNLCLVGS SDSPLSL*RWVGNSHFIFTSLLSVSPRS N
7995	21896	A	8055	1	125	TAVILIFMI*EAFASKRKVLIVEEPSI NLE*LYGCPPPTH
7996	21897	A	8056	400	260	HMSPHLAFFFSFLFL*RLDMLPRLVSNS WPOAFLQLLLPQVLGLQV
7997	21898	A	8057	396	263	FLQPGTVAHACNPSTFRGGLIT*AQEFK TSLGNKVRPCLYKKQY
7998	21899	A	8058	402	211	FSCWCTKPKAAG*FPAPWGPPLNNPP GAGTNFPGPSPSGGFGSPPPWPGRPRP CPNGIFFC

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7999	21900	A	8059	1	279	VLLYHPGWSAVVQSWLMQ*TPSNADIWR IARGFKRSSHFSLLSSWDHRHVTPCLAN FFLIL*IWGLAMLSRLPLRLRKPVLLD *APSPCGLI
8000	21901	A	8060	408	315	SLTMLPRIVFNS*AQAILLPWPPKVLGL QV
8001	21902	A	8061	198	2	RIQHVESNCHLEVEGGWAQWLTPSTLGG RGRMIS*AQEFETRLGNTPRCFYKNLK SQPGMVVRI
8002	21903	A	8062	3	294	GLSPTAHPITAFTSQPLPSGLSVCRLFL WAMCEQCPLPIRPCCPRIIGPECALYT TSCLLHQLKKREGF*KKKKKKKKKKKK KKKIF*WGGGKK
8003	21904	A	8063	197	184	IHDFFLFFF*GRVSLCCPGWSAAQSRILT AL*PGELKETFYI*IRSWDHKHAPPLP APF*LFWVTLIITPSTHEVSSAVCSLLY VKSEQKCQ
8004	21905	A	8064	3	373	TSGSLAKRPADCLSAQPTFPSSLCGCSP VRVCITVPRCTHARAHTHTHTHTHTHTH SNHG*APGALYIQELQRGKVSHVPEKEK SDPETA*TKGG*HVTNPHGRQSRGEE HRI CVGRCCSG
8005	21906	A	8065	532	106	ENKPIHNLSINKYIGKILRDKALLYCPG WRAVMQS*LPVASNSWAPAILLCPGFLS TWDYKRVPPQLVKIFSKKKKNKPTNILR PKCHTRNQDIYKRGKVGFLCSYCPALL LLLSLLLLLLLLLFSFSTRDSASGACSS LP
8006	21907	A	8066	411	130	PHAQLIFLRR*SLTVFPRVVSNSWPQAI LPPWPPKVLGPQARAMVPSPKLVLESIL RIPTSVIFFPLNLCNKLAEIKEGCSA AFLFNQRFAN
8007	21908	A	8067	3	32	DAWADAWGSLTDEWVEKIWIYHAMQYYS SFEKREIL*YVRTCMNLEDTMVSEIRQS QRDDYCMIPHI*GRTRGVH
8008	21909	A	8068	410	116	STFNITQWPGTVAHTYNPNTLEGQAGRI T*GQELETSLGNITRPNFLFCQACPGQ GLSTVRMCGSLHYFVLPLRPLLKCLDNR KSPFFYHPVILPCYE
8009	21910	A	8069	158	289	DLCSLRNIVRPQLYKK*KISQVRKKKK KKKKKKKKKKKKKKKKKKKK
8010	21911	A	8070	388	1	AETPPCFLLFKPFVLGGPPFGKAFFQKFP GGGFFPSPISGPKPPPPRNPISLKGKRV PSPQSPIMVFPAGF*RPPPFPLMVG*KI KIFLPPPPPPKTPPALSPPFFFEAEFRS CWPGWNAVMRSRLSATS
8011	21912	A	8071	15	336	KLDKRYDRTGSPGTTHASGYLIEPLVAE ASYELILSLAFFFFFERRGLALLPRLEGS GVIVAHCTLKLGGSGGPPASAS*VAGTA GMNHHEGHEPGLFEKQNSGFIF
8012	21913	A	8072	396	274	PHLHTWESSL*RQGLAMLSRLVSNWPQ VILSPWPVKVVL
8013	21914	A	8073	189	54	NKPLGPGMVVQACNPTPLGGQGQWIP*A PEFKISLGNLAKPCFY
8014	21915	A	8074	3	257	HAFVLLFETRSCLSLRLESSGAMIAYCR LELLGSGDPLTSASQVAGTKGM*DDAWL RQVSNSWPQVILRLSHPHMFLFQFSLET
8015	21916	A	8075	1	119	TLPATWEAGAGGLLEPKSLRV*CVFTAT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VNSSRTPAWAA
8016	21917	A	8076	232	266	LPYCSGQWCLGLPIIQGVQWHDHGSGLQP RLPGLNQSSCLSLPKCWDYGREP*YLA* YQARYHGSLARQNVFNIRPGIMVHARSP STLGG
8017	21918	A	8077	390	143	LGGFLVFCPPAKKGFFPNPINLGTPRFF PPPPF*KPAPEINFGGPKKKKIPSPPPG VKFDPLKRPPPPPPPPPPFFIRLLV
8018	21919	A	8078	424	144	LKNYIFFTFL*NRDRVSLCCPRLVLNFW AQEILLPWPPKVLGLOA
8019	21920	A	8079	182	45	VHKAGMVAHAYNPSTLRGRGGWIT*GQE FETSLASLDNMVKPRLC
8020	21921	A	8080	405	163	YFLEEMGFHHDQAGLELLTIGDPPGGM SHCTWLNLNVLNIQKHPHRIQNNV*PH ISGPVKLTHEGNHHNWHMSTQKHSP
8021	21922	A	8081	39	240	QSKTVSKKKRKIIFCRYRVS*SPGFKQS SHLGLPKGWNRYRREPPHPASTFSQSPV KDHFCSGVSS
8022	21923	A	8082	2	263	DCCVSSE*GSVGVLSEPGAGYNLLVFR LLRPLEKRSIRVGGSRFSRYLSWLPLA RKGNSPTPCTSQVRQCPTELLGLHPLCD KPQ
8023	21924	A	8083	1	248	SVGVGPSEPGA*YNILVCCLLRPLEQHS IRGGVSQFSKYRQSWLPLARKGNSPTP* ASCGMRGPALLWLTLLGLHPLSNKPQ
8024	21925	A	8084	3	255	HLSLPSSWDYKRMPPHLANFFFFLKKK GVLP*GQTGLEL*N*KNPPA*PPKGAGV KGVTHRPKP*NGGKGRFEKDTGGGFL
8025	21926	A	8085	409	145	LRGPYKKNFSFQAPGRKIGSFKKAPPPF FFFFF*GQSLCCPVGLSTGVIIAHCSLE LLTSSDPASSASRVAGTTGACHCS*VLQ TFTF
8026	21927	A	8086	199	26	GFP PPPNKTEIF*RPPDFLNFFFLVEMN LTSLSRLVSNPWAQAVLLPWPPKALGPQ A
8027	21928	A	8087	222	3	SVGITGVSHHVLWYFTLKGFLGRGAHSC NNSALGGRGGWIT*AQEFETSLGVARH HLYKKYKNYPVAVVRL
8028	21929	A	8088	415	197	TILCFYHQNNVSFSSNPFSL*IFIF*D RVSFCHPGWSAVVQSWLTVFPILCATVK YFTCQQYIIMIFALNS
8029	21930	A	8089	297	71	FIFPENKNRPEVVAHACNTLRGRGGRT *GOEFEKSLSNIRPHLYKTKTQNILSK YIQYLGFLTLQIDLANIY
8030	21931	A	8090	185	415	PFGLKQSPHLTLLSS*DYKHTPPCRVNF FFFLGGFGFFPKAGFNLG*RNFLASPS KRAGMAGINNLAGPIFRFFKK
8031	21932	A	8091	2	125	RKQASKKERKE*KK*RKKERKKERKKER KKERKEKERKEEP
8032	21933	A	8092	8	412	KGPQGTTLTCIFDLSYSSSLSHWSQSLC VAFPLPECIFPHKPLCPACHFFQSWG LALLPKREYRGKIGVNGNLELLG*NNPP SGTSKIAEPAELFHHTHARPFNWIKTD FPYIAQTGF*LRPSRNPSTLEV
8033	21934	A	8093	249	143	NIFAATWMRLLETIILSEVTQG*KTKHQM FSLICGS
8034	21935	A	8094	3	280	PERWDYRHEPPGPASFT*LLLFVFNL*R KGLYVGQRGRQLLASSSLPAPASLSAGI

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						IRMSHCTPAWVTVRPCY*INK*INGKDT IRQNLKKM
8035	21936	A	8095	404	16	QMGFCLFFLPSSKEVFFFPPIFFFYRESF FLFHFFLDPRQY*LYFIKKNIFLPSPF IFFLFIRVSPYIFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFWGSME LSKAHQCISSHGSG
8036	21937	A	8096	358	200	KSYFIFSLIIFSHYFLLFLKHLATYY CFLIDCTLFSSFYCPFCCLFVLLSGRFP RSCL*TFH*RLYFSFPIFNQKLF*LS ICFCCIYLFYLFYFETVFCSCCLGWS MMA*FNGMFKDRI
8037	21938	A	8097	2	132	KEKKKERKE*KKRKKERKKEKREKKR EGGRKEGKEGKNSST
8038	21939	A	8098	48	331	PGTWHACLGGEDILKWQTKGRGRRAGSH RTSWIEPLETVFLELEAGGRLESPGK SRLGAVAHICIASTLGGRGRQIT*GQEF DTSLADFCST
8039	21940	A	8099	7	373	NGRLRRGFAMLARLVNLF*PRDPPT*AS QSAGITGMSHHARPTIESFIHCWECKM E*PLCKLILYFHLPIFKRQKLGWHCH SLLOPPTPGLQRSFRLTPSGWDYRRGP PCPANI*LII
8040	21941	A	8100	116	432	YLRNLFYQRQAFSPAILNLMCSAL*ESH TVAQAGVQWHNLGSLQPLPPRFKRFSC SLPSSNIFAPLSYFFRNSSTFNISPSEI GPQITDPLFIKKKIKVSMVE
8041	21942	A	8101	361	138	FNLLGRKKKNFGGLKEGESRRPPNPGPQ FFFFFFFFFFFFSG*RWGLTMLPRLVLNS WAQVILLWPWKSLGLEV
8042	21943	A	8102	1	199	PTRPFVFLMEMEFYHIGQTALELLTSGN LPASASQSAGITGVSDR*LA*YLFFPHE LFCYFALLI
8043	21944	A	8103	412	46	KGGSPPPPPPKIGRKGPNNPGDPFFFF SPFFFRGF*GSPFPK*KVLLVGLKPK PPFPLGWNPPPPVGGFSPQSLQFFF FKKVFGWVFFPLFFFFFFFFSPFLFS ETESHIIAQ
8044	21945	A	8104	192	2	EETELSFIIKYYLPRNQKVKRL*RRL GPVAHACTPSPLGGQREWITRSGVQDQP GQDGETP
8045	21946	A	8105	373	183	GGPF*FQYILILFDNFFFSLSFPFSQD FFFLSSFFFFFFFFFIINYFYF
8046	21947	A	8106	373	281	SFKTAPPPFFFFFW*RLSLTMLPRMVS NWAQVLLPQPPKVLRL*ATQRKKHFRQ EQI
8047	21948	A	8107	3	114	FLIFVHIGPNYVAQAGLELLSSDDPPAL ASQCAGITGMNHHARPYLL*TLNIPLP YDPEIFLLGIYPR*MKTYVHTKACT*FF ITPLFVIKTKQPK*PSVLGLQA
8048	21949	A	8108	416	243	PGVFPFPPF*NPPPEIIFWAPKKKYFP PPPLNPFVFFKGPPPPPPPPPPPPPP L
8049	21950	A	8109	2	211	SVTQAGVQWHVSLQLPRLPGLEQSSCLG L**CWDGHEPWHLALVTTSKHTESCSL LCIPTATFLGLVT
8050	21951	A	8110	172	28	HVVCFITSEFFGYFL*ROGLTKSPRLVP

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						NSWV*VILLWPVKVLGLQA
8051	21952	A	8111	2	225	QKSAKNFYHLSIYLSIYLSIYPSIYHLS IYLSIIYLSSTYE*VILEQKWNISIKKG CL*CTIQTNCL*QLKE*VIRLIPKL*YK IKLPTCWSVHLNWFLLCNISWYLYLAM **RKLVCFA*FVVYNSNKLITIKRIGH
8052	21953	A	8112	392	221	PFPKRESPPDKVNPPPPDIFGGGKTKKK TLANN*FPPKEKEFFVFFFKKEDFF*NI VGNFKTPSKI*AVCF*NPVFKKKKGAPK KKSSFKNF
8053	21954	A	8113	369	112	IFFSTIYFXHPFFFFPPPLFFTPPLFF FFLKKKKFFFFFXXXXXXXFF FFFFFFFFFFFFFFFFFLAF*HVV SF
8054	21955	A	8114	418	248	KYYLPTPGY*NLILLNGPPFFFFF*D RVSPCCPRLP*TPRLTQSSCLSLPRSWD HRCMPLRLVTF*FTFKLSHQSLRTLTY TLAGTTLG
8055	21956	A	8115	229	78	SFKGAAPFFFF**RQNLTMSPKLVSNS RPQAVLPWPVKVLGLHRGGWIT
8056	21957	A	8116	356	66	PLFPPFYIKNFKKKFFFFFYFFFPFP PKHYSHKDIFFFFIKFFPSSSFSPFPF FALSSFFFFFFFFFFFFFHA*FPVF FLYKIPMLYPQL
8057	21958	A	8117	212	81	ERLSHCSLNLDPSSNPASAS*VAGTSG THQLVMVHAGSPRF
8058	21959	A	8118	367	2	GVFFFFFFSPAKGVFFHPFFFLGPRFFP PPPPFFPPLWFYFWGP*KKY*FPHPRGY EFFFF*GGPPHFFFFFFFFFFFFFFFF FFFYAEGIGVSPCYIMLGYNFSSFCGT ISPRVRPRV
8059	21960	A	8119	38	215	FFKSAFHHTRLIFNFFFLEKTGSHYVA QAGVELLG*SSPTSAFEIGGITGLFLS FKN
8060	21961	A	8120	266	2	PQIFLFIFETRSHSITQVGQWCDHSSL QPONPGLKQSSLSS*DYRHTLTAPG*FC FL*RCGLAMFPMLVLSSWPQAVLKIHP CGMC
8061	21962	A	8121	3	332	DAWADAWGHVPPCPANFVFLV*TGFLHI GQAGLELPTLSDPPASASQSVFIYFLET ESHSPAWEATERDSVSQKKKRGRFKGS NFTSAGLQRFIFFMGPPKLISRAGV
8062	21963	A	8122	378	66	LFIFLPPIREEVFCIPG*NWAPPGVLYN GRPFFFFLLETVFLHAGQAGLELLGSSD LPVSASQSVGITGMSHRVQPKLRIFVNI SFPFEIFCEIMLLVPLAQP
8063	21964	A	8123	2	316	ISMLLALLLRITITRLPQLNGYVEEFTP YECGFNPISPGRAPLFIEHFLVDITFLL FDVQIALLLPLP*ALQTGNLPLIVMPSL LLIIILALRLDYERLQNGSD
8064	21965	A	8124	331	14	ITSILLIITTF*LPQLNGYI*KSTPYEC GFDPIPARVPFSIKFFLVAITFLLFDL EIALLLPLP*ALQTTNPLIGMSSLLLI IILALSLAYE*LQGLD*AE
8065	21966	A	8125	2	228	IIITTF*LPQLNGYIEKSTPYECGFDPI PARVPFSIKFFLVAITFLLFDLEIALLL PLP*ALQTTNPLIVMSSL
8066	21967	A	8126	451	200	KA*WNRFAILNVTKYTCESQEEVKIPTF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AGVWKKLIPAHITDDFVHFKTSVQEVATD VAKIASLLELEVESEDVTE*LQSQDKT
8067	21968	A	8127	2	396	LIVINTLLALLLIITF*LPQLSGYIE KSTPYECGDFPISPAPVFFSIKFFLVAI TFLLSDLEIALLLPLP*ALQTTNPLIG MSSLLLIILALSLAYE*LQKGLD*TES GWEKLVKKEKADKLGGRF
8068	21969	A	8128	1	350	GTRGLQTLPLIAF**LLASLANLALPP TINLLGELSVLVTTF*SNITLLTGLN ILVTALYSLYIFTTQ*GSLTHHNNIK PSFTRENTLMFIHLSPIILLSLNPDIT GFSS
8069	21970	A	8129	375	1	LTCFSEHRPPPRANFFFSRKTRAPFFLP GGFQIPGNFFAPPIFPNGGPIPGLDPO PGPLNFF*KSFFPDPKFFFLFFPPPI*N SGVFLPRNPVFPKTPNLEFFFSPPFPGD GVLLCHPGRLPRA
8070	21971	A	8130	32	211	GIRHGFAMLPRLVLNSWPQAILLPWPPK LLG*QAGVELLASSNPALASQTAGMTG VSTRPPVLLPTLGTHLCDACLGSSL
8071	21972	A	8131	396	5	KYRDGPPPPGKFFFFFF*DGFSLCCPGW SQTSCP*KSSCLPEG*DYRHEPPHMTLS SSY*CSQMCKCINKNCLGSCVVAHACNL SPLGGRITWGKKFETSLDNIVKNRLKK KKKKIYQGGGDHPCIFTN
8072	21973	A	8132	347	34	KAGFVIRPGPQEFFFFFPQDGIILCFP GWRAVAKS*VTATSNWAQAITGMLPPC PANF*KIS*RQSI SMFRLVPNSWPQVI LPPQPPK*LGLHVCLVPSLA
8073	21974	A	8133	102	270	DYRRTPPHLANFFYFL*RQILTVPMLV SNSWQAILLQDFFSVQLKMGFLSVP
8074	21975	A	8134	338	47	FLSTQKESSPLHTHTHTHTHSHLLTH HHGRGQERGRGR*GG*WRTGTHSPHGP HCVRLRSRPSGELGAAGGCSLIQPKI EDPGQSGGPREV
8075	21976	A	8135	68	467	SLNLRIPFCLCLNSFCVFLGLLFEAG FCSVAQAGVWVYEHGSLQP*PRGLK*SF HLSLPKFWDYRNEPPHPPFSCFKALNFK DYCDSGTVPCPFMKELSMFLIHALTESF VLFIVMSKLITTKHLTIISNV
8076	21977	A	8136	500	355	FHHVGQAGIQLLTSGDPPA*ASQSAKIT GVSHRARPQTSFLNKLPSLR
8077	21978	A	8137	58	222	IYGYEGRGSVAGSLSSL*SATDSDLDY DYLQNWGPRFKKLADLYGSKDTFDDDS
8078	21979	A	8138	345	196	KGDQAQWLRPGMVAHCNLSLTLEGQGG IT*AQKFETSLSNTLRPPISFK
8079	21980	A	8139	500	355	FHHVGQAGIQLLTSGDPPA*ASQSAKIT GVSHRARPQTSFLNKLPSLR
8080	21981	A	8140	3	231	HASADAWGRNEWPCAVAHANPTTSGG* GGWIA*AQEFEFETSLCKIVKPHLSKKK KKKKNFSPGWGSPPCPLF
8081	21982	A	8141	416	26	ARIFPNNSFWPGQGPPFPPLPGLPGG VIP*CQGVQARPAPPGEPRLFPKPKIV GGGGEPLFPPPERAGPQKCRPFEGGGF N*PKPRPCPPGWAQGGFVSKKKKKRNE DSKIPLIGKYPVGIRNMA
8082	21983	A	8142	413	35	RGAGGGGSPGPRYPSQOHLRLARTPTP FARSRCSPGVRGSCWRGGLGG*SRERP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LPSLPPrALPRSGASSGPLDGGAGQGPGR RERWAF LGGIRADARGCRAVTSPEPYRL PCAGAARARR
8083	21984	A	8143	166	368	ENILWAAMVVLDCHPSTLGG*GGRIT*G QEFKTNLANIERPHLFFFFFFKRDLSLFA PRAEGGGPILF
8084	21985	A	8144	1700	621	DLRDHSVLQGGPACLTTRCGEPILSHSEG SKIGSERESGEHSRHPPEAPPSPVEVGSR RS*QDS*GFGPGNGQDTRGPLSHAAPN WTPDPAAAVAAGGTS LPPRGGGGI*RGR SHTARSGARVGSANAHARGGSGFSRHSG SHGCLRNQSPRLGKAGALCGSAWVSGL* GSGLTSPRGRERLRMPGVAKGRPR*GN PRRGRGKQHGIPASGLPGRCWLGIKMT LQPRTRAPEELFVPQESSGSTPEKMLVS FHGSSLRNEATPRYSQQEEAGNGRWQQS LSLERWPPWTSHPLGTPPLMPVAVARCC ILPGLWPLLSPPSGSASPVSQGGPGLSL WPNAFKKDDFPVRQGDTSWRSVS
8085	21986	A	8145	390	38	NTTTFNIYFFYFFFFSLFIYFFFFFFFFFF FFFFFFFFFIFILFIYSLLVFGVWVLGL GLALALLAKLFLVNSLCRRYRG*SLLYY AWL*FFIFPLRYIYICARQFLSPILYL GKWF
8086	21987	A	8146	20	187	KLTTSTGRNPGRPTRPNF*VF*RDGDLI MLERLVSNSWPLVNLFWPPKILGLQM
8087	21988	A	8147	417	64	VRPRVRPRVRPRIRKKKKKKKKKKKKKK KKKKKKWGGF*DFWGGEGKPPPLQKND LLFWGFFLKSSFFFCGGLFFWGGPFFFP PPPNFLGVGCKKKTFRLLCGPFSAFFGG EKN
8088	21989	A	8148	351	187	RLGTFYLSNLRFYLSITHGPPIPYIGRL TSQNLPLLLDLT*LEKLLPKKSQTYN
8089	21990	A	8149	465	60	PPHFVGNPKKNSQFFWAKKKKKIFLGP *KMAKKGVVFWGRKKGFQRGKKG*KG GQLFYPLVLSQVLGGGQNHGPPGKAGFGE NFFFFGQGLGWAISRWLRTPLFLAGGGE DPKKNFKPPPKIKTLGAGVKKK
8090	21991	A	8150	1	175	WDYRHVPYPYLANVFFVIFRGDKVSLCCP V*GPTTELKRSSCLGFP*GWDYRREPPH LA
8091	21992	A	8151	59	35	RWNSRPRRPGKFLTSGDLPASASGSAV ITDVSHHAWPETFFR*RA
8092	21993	A	8152	269	159	ARVEVSKYIYIHTHTHTHTHTHTHTHT HTYTTKKLPS*LFQVCKMEKFGRLVVQ
8093	21994	A	8153	1	256	PGPPPRFFFFFFFFFFFFFFFFF*TLKI RFIWRKQKTHNPKDGIHQDISQVISLQ ITNHFHRRYFCTNFTCIQERDINQSLFL F
8094	21995	A	8154	252	41	LIIPVLICIVFIVLQKRFISVISLNKGL FRNHFFIF*RWGLTMLPRLVSNKSAQV ILPPWPPKVLGLQV
8095	21996	A	8155	21	443	HELSLI*FISTLAETNRTPFDLVDGESE LVSGFSIEYAAGPPALFFIGEYTNIIII NTLTITIFLGTTYDALSPELYTTYFVTK TLLLTCLVL*IRTAYPRFRYDQLIHL* KNFLPLTLALLI*YVSIPTITISSIPPQT
8096	21997	A	8156	2	205	LLHLMKHFNLEIQKAQ*TRINLKRSISR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						HVIINLSKAKHKG*ILKAVREKMLIMYK KPLVKLQVISN
8097	21998	A	8157	2	205	LLHLMKHFNLBIQKAQ*TRINLKRSISR HVIINLSKAKHKG*ILKAVREKMLIMYK KPLVKLQVISN
8098	21999	A	8158	2	222	VYTWGTGKARVFPGEF*LPVWIPTRHLK FYNEPIRDANESASAETENPQSSIIHPQ DEQNGDIRRTDKVTIHQ
8099	22000	A	8159	1	297	GFHHVQGSGLELLTSGDPLASTS*SAGI TGMSHHAWPLNCSYGDSEFSWLKCPBLTV ACWEEGWKRKLLMENEQGREAHQKLESV INFYIKDSMTKRKYK
8100	22001	A	8160	138	437	NEYDHFSTIKERRDFIVCVFFFFFSKKS LTVGTQGGPSYLEPPFLGNKEFSCLTFL GSWDNNGGATTRLG*FFVFFRKKGVSPCG PGWS*TPDLRKTPPSA
8101	22002	A	8161	330	148	QOSKTPFFFFFCKKKKIYIICMVVHAY NPSYSGG*GGRIT*AQKFKTSLNNTVRP HLYKK
8102	22003	A	8162	391	255	RPAPADF*FFFFYRLGLAVLPLRVWNSW PQATLLPQPLRVLGLQI
8103	22004	A	8163	131	3	HKVSLCYPG*SALMQS*LTVASNSWAQA ILOP*PPE*LGLQA
8104	22005	A	8164	97	440	NKGSCLCPPGGRPGALSHPTARSRGSPGP TPQKTGNNGPGPPTPVNLEFFEKRGFT VGQGGGLKLR*RSPPPSAPQKAGITGGS RRPGPIQKKFLKTLGETKWMKLIKTY LK
8105	22006	A	8165	541	295	FSQQKKKIFISTNLSHQESKIYICKEME SHSVIRLLEGGSAIMNHCSLKLPSSSDP PASVS*SAGIIGVSQHLANYTFKKIF
8106	22007	A	8166	440	259	PPQKFFFFFFFVKTFGRHV*AGFRLLD SSDPPLAFQSVETGMSPSARPMFGV HSLR
8107	22008	A	8167	23	405	FRICHLRLVHLLVYFIPSFTDNHLLSTS AMFLYSNDVIAQNVSGPFLGIIFRTFF FFFLKGEFFAPQVGGQGGNGL*LNPPP PGLKGFSGLTTPGGGNSGGGPPNKPFW IFKKGGGSLWPRII
8108	22009	A	8168	23	388	PYFSCALPRHHPPTNLGPHLGMGAPWG QPSVAHHTLLFFFFFLKRDFCFVPRVEK LWLEESSLNPLLGLKEFSCLTLWRTGN NGGPPPPVIFCF*KKGGVYPWPGGGE TPALKETPGL
8109	22010	A	8169	612	498	NIHFSLSFSHTHRHMTHTHTHAPTYI RTP*DNVPQ
8110	22011	A	8170	2	288	VNLITFFPQHFLGLSGMPRRYSYDPDAYT T*NILSSVGSFISLTAVILIIIFI*EAF ASKRKVLIVEEPSINLE*LYIKKKKKK KKKKKKKKKK
8111	22012	A	8171	381	101	QKSLQQPSNIATILEEVQVIFLGSFYHL QRWEMRLTKWLRGLGAVAHACNPSTLGG MGGWIA*AQLETSGDPPSSNRQLFTG EHNNDNKLI
8112	22013	A	8172	136	360	TKKHFGLLK*TKKHFGLLKKKKKKKKK KKKKKKKKKKGGGAFKKKKFFPRGGGK IFFFGAPKNKFGGGVLKTGGGKKPGVT KK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8113	22014	A	8173	358	58	EKVSVFFFLMKCSGIILLPCRLTLPGST DSPASVCRMPAIAAGPRRHA*LVLVETGF RCVGRAGLQPLTASDPPTSASPGAAIAD GVSFTQCSMVPRIRVQ
8114	22015	A	8174	254	370	GLTVLPGLVSNWAQVILLSWPPE*LRP QAYATGAGFLL
8115	22016	A	8175	48	269	FYVILCLDRVLLCCLGWS*TLGLKLSS YLSLLSSWDLQHVPVPHSASCLTF*VKAC FLLKYLKRLKIYAKIM
8116	22017	A	8176	1	338	PTRPINTLLALLLIITTF*LPQLNGYIE KSTPYECGFDPISPARVFFSIKFFLVAI TFLLFDLEIALLLPLP*ALQTTNLPLIA MSSLLLIILALGLAYE*LQKID*AEF
8117	22018	A	8177	426	130	QSLDPPGNMVTLSLQN*KNPPP*GGAVF PPFGRLLGGENPPGGSKEQKRRPAPQGG* PRQPPSPKKKNADSEFSIFNLQPALCK QYCVLHALENKILF
8118	22019	A	8178	396	244	KIHLLYICMCIYIYVISRHVILR*HHTA HTYTHTHTHTHTHTPKNTKYTLW
8119	22020	A	8179	2	119	TRPGNWPGVVAHFYDPSTLGA*GELIT* GQEFETSSSLY
8120	22021	A	8180	2	80	FLPLTLALLI*HVSIPITISSTIPPQT
8121	22022	A	8181	438	333	SPLGRLRHYNCLNWGGKGCN*PKSCPCP PAWGK
8122	22023	A	8182	393	19	IEFFFFPPPSPAKFFFIKKKRFPLWG GVF*SPPPGFQKTPPPQKVGFSRVFPFP PPKKFFFGGKYFFFKPPPPPPIL*K GGAKISPPPPGKKKNPFLLKGGKKKT PFIFFFPPKKIKN
8123	22024	A	8183	24	269	GSQQVLGFCDRDRVLLCHPGWSAVM*S* LTVASTSWA*RILHCSLLGSWEYRHTPP CL*NRNPQLTVKWRVKDHNKKSHR
8124	22025	A	8184	154	361	WHNHDPLOPQTHGLKRSSHLLGLPSIWHY RHVPPRLANFLNLSFRQGLAMLPTPSVC HLLVFLS*HIYWTFGYLS*SVCSHLLNF L**WHNHDPLOPQTHGLKRSSHLLGLPSI WHYRHVPPRLANFLNLSFRQGLAMLPTP SVCHLLVFLSETLGFK
8125	22026	A	8185	228	337	RPGMVAHACIPGILGGRGGWIT*GEKFE TSLANMVK
8126	22027	A	8186	314	127	DIQPKNEGEQELWLGMTAHAYTPS TLGD*GGRIA*VQEFETCLGSLARPPSL QKNFKN
8127	22028	A	8187	10	420	TQEAEVAVNWDHATALQPGRQSETPSPE KKKKKRGPPRWGENFFPTPGGF*KDGGN KKTGFPPFKRDGPPPKNWTWPWFQKRG APPEPPPLGGALGREPLGGFFGKGGVET PPPIFKKNPPEKKPHRGFNFFAF
8128	22029	A	8188	398	1	LKKKRDPQTFSPKIQF*KFFPPFFPKKS FPKNNLLKKRAPGGPIFFFFFFYPLFK NPSPL*MGSPPPPLFNPNK*KKPPLKK GPGF*WPFQKKKPPFFFFFWRQGFV LPRHTPSCLVNFCIFCRDGI
8129	22030	A	8189	30	153	AWYVRREDHVSLLGG*GCGKRWLCHGTPA WVTEENPKGKIK
8130	22031	A	8190	206	45	HPSQNSLSKN*ERVSVCCPGWSAVAGSQ LTAASTSQAQVILLPQPPE*LGLQA
8131	22032	A	8191	3	228	TCVCLCVYICDVCVGCVCYIDEYIQ

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						IYRYIHTYIDIYTHI*YIYHTYIDTHMWVCVYIYIYIYRCMGVRET
8132	22033	A	8192	41	416	ICRVKEIASRPLLETHSLSLVELS*FCLTAQ*RNDFLALKHLTAVLYNLILHSSGFWSSLKSHFIFLAL*YYL**FI*SN*RRDLAVLPRLVSNWPQVILPPQPPKVLEIRYEPPSLALILFFN
8133	22034	A	8193	2	183	KRLSIWQKKVEGEGFGQMDVGPVSVAHACVSSSLEGGQGGKIA*GQEFETILSNIVRPHLY
8134	22035	A	8194	2	465	AGVQWHDLGSLQSPPPPGFK*FSSLSLPSWDYRSAPPCPADFCIFRRDWAGWGVGCGFHRVARAGLELLTSGDPPASASPGAGIAGMSHRTQRGQDNFASWRRGGPQMSPPSCLFLQNTFSLKPSWVAPYPHASALGGGEYGGPPSPQPHLE
8135	22036	A	8195	397	149	LICLTDLPIRFLSLLALVFTVFNTKVVDKLIKLGVAHTCNLNLGG*GGRIA*AAHEFTSLGNIVRAVIPCCFSVILSR
8136	22037	A	8196	355	95	KKIMPTLCLKIPS*YRCEEIIQLSLQSSCDHRHMPHPPTNPF*RHLSMLRSLVLN SRPQAVLPHGPPKVLGLQAPATAPGILSLF
8137	22038	A	8197	382	112	KTDFGKKGSPSSPPPPFFFFFKSFAPSPRGEKKAPLKSQRGLCPKPKDPPPPGSG* TQDKGPPPPGQPIFFFFLKKGVCLFSRGGSKTFI
8138	22039	A	8198	32	361	ASRIGFILQEFLPVRVWTTNPSAGADGYNFLEKQKGTEKTSQVAQAGAQWCHRNLL*P*TSELKQSSCLSLSSWDYRMVFL LGKQVTLILGKRALSVPYPRDVVSLC
8139	22040	A	8199	1	314	INTLLALLLIITTF*LPQLSGYIEKSTPYECGFDPISPARVPFSIKFFLAITFLLFDLKNALLPLP*ALQTTNLPLIGMPSLLLIIILALLSLAYE*LQGLY
8140	22041	A	8200	3	109	FTSKHIFGFEEAA*YWHFVDVV*LFLYVSIY**GS
8141	22042	A	8201	3	216	DAWAAVGHHTRLIF*IFVEIGSLCVSQAGLEILDSSDPSSASQSAGIRGMSHGAQGEHLFHRPIGKIK
8142	22043	A	8202	1	267	RIHTGEKPYKCEECGTGFKGPSTLTTHKFFVYCREVAVLLKNCYSHLYPH*IIVNGSEADKREMCLLCIFFHPLAEQENVENK RKYNP
8143	22044	A	8203	422	92	PLVFALPPKIGFAPTTPSSSPPPPLFFFGPPVPFPFPFFNPPFFFPSPPKKKFPSPPPRGKIFPF*TPPPPPPPPPPPPPPPPPPPPPFLYLLFILC
8144	22045	A	8204	445	260	VCSPPLFIWVAPGFSPPPLFKNPPPNFFFGAPKKKNFFPPPPA*NFFFLKGPPPLFFFFFF
8145	22046	A	8205	103	248	GPGVVAHACNPSSLGG*GQWIA*AHFEKTSLSNAVRPISAKKKGGPF
8146	22047	A	8206	407	197	QLIFKFL*EQASHYVAQAGLELLGSGNP PASTSQSVKVTGMSHGAWLLAPTLRSTSLNYSLSVLLLP
8147	22048	A	8207	1	142	SCSVAQARV*FRDLGSLQPPPPRFTTFSCTPAWETVRLHLRKKKKNN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8148	22049	A	8208	2	370	PEVFDYPN*FKNL*LHKTCTQ*L*AALF VITKTWNQGCPLTGEWINKLEYIHTMDY LAIKINELANHKMM*RTLKCILLSESR* SRKATYYMISIRHPRKGKTITETVQNSS CQGLGERQKGL
8149	22050	A	8209	363	108	KKPRVEACLSPGVGRERAKRER*KRERE RERERERERENEL*KLSLADLCIKNG*R EFFKEKRYVKRYAKILRVSGRKQKYGNV
8150	22051	A	8210	386	254	LNPGGGVCSEPRLCPCPTPAWVIR*DSVS EKGGKKRKGPENSLTATNF*ALSCNLDY LRCSMLKMQRQRKRKERTEVRFWQLHHN LTLGFV*LIVYQRE*RRTGWFVAKYMLY TFS*PGSFPRLRKCEVHFVGYEPACSP FPLIHNQLHKAAC
8151	22052	A	8211	3	131	AHLFIAWFTEYFKPTVITYCSKKKIPFK MLLLIDSAPSYPRALMENYKGMNVVFMH DNLTFILWPMQ*VIFTS*SYILRN*FC TIAAIDSDSDSGSQSNLKIF*KGFTTL DAIKNICDS*EL
8152	22053	A	8212	86	286	WSIWECTVISVQLFHKPKTSFKNTSYWS GVMAVTNNLSTLGSQDPQIT*GQEFETS LANMVKSCLY
8153	22054	A	8213	393	344	SFFPSLPSKWGFKNLVPSPGYFLFFLNK GFRYFGQGGFKILNSNYPPLASQKGGI SGISPPWRALVFF*WRNLGPN*RTIVSP NYGLK
8154	22055	A	8214	3	313	QGLVLWHSGLLQPP*PPGLRRSSCFSLP CSWEHRCPTPHLANFLILCVCVCVCVET GSHFVAQAGLELLGSSDPPLSISQKSWD YKV*AIIPRAKQNYLMLFY
8155	22056	A	8215	165	348	RPCPLFPEDLLTFSREGPGTMAHACNLS TLGGQGGGIA*GQEFETTLGNIVRPHLY FYLLK
8156	22057	A	8216	379	218	VFLVETGFLHVGQAGLKLPTSGDPPASA SVSAGITGVQKCRF*YNVFIFQKSSLL NALPICSLTMLGNLFMFMTTPKFPTCS
8157	22058	A	8217	32	276	RYLPITIAALETIAKI*KQPKSSLLDKWI KKLWCIYTMYYSAKVLITVVTWMNL VGFI PGDINHIOKAKYCMISLICGI
8158	22059	A	8218	171	2	KGVFGLGRLEFFFLDRVWLCLPEWSTVVQ SRLSATSAS*IQAILPPQPPEELGPLCP
8159	22060	A	8219	530	73	TKPTVGSNSRSYINQTYFPSTLTFFGGL MRLTIYHFFFLVYYNPRVMVTPAYM*L LILFYSSSIRDLLIAKQCLPNEGFSPH AC*TNATLLFPYSI*YLGLPFHLIFPV CFSFYFL*R*GLTMPMLVLSSWPQVIL PPQPPKVLGLQA
8160	22061	A	8220	350	135	FFFFSQTGVAQNRVQ*RDHNSLQPP*PPG LRQSSCLTLKPCWDYRCKPLCLASWIYF KDKVYTSTPVHTQEY
8161	22062	A	8221	185	331	PGMVAHAYNPNTLGG*GGKLT*AQEFET SLGNINSVPKKRRKRKEMM
8162	22063	A	8222	73	232	YCSFKFITLTCLSWLGTVAHTCNPSTVE GGGGRIT*GWEFTTSLGNIVRSCLY
8163	22064	A	8223	418	211	AMPSLLTYLLTFIFCRKKKIFFYWGEFT MLS*LVLNSWTQVILPPWPAKVLVLRPL ALFYSLLVLPFSF
8164	22065	A	8224	227	33	ESHSTTQAGVQWHDHGSGLQPPPGMSLY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						CH*CLRFWSWRPAEKPWCSSSLRFMELE SWSGASDAF
8165	22066	A	8225	244	287	TDSPTSAFRSAGITSISHHTLPKSTF*I FCRAGGLAMLPRVLVNSWPQVILPSQPP KALGSQA
8166	22067	A	8226	53	235	NNKWQGVVAHTCNPTTLGG*GEWIT*GQ EFETSPANMAKIPPLVMFAFCFEETDNK SHTK
8167	22068	A	8227	275	25	GVLMFNFKFCI*QNSPFMLPGVVLNSWI PAILPPQRPKVLGLQAWTILYKWWYGKE MWHKEICEGTHDVL SKL LTRFRKRL
8168	22069	A	8228	386	211	QLKLPLPKGNKLRPP**KFFFFFFFQ GLTILPRLVSSSWHQMIFFPPQDPPEVLGL QA
8169	22070	A	8229	1	117	VFILFYF*DGLAMLPRLATNSWAQAAILL PSAPKVQGLQA
8170	22071	A	8230	356	26	WHVHGSQQP*PPGLKQSFCSLPSWDE RCAPHPINIFYQICRDRVYKRWANMVIS PNPLVLISQSAGITSKIPCPGSEISTIF IFSHQLLLVRGVYPDMLVLQLGKTCI
8171	22072	A	8231	3	188	FPSLRPA*IFFYIYFFFLKNKVFLCHPG WTQLLDPNWTQAAGLKQSSHLSLLSSLN FRGSA
8172	22073	A	8232	2	253	KLDYINCGTNLAQKCLFCLFGSLFFQR* GLTLLRLFLMNSWPQAAILLP*PLTVLGL QATMLGSQVPVFDLGITLCRCRFGKLE
8173	22074	A	8233	373	65	PEKAGSCLELAFGLQMQHPPWASTLPAA LTDPLATVPHVSVQFLKSHTHTHTHTH THTHTCTRLLVLFL*EALTTTPLLRSI CKHRESACSLSLTWPLCC
8174	22075	A	8234	390	46	RVFKPG*NPPLVKAPAPPLFFGGV*GRS PKKKNPQGGGGPPPGFHPFFLTPFFP IFLRREPPPPFFRGGGLPPPPPFKTPFF FFFVWKGKFLPQKKKKFFQSISTRSV IHK
8175	22076	A	8235	387	216	QKLGVLVPPGRVIFFFFFFFCC*GGGL TMLPRLVSNWPLAILLPQPPKVLGLQV
8176	22077	A	8236	1	201	RFFFTIPPQCFFPQFILSF*RRGLAVLBR LVLPNPWPQAILPPQPPPELLGLQAHPTTL GPVFYSYCVRA
8177	22078	A	8237	399	229	SVGGGGLTMLPSWSQTPGLK*SSHLSLI KCWDYRPEPPHLAHSLLNLQLYCHTKL S
8178	22079	A	8238	192	335	SHTLPHSSNFSYFW*RQGFAMLPRLVLN SWARAVCLPQSPKVLGLHA
8179	22080	A	8239	442	254	GRDRVLLFCPGWSQTLGLKRSSCLGLPK HWDYRHEPPHPAENIKFCVWPTLYFYWP ALVQINLP*QLQGTCEVACMC
8180	22081	A	8240	381	180	VLKLIFFCSHRGPTMLPRLVNSGLK*SS HLGLPNCWD*RCEPWHPASLCLLTSTFW PPTLICNIHK
8181	22082	A	8241	388	260	NAIPFYITKCCNPSTLGG*GG*IT*GQE FENCLANMVKPCLY
8182	22083	A	8242	1	145	GFTILVRLVLS*PLDPPALASQGAGIT GVSHCAQLIYVFQRLQLLW
8183	22084	A	8243	1	173	GLTVSQAGVQWCDHSSL*QTLGLKQSS SLSLPSSWDYKCKPQHQAADFFLMEFFQ M

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8184	22085	A	8244	202	327	TLFITFIFFF*R*GLAVLPRLVLNSWPQV ILLWPPRVLGLHV
8185	22086	A	8245	42	289	KBKRSIILFIFFCRDGVLLWLPRLDLNS WPKTIFPPWPPK*LALQAHTTIPRGGS ILICIRDVKRERKQYAKSKNPEGET
8186	22087	A	8246	592	485	NIVSQAGVQWHNLGSLQPLPLGLKWFSC LSLLSS*DYRHVPPCPANFCISVETRFC HVGQAGLELLASNNPPAPASQSTGTTGV SPCTRPRVYVFLWLILANGPS*RAETLV NLATNQEDADSSILAPGLSGHCF
8187	22088	A	8247	307	12	MCSPVFSPPKQKNPLFLNFFKKEFLFFFP GGRQGGHFGFLAPPLPGLNKFVLDPFG NGDTGKGGPPARGNFFFFFGIFSRDFV SPC*PGWSLIPDPR
8188	22089	A	8248	392	237	HYQASLAPLTSGDLPASAPQSAEVTGV SHRAWPTVLI*SFS*KFNWV
8189	22090	A	8249	153	386	FFPPGWPKPSLLEPPPWLGKFPPTIL GGGD*KRPPPPGNFCFFKKNVSPLWE GWF*TSNLGNPLPSPPKRVGIT
8190	22091	A	8250	387	166	IETILDAIKNIHDSWEEVKISTLTRVWK N*IPTPMDNPEGFKTSLEEBVTADVGMIA RELEVEPEHVIELLHDIS
8191	22092	A	8251	405	266	LFAIVKR*NHPKCLLIYARINKMWHISI GWNIIISLISKGMKFSYMLTWMNLEVIM LSEISHSQVT*YMVPLA*GHLEKLNCL PIKQQTPIPSSSSP
8192	22093	A	8252	379	201	PGANYACNPSTLGGRSWGIA*AQELETS LSNMTPKQPCSTPQCFLVNQLLLQNLYP YFP
8193	22094	A	8253	78	311	LTLYFHTRRKKGLK*IFYFI*SILSQKD LKVGTGPGAGAHTYNPRTWGGWGLQAG KRIT*AQEFETSLDNTVKICL
8194	22095	A	8254	303	81	TPCAENFKLRKRFFHHIISLQRKMNYLIS FLYF**SHSLTILPRLVSNWPQAILLP LPPKVPGLQVSATLPLGL
8195	22096	A	8255	2	376	MGYNLVCHLLRPLEKRSIRVGVTFSG CPPSPPLPARKGYSLTPCASQVRQCLAL LWLTGLGLHPLSCPHCPTSPSMNPVPQ LEMQKSPVFCVSHAGSCRLEFLFGHLG TQSSLDSEFFKKVI
8196	22097	A	8256	70	356	LIIAYNLTYDLSWKMFVYLRKIYTLH WVECSIYTCWV*FVYSMVSWNRIDSPGK KKTNIYDQLIFNKGAKSTKLKNSLFNK WGQDKISTYKK
8197	22098	A	8257	403	85	PFCPWFPFVFIPPLRKSGTPPGPGPEF PGPGFSNGGNPRPLKKSFKFSPGWGRGP LFPPSRGV*AGNFLGPRWRGPWAKFVP LPSCLGHKARFFFFPKKRRKIK
8198	22099	A	8258	249	2	YCEGDLGSYRPGVSKCMFEFSPPRDIRIM PWPAGVCYAYNLSTLGGRDGIA*A*EF GTSLAYIVKPHLYTHTHTHTHTHMY
8199	22100	A	8259	2	189	IQCVCTKSHFCHPGWSAVAQSWLTAAS TS*A*VDFSHLSLLNSWD*RRVTPRLVN LILFPS
8200	22101	A	8260	453	128	FFFFFFLIETVSHDVP*AGLELLSSSH LASAFQSAEITGVSHHAQPSVSWLIHS S
8201	22102	A	8261	420	79	KNPTFFFFFLLIETVSHDVP*AGLELL

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						SSSHPLASAFQSAEITGVSHHAQPSSVS WLIHSS
8202	22103	A	8262	1	262	NSRTERLGSWQSHFCHKEMEAHFVVQSG VQWCDLGSRLPLPPGFK*FSCPIILSGW DYSQCRPCRTCSLIFMHSRSPSPSEKK WTC
8203	22104	A	8263	321	100	SATKNYLLSRQSFQIK*NNGLGAVAHAY NSSTSRGLGGQIA*A*EFETS*GNMMRP HCYRKYNLARHSTYSR
8204	22105	A	8264	145	275	KPRDYSFFF*WKRDLMPLRLASNSWTH AILPPWPPKVLRLQG
8205	22106	A	8265	73	351	SLCYRSFARCDRPPKKGQHFSSYLQDAQ WARTLLSTIAQNNSAEHLKTTDW*GAV AHACNPSTPQGRGGRIA*VQEIETSQGN TGRPHLYKK
8206	22107	A	8266	382	232	LVETGFCHVGQAGLKLTLTSGDPPASASQ SAGITGVSHCAWL*T*YS*DFQ
8207	22108	A	8267	397	130	IGQAGLKLTLTSGDLPTSASQTAGITGMS HRAWPTFSLIAR*NASFQVGHFSPKYQV GTLAKSLKCHQVRSDTLEFILCCRIIYE TLGKF
8208	22109	A	8268	309	97	DTWYRTRRKDHCTITETRIQSVRPLSPR *AITSRVCTYTSR*PEANEPPQKITFR HCDLFLPTLTDQLTL
8209	22110	A	8269	2	224	DSSGIPGSPTRPPTPRPKQKLPDPTVS LLGICIDYDQRQ*SVFQRDICHSHMFITA LFTIVNIWKQT*HPLMDE
8210	22111	A	8270	374	2	TSWESARKPPPIHSHTLKGGFFFLFMFF FF*NKICKDGLTMLPRVVLNSWAEGIL LPRSPKVVGIQELATQRRASILLCNPT ACGIFQHVVVNVKLLMKQCPFCPAAPT TKTQNFPPRV
8211	22112	A	8271	1	379	PTSASQVAGTTGTHHHIVLFFFIFGIFEK KGVFFFPSPGGF*TPKPKPPPGFGPKRGG KKGPPPPARGMGSGVFYPPQKPFV LIGGQILFKGRTLDFKKRAPPPPSLF LPKHTPSFWIKWDP
8212	22113	A	8272	80	401	AWGMRFCLLLYSCQYLISDIAHFSAFF FWKREPPAPQVKGQGNLS*WNPWLQG *RGFSGLTPKGGNYGPPPPPLIFFFL RKNGFFPGWPGWSKTPDLRKPPC
8213	22114	A	8273	405	95	PPKRFWGSCKGFPQREKILGSPTFPKKK KDFIYSYLSKSLKKE*INRPSAAHTCN PSTLGGQGRIT*GQRFKISLSNIGRPH LYEKIKNVKKLKIKKPNKL
8214	22115	A	8274	167	52	DREQRPGAMAHTCNPSTLGG*GGWITRF LANMVKRLRY
8215	22116	A	8275	276	23	KYVSSRPGTVAHSCKPSPLDGQGEWIA* VRKFKTILGNMMKPHLLFYKKLT*KNVK CTFKKYCATESRYVTKEKQKDRKKGTKE
8216	22117	A	8276	1	114	FTMLARMVWIS*PRDPPASASQSAGTTG VSHHARPLS
8217	22118	A	8277	2	87	TMLLRLFLNS*AQAVILPWPPAVLGLQG
8218	22119	A	8278	357	347	SEGLALYQLEAFTVCDLRERGFRCGRSL WPLITWAWRGGVFLLVQFQEVCCRLALG SLSPDPVLLPESGGPTASQSAGIIGVR DRAQPNCFVEIGSYSVTQAGVQ*HNHGS L*P*P

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8219	22120	A	8279	371	125	FFPKKNEPPG*PPPKK*RKPGKFILAPS PPFFGGGEFYKLKRGVLKQKPGPPGVPK ILKTPPRLGKNKPISPPPGQKKQNFF
8220	22121	A	8280	377	63	PPVFPFPWGGQGGGFF*ARGLRTPWPTR ENPVFF*NPKN*PGGGGPF*IPPPWPG* ALKFPLPPRGGVPLTKNIPPPPRFSHR RVFFPKNLKKKNPCLIESL
8221	22122	A	8281	2	284	LPK*VKNFVHAKICT*MFVAALFVITSS WKQPRYYSIEKWINKLWHISAMEYSS LKR*ELSSHEKT*KNFKCGLSEKSSQSE KDTWCLIPVI
8222	22123	A	8282	318	40	APRLSLVVFVFIKRLDSSPGSRITWT NCFENHLCVCVCDRFLLCQAREQWRVLG SPQSPSPKFKRFSCLSLPSSWDSRCKTP *PANFCGLC
8223	22124	A	8283	30	343	CYQKASHATEKSFMR*RVNPCSILCCCY KILPQQPQSAVITLISQNKKKKKKKK KKKKKKKKKKKKDGGGALKKKKIFSPR GGRIFFFFWAKNNLGGGL
8224	22125	A	8284	163	392	FVVLYNFSVIYSISDPCWYKEQLCKSVF SFLSS*SLLEPNPNPNSPANSQAQLVQE NKREYEKRVSAIVEQSWNDS
8225	22126	A	8285	406	63	KKKLILAKPGVNNLDSLKRAPPFFFFFF RHGVPLCCPGWSKTPEPK*SSCLSLWSS WDYRREPLCLAYSPVLNITHLSSPNVKL CRDSQESYDPIIMMVIIITEGGMICGV IM
8226	22127	A	8286	1	322	TNTLLALLLFIITF*LPQLNGYVEKSTP YECGLDPISPARVPFSIKFFLGAITFL FDLEIALLLPLP*ALQTNLPLIGMSAL LLIIILALRLAYE*LLKGLD*AE
8227	22128	A	8287	395	181	HGSLHPGTPGLQQFSRLSLPSSWGVRHV PPCLANF*IFCRGGVSLCCLGSVEGLEC QARLPVLVRAELGLD
8228	22129	A	8288	3	246	SSTLSFSPG*DYRHVPFCPANFFFFWIL EKTFFCFVPQGGFNLWA*TSPLNPPWA SKGAKITGGTPGMGLINLANGRPP
8229	22130	A	8289	138	421	LLSSVFFFFERDFCFVPAQQGWGNLG* WNPWFRGLKNFPGLTPPRSWNNGGPP PLIFCFFLKKRVSPRGRANFLDLGT PPPGPPKERE
8230	22131	A	8290	141	375	RTFFFFFKTEGYFVAQAKQGQGDHGS LQPSPLKGSLLRRWDYGSMPPCPSIFF F*IF*KNGASLCGPNNSKTGG
8231	22132	A	8291	407	209	IGGPPGFSPPPVFKNRPPNLI FGPPKKK KNFPPPGGKNWFF*KGPPPPPPPPPP FFFFFYTL
8232	22133	A	8292	86	433	PPXPKNLIEGGAF*KRHFFPPPRGRVR FFFFGPKKTPAPGQNPGGGKPGWSP FSPGEKNXPPTHXGGPVLGAPPPPGI VLI*KKTGLPLFVGRAGTNPNLGGPPAP PPKG
8233	22134	A	8293	147	342	LVKFEYTVLPKNRYRLGVVAHAYNSSSL GGQGRIT*A*EFKTSIGNILRSHLYYK KRKEKKLN
8234	22135	A	8294	6	152	CCGHAPHPANFYSL*RRSLAMLPRIVS NSWTQAILLP*PLKVLALQV
8235	22136	A	8295	18	205	IPTRPPTRPPIGRNLNHTFTATRPGVYY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GQCSET*GANHSFMPITVLELIPLKIFEIGPVFTL
8236	22137	A	8296	1	199	YLYIYLSTILLSIYLSIYLSIYLSIYLSIYLAT *LAI*KBIYYEYVLVMTEAEIFHILPS PSWRPRKVMV
8237	22138	A	8297	1	318	PTRPPTRIILSRPIKIQTALHKFSCLCEY LQ*ADYLF*SLWIRPDVAVPHACNLSIL GG*GGRIA*AQEFEISLGNIVRPCLYCI IKNKIKKKKPLQIIAFFLCFKD
8238	22139	A	8298	416	304	GFLHVQGAGLKLLISGHLPA*ASQNVGITGMSSHARL
8239	22140	A	8299	352	31	EMILKAAREKK*IIPYNEPLICTVDFLVETLQARREWDIFKVLLKKKNKTKNPFYT KIEYLVKLSEFYKEKVTKTLTLD*Q*LRFINTRHANRNTSNRRKRPIIKHK
8240	22141	A	8300	382	266	RWDFVMLPKLVSNS*AQAILHVGLPKCW DYRREPPLHA
8241	22142	A	8301	2	273	PLTRGPSSASDALSSGGPYHPSECCTYT TTYKIPQRIMDYYETNSQCSKPGIV*VVHTHTTGGRGSQQGLLEGSREWNNWNGDP QRTSQV
8242	22143	A	8302	77	430	GMGLSMHRTHFQYLAHIHPCVHVHTHTHTHTHTHTHTLCM*HTEIHKSVRYGTE HAQDPFSIFSPTYPMCACTHTHTHTHTHTHTHTHSVYVTHKVCETCLSFFYPESG TISHAQEIILKRCLENKTHLGVWCFTSLLSVANIVFFSYKRQVAARGLFFFSLSQAE
8243	22144	A	8303	137	396	SSVKTMNYLKPVVHMVADRCLFQCLPS KKKKKKKKKKKKKGGLPKKKKILTRGG GGIFFFFGAPKKISPGRV*KKKKKKKKKK KKKKGGPLKKKNFNPGGGGNFFFWGP KKNIAGARLKKPGGGKNPRS
8244	22145	A	8304	329	144	NGPPFFFFFF*DGVSLCCPGWTAVARSRLTF FAVFFTLNCSVVGIHSELQHWFQDYLKLKTF
8245	22146	A	8305	404	157	RTYNPSTLRGRSQGIT*GQDFDTSLGDR VGPHLRKRKNYYSLVECFYRIKEKYPE SHKKAMKMLFQLKPDFLHFQHIATN
8246	22147	A	8306	394	294	SLCFLTTPRPDLNALIKNFYSPTPGWVSC VLSKGGPFFFFFFFFKIDGVLLSCPH*S QNPVFVALEWSGTPELK*SSHPGLPKAW DYTYEPFHQAQVELLRY*RSFPVLLLDG ICIFHSFFSPRGSLIP
8247	22148	A	8307	280	2	VVDSHVTTFFTSVITVMLFSIQYVKQLEN IKSWPGIVARACNP SALGGRDG*AQEFD SSPGNTAKPCLPQKNKTQKTKNKVGGT LETBSWRL
8248	22149	A	8308	136	330	MSYQRKSVNYKYSNNACEVTTWARHSG SCLRLYNPSTLVGSGGKIP*TQEFETSL SNIARPPLY
8249	22150	A	8309	3	118	IFVVLVQMGFHHVQGASLEL*PQVIHPP QPCKVLGLPA
8250	22151	A	8310	2	366	TRVDPRVRVSTRNLCLPGSSHAS TSA S*VAGTTSACHHARLIFSFSFFFLGFSE KTGENFFAQQGFELGEREPPPPFGPPGF WGCGGGGTFKRPRRWKFQKDIIPPLVSN RGDOPEPFF

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8251	22152	A	8311	253	446	SKTFQARGGVTEMGFRHVQGTGLEILTS GDPPASACQAAGITGVSHHARLRI*YFI RIFILMTC
8252	22153	A	8312	430	88	GVGRIQISWSPWLPKPKNSPGSPPPQ*VG APGGPPPPPGPYFFFFFQKGFPLFSGRV *GSGSKNFFVFPKKNWGTSPPPPEGR GFFFFFFFLSRDGASCCPPRPPKVLGL QV
8253	22154	A	8313	400	323	HRLMPPHPIDFFLFFVETGSCYVAQGAC ELLGSGNLPGSAS*NARITDVNHHAQP* KSSSGPGTQQC
8254	22155	A	8314	4	421	GGRIARTQEAQVAVSQQCTTALQPGRHS KTPSQTKKKKSPGGPPGPPGRFFFFFF KT*KKGPFLKPPQRRGGDPRGKKRGGG LWKKPGGKLGPTKKKTRGGGANPPPLW GKGGGPKGAPRAFPFTKKKPPPSGRNQ
8255	22156	A	8315	213	32	RCPGTVGHGCHPSPLGGQGRGRI*GQEF ETSLANMVKPYFFLNSKKKTKNHPTKKN SQAW
8256	22157	A	8316	422	153	AATLYTHKTPHCYFFLDRNLLCCPGWS QTPGLK*APCLSLPSSWDYRHKPPRPVT SPIFRIKSYDVIPPPYLE*NPMMLYLP YCHHI
8257	22158	A	8317	1	284	BRQDWESRLAMECAFHLEKSVNQSLLE LHQLAMEKGPQLCDFLESHFLNQVKA IKKLG DYLSNLCKT*APEAGLAEYLFDK LTLGGSEEDT
8258	22159	A	8318	187	37	TRDFFWPGVVAHA*NCSTLGGQGRRIA* AQKFESNLGNRVSHCLYKKFKN
8259	22160	A	8319	2	250	KYEQSLQEVWDCVKRPNLRIIGVPPEEE KSKSLENIFGGIIIEENFPGLARDLDIQI REAQRTPEKSIKRSSSRHIVIRLSK*E VWDCVKRPNLRIIGVPPEEEKSKSLENI FGGIIIEENFPGLARDLDIQIREAQRTPE KSIKRSSSRHIVIRLSK
8260	22161	A	8320	371	196	NNFSILFFFFETRSH*VAQAGLVLLGSS NPPCSASRVAGVTGVHQRYYQDDFKNFR HN
8261	22162	A	8321	3	235	FISVSFKYSKHIPNNMHLKFLVLFNFF FRDGFWLRSG*SVVAILRCGHSSLOPLT GLKQSSHLSFQGSWDYRRAPH
8262	22163	A	8322	1	395	LEVPLNTSLLLASGVST*AHRLIES NRNQIIQALLITILLGLYFTLLQASEYF ESPFTISDGIYGSTFFVATGFHGLHGII GSTFLTICFIRQLIFHFTSKHHFGFEAA A*YWHFVDED*LFLYVSIY
8263	22164	A	8323	322	83	MHQSFVLAKVKKGKGRWFYSCLMIKSA PVLSTVHTNLLCWPAGVHACNPSTLGG QGRWMA*AQEFETSLDNVGKPHP
8264	22165	A	8324	12	249	GFFLPPPPGRGEGKRGPPPPPLFFWFFFK KGEFPLGGGNFLTLEPRLAPPKGGK*G GDPPPPGFFFLKKKPKPLLKG
8265	22166	A	8325	139	335	ENILWAATVVLDCHPSTLGG*GGRT*G QEFKTNLANIERPHLFFFFFFLKRNFFFA PRVEGRGPV
8266	22167	A	8326	1	246	FRRGLAVAPRVLLCYPGWRAMVQS*LTA ASNSWAQAIHLSLPKCWNKYHTPPYPTC *NSACWDESSFLLVSAMEVCGQPHS

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8267	22168	A	8327	422	107	TYVVRQQRKKRGLFFFFRFLPPGGGQ WGHFWFLQPPPRGV* RFFFLNLPRNRPW DFKGLPPPPAYFAFFLKKGVFPFGQGF *ILAPKGPPTSTSQKGWGFKD
8268	22169	A	8328	1	161	FRGTRWVCHVLFYLSFFLRQGLAVLPR LILNSWAQATLLPQLPE* LGLQTSS
8269	22170	A	8329	422	103	PPYSPFFGGPGGGVPKVRESGPPGPPQG NPPFFKKPKNNPGGGGGLIPSSGG*A KGMGLSPRRLPLS* NWPFPFGGQNK LPFPKKKKERKKEKFNFEHRG
8270	22171	A	8330	46	422	STPFFLASQSAGITGVSHRARRSSSFQC TQIPLFPETLPLNGFGSRHGRGFSSQVL PAQSSSFDLDSLVLGY*MLSHISLGN RALGFIPPHLSKWENGSTLRSIVLSQIE GLSSTLSFPHVPS
8271	22172	A	8331	429	112	FSHLGSSPRQGFTMLARLVNS*PCDPP TSASQSAGITGVSHHAQPHAVFYIRLPD SQVLCHQMPYWPHTAHYPHRWIFSLVLQK NLSVPPPLWPIQSQPKASILLN
8272	22173	A	8332	291	19	KTFPPPKI*KFPNFKFTPGCGGPPPP FLKKFVSPGNPPPKIFFFFFFPPPPFF FFFFFLRRGSLISIAQDGIQWHYHGS LQQLPGLR
8273	22174	A	8333	307	123	KYFRGGGGGR*FPPLGGVKQKKRGNPG GGGSKPKLGPSPPTRGKKKNFSPKKK KKKKK
8274	22175	A	8334	3	169	HASADMCHQAQLLLLLLVETGLCHDGRA GFGS*SQEIHPRPKVLGLQHFLIY
8275	22176	A	8335	1	208	LCVCVCVCVCVCVLF*WRKGLALSP RGECSGTNMAHCSLNFSGSSNPSVSPSH VAETTGVRPLG
8276	22177	A	8336	1	352	ILFYFIFYFSCFEMGSRVSQAGVQC PDLSSLQPLPRFKRFFCLTFPSSRDYR CVPPHLAKFCIIRRR*AAIGQAGIELLT LSDPPASAS*SARNTGVSHCSGSPFINF LNWQI
8277	22178	A	8337	420	272	KAPCQFSGEKTVPKHCWNSVPPFRKKQ QQKKNLCPCLVLYTSINSQ*TMGLNIKA RTVNIS*KYKEDP*TGKK*INKSCPWTG KKKKFLARTQKTLAIWDTLINWTSPLK MSTKQRHHLKMN*PKWLLFFVS
8278	22179	A	8338	427	202	LTIYFCHQSQKKGVLPLQEREGWAEA SLKISNISLSHTHTHTACAHHTHTHT HTSS*NGIKTVVITIKSFA
8279	22180	A	8339	2	164	TPGHGISLCRPGWSAVAPSRLTATSASW VQTILLPWPPE* LGLQESRLLRDHL
8280	22181	A	8340	422	1	PEGPPGKTKRAPPPSFKGNPPLKKGK GPGAKPPPKNGVFFPPKVKGPQKNFG GTQISQPNKRG* KFTPFFL* KPPQKKK GPPPGKIFKGPKF* KFPSPGFFFFFLK QGLTSPRLERSGANTAHCSLKLSSSD
8281	22182	A	8341	1	456	RTRGAVSQGHAIALQPGQSETPSQKKK KKNPAPGGKGKIGGTAKKGRNFDANI LGPNSRPGGAFFGG* TAPPKKRGSPPG IFGGGKGKPKKILSF* KAGGGAFFPS PVGTPFFRGF* KGKILKKKKFSKPGGG NPENLSPTNFFF
8282	22183	A	8342	407	2	RQFILGAPGVFPFPGF*KPPPKIIFWGP

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						KKKNFFPPPRGEKFFSFKGAPPLFFFFF FFFFFFSPFFFGALFFFFFFTILFKTKFG VFSCCKGIPPKFFKRSRPPNGAGRLPLL VGPLPGVPGGGEAERKISQGSFQ
8283	22184	A	8343	441	1	PPPYILGGPRVFSPPFFKTPPQIFFLG PQKKNSPPPPGKKIFFF*RAPPPFFFF FFFFFFFPFFFGALFFFFFFTILFKTKF VVISWKGIQPKLFKRSRPPNGGRLPLL GGCPPPGVPRGGEAERKFSRGSFQRTGG SAPEFRA
8284	22185	A	8344	466	323	FGVAGTQNPGRNPRVFSFRGGPPPGVPQ GRNPPPPWFPLNPPKHFLTP*VFPPLE PPIEWVGPGRP*PSYGFSSPVARK
8285	22186	A	8345	657	347	LEFWFFLRQSFTLVQAQGVQ*CDLGLSQ PPPPGFK*FSRLNLPSSLLDDRCAPCPA NEVLLVETGFHHVQAGLELLTSGDPPA SASQSAGITGVSISAQPAQ
8286	22187	A	8346	3	212	DCSRGPPPHLANFGLLEKTGSNHVDQAG LKPLSLRDPPASAS*SPGITGGSHRAQF *FIFKRGMAPKGF
8287	22188	A	8347	9	255	IPGPTHPSDFFLYEIDLFPKN*KGFPFP PRGGGKNPPPPPPFFFS*PPWKKKITF QTPLTGVFGAPKNFNFWGGFKKIGF
8288	22189	A	8348	79	312	NAAGFEVGISKA*ALETQIITREHGSN KPRYAVTFESHMGTVLHLVEQEHTVGY ITASCALKC*IESGGFLNDYI
8289	22190	A	8349	1	369	FFFLKRDVRVSPLSRVYKWHDYSSLQ LQTPGLQ*SSCLRFLSSQDYRHIPPCPT NF*KCFVEMGSCCVTQWSQTPGAQAVL PPWASQRHWGLQGVRLCSLLSNCPHS RLVWSWLFSGC
8290	22191	A	8350	434	324	LEILSPVWWHMPVVPGTREAEA*EQ*SL EPGRRLQ
8291	22192	A	8351	3	253	YMCSKFFFLCSCGAISACHLELPSSD PPPT*NF*VIGTTGTCHHEWLLFELFG KMKPHYIAQVGFKLERNFLKTKKVPF
8292	22193	A	8352	3	1431	SPRGGIPSLKQVYSSLTNSRPSQHLF* EEALQRAREEEKREKETSHTFQSTLTDI QQQIEQQSERNMKLCQENTELAEKLKSI IDQYELREEHLDKIFKHRELQKLVDK LEQAQEMMKEAEERHKREKEYLLNQAAE WKLQAKVLKEQETVLOAQLTLYSGRFEE FQSTLTKSNEVFATFKQEMDKTTKKMKK LEKDTATWKARFENCNKALLDMIIEKAL RAKEYECFVMKIGRLENLCRALQEERNE LHKKIRDAEISEKDDQSQHNSDEEPESN VSVDQEIDAEBVNSVQTAVKNLATAFMI IHHPESTPHQSKETQPEIGSSQESADAA LKEPEQPLIPSRDSESLPPLTPQAEA EGGSDAEPSPKASNSPAGLGAETQCEGL PVGAQADQASWKPEAEASGQAPQAPTEA SLQKMEADVPAACAAEEHVAAMVPACE PSRQPPRAAABELPVGASAGQPQPRNVA
8293	22194	A	8353	376	65	IHCGDHVQEVPKLKVCAHLMSSWACSQI PKAGDKILTFDQLTDLTKGCGTILLSG PHKGQEVYWHFSKALGTQHSHTKPCVHS RDQKFKHIRG*WASQGYKN
8294	22195	A	8354	459	85	*LEEVESELRVLEKKMIESEELKSKQTRF

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						LEETIKNQDKLNKSLKEEAMLQKQSCHEEL KSDLNTKNELLKQKTIETLTRACQKQYEL E*ELAFYKIDAKFEPLNYPSEYAEIDK APDESPYIGKSR
8295	22196	A	8355	231	158	PPFIFLYLYQSNDIARGLERGLEPEKVG ATDSCGDLMLMKW*ESVAPMTFSGSRP LSKPRAISLLWYK
8296	22197	A	8356	2	164	THRGVENQMAEQGWKDVSVYVWGA HACNPNTLGGQGRWIT*GOEFETNLP
8297	22198	A	8357	23	291	CTHTRAQAHATHHLLFYFLYIFNFFEB TGSH*IVQACLELPASSDPPASFSQSAG ITGMSHHAWPTSCILKVKMALCSINCSA ACFLY
8298	22199	A	8358	1	307	FFFFEIESCSFAQDGVQWCDLGLSQPPP PGFKQFSCSLSSWDYRHVPPRLANFC IFSRDGFHHVQAGLQLLTSNDPPT*AS QSAGITGVSPRAQPCPAF
8299	22200	A	8359	75	266	FVKTRNLFITVLEAGKSNIKARAG*VSG EEHGLCLQDQALLPLEGRNAVSSHPRGQ NMMRAKC
8300	22201	A	8360	1	295	NTWVFCFVLLFRDRVSLCCSVRSTVASS *LIVNMNLSFPSS*AYRHVSSHLDFFFF FKIQRIILPRLISNFWPQEILLWLQPG LGLQPRPQVLVGN
8301	22202	A	8361	376	293	MGFHHVSVQAGLKLTSGLDLPASASQSAR ITGAGHHAQPDF*HSGDSWQAPPEPRDQ G
8302	22203	A	8362	375	142	PQEEFLRFATDVGEYRAVTELERPVSES WNTQKDLL*QKRGRVSTYCRHTYGVGES FSVQRRGEHVGGRLGPCELEI
8303	22204	A	8363	36	363	QLSFNPLIGKKVLRVTFIGKQFLFLIG GGVREAGAHSGAQATVRWHNLSSHAKRP SCLSLPSCDHRHLLPHDPANFCIFWTD*I PPCRSGWVQTPELKQFTHLGLPKR
8304	22205	A	8364	455	235	GAQARAPPRGIIFFFFW*RKGFCLPRP VSKFWG*VPLPWPVKRVGLDSWAPPPR DIFFFSFFVKKRVCILW
8305	22206	A	8365	432	175	STDQVSVAMGPS*PGAGYNLLVCRWLRP LKKCSIRMGVS*FSRYCLSWLPLDKKGN SLTPCASRVRRCTVMLRLMLRGLHPLSD KP
8306	22207	A	8366	383	83	RRLIVFICYFSKK*GLPLLRLVSNFWP QVILVPWPPKVLGL*ALKKLWLDVTHA YNPSTLGGQGRIT
8307	22208	A	8367	27	304	FFGFILTLKKSSN*CTLRFCFLSIGKVR IHTLGNILSRRGYGERCSLPHCLWESIC LPVQSN*ALHKKVQMHIIPFDQAIPSRGI LPTDTGKH
8308	22209	A	8368	165	204	QNIPIAVSFFFFFLKRVSFCCPPG*RAGG QSLFIGALTQV*GILIPYPPGNWELRG PPNLTNEFF*FLNLRFLGLPINLHYVHD KTSPLLYLFFFFF
8309	22210	A	8369	400	201	KERPLPFLIGSPFQGTWPRFFSKGEVK NSNFSKY*PPPFINAPRVCFEGIEVIT KFFQVRPFFP
8310	22211	A	8370	21	408	LIPLSTYVCVRVCEVCVCVCVNI*GYA CNTLLIACNILQDVPTSPTKDKIFSGD FLTTLVGKK

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8311	22212	A	8371	1	94	NTLGHEN*LNSGFGGCSEPRSCHCTPTWATE
8312	22213	A	8372	546	972	PIHSLYGR*PSFCLGLALFKTLQVMHFLKDSVRNLKSSNLKVGLNFRSPQIQATIS.PPLQPKTKTYEEDPKSKPKKEEKNMEVN.MKEWILRYAEQQNEEEKNENSKSLEEEEKFDPNERYLHLAAKLLDAKEQAATFKLEKK
8313	22214	A	8373	502	178	QHFWRRLRQKDSFALGG*KQPGQKGENPF.FQKKAKNILG*WDQPVVPTTQKGGGGESL*PGRTKSPCTSGWGKKQNPVLKKKKNPQKTNCIPLCIYHIFLINRKTNTV
8314	22215	A	8374	362	112	YRMSVNPQVRAKRVSQRTNTTPNFFF*D.RVLLCRPG*STVVQSQTLVASISWAKAILLPPQPRQAKYFLRLVKCSSEKGERIE
8315	22216	A	8375	411	21	VLGIYPTLVSPSPGLKMTRVKLPSPGSKK.VISSNRNPVFGVVAAGG*FDKPILKAGR.ASSKYKAKRNCWPRVRGVAMNPVEHPFG.GGILQRIGKPSAIRIYAPAGRKVGLIAV.RRSGRLRGANTVQEKEN
8316	22217	A	8376	450	108	AEGGRGPRK**LRSCRVDGSAGQSPGP.LRTESLETPGCSPQGVVQLEPPRRPQ.WWPGPPGHRDRRQHRPGRARSROQGPESH*QRSGESRPPAVPRPCLPWKKGVLE
8317	22218	A	8377	25	306	EQQPPPVAVHQSGPPGAPPEASPSHPGS.SEKPPQVPPPPRAPLVPQPKP*LSPPHHP.AAGLLAVHALAGGPGTVQRGLPGRAARA.VSVRVPAARC
8318	22219	A	8378	376	149	PAHCSLLIPGFRGSSCLSLPCNWYPGRA.PPRVGNFFFF*EMESCYVAMLP.SLVLT.SWALAILPVLPPKLPGLQA
8319	22220	A	8379	98	374	SVPPPVGTVEGDAAPTGGGGLPALGR*G.AAGGHVQGHGPHRGHAAPKPSAQGGP.GHSRECLEPSGGAAGGEREP.PRAGGQS.WMRAPSM
8320	22221	A	8380	2	807	RPQCCVRAPRAGAVSGVPKLWSVP*SGR.SAPHPTRS*VRSWRWLRTQSWQTSRTR.RRSESKVRVSYQAWTASPPPAASASARP.A*RTSSRSYSSSSTCCSWLPSSWSTGP.SQTFVRNSSTLSCLCLTRKWIAMMPQVL.PCTPVRPSCSAVSTITRSFLL*QALASR.VT*IAPPRGSTTRTPSPIRL*NLP*LSR.GPGK*KSGSWSSSSSA*TRVVRTSAPLI.TSSSLLSRSSCKAQTG*ASCRPVVPPIP.AGSSLGASAPGSRCHW
8321	22222	A	8381	104	327	CIAPPEMLGIKYEVGKCPGSLKSLKILK.NTHTHTHTHTHTHTHTHTHTHLIRE.GRKK*CVCMRKTDSTCVS
8322	22223	A	8382	400	270	KPKLEVRAAGQVQWLSPTIPALEEAKAG.G*LEPRSLRHFMCVN
8323	22224	A	8383	178	588	ADLLSGAPGPPGGSQDNANSSEHSRACA.PAAPGP*WLQPWLC*WTQSPLEARGS*NPQVSHSRIPGIPGAAGTSRPSGALPP.QPAGHGGSSGELHVARGCACGRPLWSHR.PCCGQLLRVTAADSHRCASGAAPM
8324	22225	A	8384	423	78	QQQELAEALTGVTVESPEEPQRLLS*GG.TVPCLACSLHRTL*TVGHGSASSFLAQG

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						DMEPLGDRGLQGTEQLH*GGDRASLQDI CFLLPVLSLLCPRSLDLHRHRVGVGTGFT ED
8325	22226	A	8385	434	176	FADDSRFDFLLLV*CAMLMLIREQLLEG HFTVNMRLMQDYPITDVCQILQAKELQ DSK*PGGKRPMPGREASRPCAVAPGTHR NL
8326	22227	A	8386	2	305	RLWEDPPGRNTPPGAR*PGPCGEGGHTI REEQACGWPRGHSGPWRHPQAGPLQLGQ WRKGAGQGARRSPQGSLSRPPPTLSAA PPAIHICSVGGVRLHCY
8327	22228	A	8387	331	91	EMRSHSVTQAGVQWRDYGSLQTRPPGLS FNVNWDWVGL*GDPSSPMLLPSS*ARP GGGWGPGGEGHVSKEAAGRLQGPP
8328	22229	A	8388	2	250	IHVRLWSQLFRRLRWEDLLSTGGGSCSE P*SCHCTVTWAFPLESCLCAHVYVYVTL LTALLGSLPCANPRQTAVSLPQAQLV
8329	22230	A	8389	388	176	YWDSQ*CMPSFAVPVESACICAIGHNFS KSVNSVIAVCVDGSSHKYVFTHDGRCHR EAFDVYRDICDDDA
8330	22231	A	8390	445	330	PPRFTPFSCLSLRSSWDYR*PPRPDNE LSLYSVLHET
8331	22232	A	8391	559	142	LRTLPVTLGKSLALSVPSPFYVGGNWIT NREPSAKGRGSGPNRGPCHAASCPARTH SLRHSPPAGGVMLTQPRPILILPETQHPS ESAVARTDISKARRWLHRSRSPWPH*DET SAGAERPGRICYIGHPAT
8332	22233	A	8392	104	400	YYEIFKKEMYSYYHILHFFFFFFF TKPNSVNGPEGKGPILG*LKPWLLG*KH FCLTLPSGGNYRHVLPVPVNGFFFFFFF KKKKVFPFVAPRGV
8333	22234	A	8393	408	169	DQVWIKDWNIGSLRPR*KGPQTIIILTP TAVKIEGIPAWIQHSQVPAAPETWEVR PSLDNPKVTLKKMTSPAPVTLRS
8334	22235	A	8394	1	269	YCCPLFSSKALTQENSPYSSFRLLVNPPG LSLHPEGEGKWINERGRELGPSAGPLL LFLHFAEAGRRQPPDWADSEADLQQRH KLGP
8335	22236	A	8395	2	204	KDCKVNKEVERVLREFHQAGKPIGCDAS TSLPAPAPWWSWNAALCCPGLSCVWCWQ GESRTCVEHQ
8336	22237	A	8396	3	285	KVTVKYDRKELRKRLNLBEWILEQLTRL YDCQEEIPELEIDVDELDMESDDARA ARVKELLVDCYKPTAFISGLLDKIRGM QKLSTPQKK
8337	22238	A	8397	1	192	ETGFHHAGQDGLELLTSGDCPSLASQSA RITGVSHCTRAQLLTEQEYFKNQNLPS APFYKRAF
8338	22239	A	8398	8	241	LNPFLYAFLDPRFRQACTSMLCCGQSRS SGTSHSIRGEKSASYSSGHSQGPGPNMG KGGEQMLEKSIPIYSQETLVVD
8339	22240	A	8399	2	240	SCLNPFLYAFLEPRFRQACTSMLCCGQS RSAGTLHSSRGEKSASYSSGHSQGPGPN MGKGGEQMHEKSIPIYSQETLVVD
8340	22241	A	8400	10	272	CNWQNAYLTVVRCAQDCEDYFAERLYRS MKGAGTDETLIRIIVTRAEDLLGIKP KFHQKYQKSLSDMVRSDTCGDFRKLVA LLH

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8341	22242	A	8401	47	248	TRGIFFFFLNRSHSVAQAKGLGHDHSS LKPQPPRLKQSFNLSLLSTWNYGGLLPH SALWKAEAAKS
8342	22243	A	8403	497	303	TVEASVSYYLYVAMVMQLPWGKSPASGA ESHRQCGGSGWPGGGMEGRGAERGGGC LLPQALLY
8343	22244	A	8404	3	235	LTLLAHCRMMAAAHMGGPPMMPMMGPNT PGMMPVGPAPGMRPPLGGHMPMPGYPM MRSPARLMMVPSQPRMTRPDR
8344	22245	A	8405	3	246	LVFSVDVGLLAHTRQRGLKRSSGMSLL GKIGAKKQKMSLEKSKLDWESFKBEEG IGBELAIHNRGKEGWIKGAQPLGQ
8345	22246	A	8406	1739	804	WEPDVSGSAAWLASAAGMATFSGPAGP ILSLNPQEDVEFQKEVAQVRKRITQRKK QEQLTPGVVYVRHLNLLDETQIFSYFS QFGTVTRFRLSRSKRTGNSKGYAFVEFE SEDAKIVAETMNNYLFGERLLECHFMP PEKVHKELFKDWNI PFKQPSYPSVKRYN RNRTLQKLMEERFKKKERLLRKLAK KGIDYDFPSLILQKTESISKTNRQTSTK GQVLRKKKKKVSGTLDTFEKTVD SQGP PVCTPTFLERRKSQVAELNDDDKDEIV FKQPISCVKKEIQETQTPTHSRKKRRRS SNQ
8346	22247	A	8407	2	241	CLRFPSSPAMGLLRSGTKLIFRRRPKQK EAGLSQSHDDL SNATATPSVRMKAGSFS RRLIKRFYFKSKPKANGNPSQQL
8347	22248	A	8408	285	186	KQGLTSLPRLVSNWAQAFLLWPPKVL RLQA
8348	22249	A	8409	1	246	RHENREELQVIADLCIKYDTLCISDEEF MNGVEYIWKGPCFCLTFTLYLKGDIFP RPPSGCLNLWIVLNPMPVIHLITSC
8349	22250	A	8410	1	102	AGSYTLHIKGGDGTGRVGTGRFTTLHR IQTSEE
8350	22251	A	8411	877	647	FFFETESHVSTQAGVKGWDLGSLQSLAP GPKKFSCNLNLPSSRDYRSPPPPLANFCT FSKNGVSPCWPGRSSTPDRR
8351	22252	A	8412	1	130	RMLNDKTLRTDIGGNFPKNGWAAIATHS FEFAQFDNFLEEATR
8352	22253	A	8413	97	401	CNPENGLTASALGRMCLATCKAPRTL DSGDTASCRFPAPVPRPHSRSSSGSHL PGRPRCPALPGLEWSNPPGPPTSGYLF TFSTPAASHQKTLGLI
8353	22254	A	8414	348	516	VSAYGFTTEGHERFSDHYDTSWKRLIF YINHDFKLEREVWKR LHDEGIIRLYQRL
8354	22255	A	8415	714	410	LGVFRSALHGSLWLLRSFPQKSPNPLA LLLFLQCNATAYQCLLIADQHCRTKYFL CLASGIPCVSHVWVHDSCHANQLQNYRN YLLPAGYSLEEQRILDW
8355	22256	A	8416	2	102	GHDPQDRLLAQDSEHNHSDRNWQRNPW PKDSY
8356	22257	A	8417	1	309	FYFENALSKSNKPIHTIILNPHVHLVGD DAACIAYIRLTQYMDGSGMPKTMQSEET RVWHRRDGKQNVHFHRSGSPVPIKPP CIPNGKENFSGGTSWQNI
8357	22258	A	8418	3	242	ARALTNAASHVDDMPNALSALNDLHAHK LRLDPVNLKLLSHCLLVTLVDHLDPDEFT PVEHACLDNVLASVSTVLTFKYR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8358	22259	A	8419	711	296	NVANS DGLTASLWKEYGKADARWVYFDP TIVSVEILTVALDGSLALFLIYAIVKEK YYRHFLQITLCVCELYGCWMTFLPEWLT RSPNLNTSNWLYCWLYLFFFNQVWVLI PGLLLWQSWLELKKMHQKETSSVKKFQ
8359	22260	A	8420	3	97	FVVSSLCNGLIAAQLLFYWNAPPHKQK KAQ
8360	22261	A	8421	1	279	GCGIADLMSAIFNFQSLTDLILLICT CAYIPSLAPNLLDRNKTGLLGIFWKAT IVERKSPYVAVCCILMAFSILLIQKLVK MPQCICHNI
8361	22262	A	8422	1	228	RHEVFIELNHIKKCNTVRGVFVLEEFVP EIKEVVS HKYKTPMAHEICYSVLCFSY VAAVHSSEDLRTPPRPVSS
8362	22263	A	8423	3	182	SED TGEEQVVTAEFINRGEYEIDIAGYR FQAKAKLYPVASLFTQKRRKDDMELSDL HGK
8363	22264	A	8424	1	70	VQFVFDVAVTDVVIKNNLKDCLGF
8364	22265	A	8425	2	151	ETTASSCTPASLESRRCCAPCRMPRTGF FGSSPLWRPSSRSRLKPGFQQ
8365	22266	A	8426	1	187	RGRVGPGEERLVPGVPGAEAAQAPAGDV RAGPLQARPPAPVGVSGRCQAAGAAAG PPRPDG
8366	22267	A	8427	520	423	GKYQLQSQENFEAFMKAIGECWTERQSC GSHQ
8367	22268	A	8428	1	627	GTSGTRGVTFYFTFTLYLETPKPSISS NLNPREAMETVILTCDPETPDTSYQWWM NGQSLPMTHRFQLSETNRTLFVGVTKY TAGPYECEIRNSGSASRSDPVTNLNLHG PDLPRIHPSYTNYSRGNLYLSCFANSN PPAQYSWTINGKFQQSQNLFIPIQITTK HSGLYVCSVRNSATGESSTSLTVKVSA STRIGLLPLNPT
8368	22269	A	8429	3	390	ILGCNILRVEYSLVICVSVPGSKKVILD LPLVIGSRSGLSRTSSMASRTSSEMSW VDLNIPTPEAPPCYMDVIPEDHRLSP TTPLLDDMDGSQDSPIFMYAPEFKFMP PTYTEVDPCILNNNVQ
8369	22270	A	8430	3	208	NGTHVILLCLKTCGTVVNVANDMIVAS NLGTGVPNQTPVSSGDLIRSNGLLIPG TCEITRLYTISE
8370	22271	A	8431	3	563	LPTSRVDPVRRLDRMKDQEEEDQGGP CPRLSRELPEVVEPEDLQDSLDRWYSTP FSYPELPDSCQPYGSCFYSLSEEHVGF LDVDEIEKYQEGEEDQKPPCPRLNEVLM EAEPEVLQDSLDRCYSTTSTYFQLHAS FQQYRSAYFSFEEQDVSLALVDNRFFT LTVIRHHLAFQMGVIFPH
8371	22272	A	8432	2	119	DGDNILVTTFIYIKSVTELNGDIITNAS WRCSEVAPSA
8372	22273	A	8433	192	1285	AGVLSTIETDSEGLQTKVVENQTYDER LEINDSEEVASIYTPTRHQGLPRSAHL PNKAMADNSSDECEENNKEKKTSOLT PQRGFSENEDDDDDDSDSDSDSDSD DEEHGAPLEGAYDPADYEHLPVSAEIKE LFQVNLQRCVPTDVLHKLKPFIPDFIP AVGDIDAFLLKVPDPDGKPDNLGLLVLDE PSTKQSDPTVLSLWLTENSKQHNTQHM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KVKSLEDAEKNPKAIDTWIESISELHRS KPPATVHYTRPMPDIDTLMQEWSPFEFEE LLGKVSLPTAEIDCSLAEYIDMICAILD IPVYKSRIQSLHLLFSLYSEFKNSQHF ALAEGKKAFTPSSNSTSQAGDMETLTFS
8373	22274	A	8434	3	251	TLQADHFNTRLSCGDAAQTLWARTGYLG FVRRTeltaATGERHDALYVVGALDETL ELRGLRYHPIDIETSVSRHRSIAEW
8374	22275	A	8435	1	225	QTFNLEGSQIYEDSIVLQSVFKSARQKI AIEEESDESNEDDEDEYHEWKRYD RLGENMCLNCIWNNGGGYIV
8375	22276	A	8436	95	340	CGCGIAGLAMSALFNFSLLTVILLIC TCAYIRSLAPSLDRNKTGLLGIFWKCA RIGERKSPYAVCCIVMAFSILFIQ
8376	22277	A	8437	1	317	GPKPLVRTSREPDKDVTSGYSSVSTAC PTSSVDGGLGALPQPTSVLSLSDSHTQ PCHHQARKSCLQWRPPSPPESTVSQQQV KRINLCIHSEEDMNLGLVRL
8377	22278	A	8438	80	213	PHLSFNAGITTIKVNIRNANSLGGGFHC WTCDAARRRGTLSQSYLD
8378	22279	A	8439	3	767	HEDNIKQLKEMKFTYLINYIQDEINTIF NDYIPYVFKLLKENLCLNLHKFNEFIQN ELQEASQELQQIHQYIMALREYFDFS VGWTVKYYELEEKIVSLIKNLLVALKDF HSEYIVSASNFTSQLSSQVEQFLHRNIQ EYLSILTDPDGKGNEKIAELSATAQEII KSQAIAATKKIISDYHQFRYKLQDFSDQ LSDYVEKFIAESKRLIDLSIQNYHTFLI YITELLLKKLQSTTVMNPMKLAGELTI IL
8379	22280	A	8440	103	354	NGCECDFLFLFLFYFFETESRSVAQAGV QWHCLGSPQPSSPRFKRFSCLSTLGGRG GWIMMSGVQDQPGQHGETPFLMQAGLKT
8380	22281	A	8441	3	160	KLYPLKIVFGMNGRVWVGKTVQQTLL ANVLEACELMTLDQRILMFLAES
8381	22282	A	8442	459	3	CGGLHPVRASWLLCLPKQAWAMAGAPP AWLPCLSLISDCCASNQDQSVGVGPSEP GAGYNLLVRRFLSLSEKRSIRVRVTRFS RCHLSPLSLTRKGNSTPCTSRVRQCLA LLRLAHGALHPLSCAHCLALPSEMTVPV QMNAEITRLL
8382	22283	A	8443	2	318	RQGNMTAALQATLLNPPINTKSQAVNDR ARGIVLNLISFKANDIEKAVQSLDKNG VDLLMNYMYKGFESPSDNSNAMLQWHE KALAAEGVTSIVRVSTALIPA
8383	22284	A	8444	2	109	VTPFPMSCDLQGDACARNPQAQEHSRKD LRGYSHG
8384	22285	A	8445	1	69	LVLNSWPQVIRRPWPPKVVGLOV
8385	22286	A	8446	1	163	PSEKHNIWVGVTQFSRCRLSPLSLTRKG NSLIPCASRVQRCLTLRLVHGACTH
8386	22287	A	8447	1	147	GQAGLELLMSGDRPTSASQSAGITGVSH RARPPSSISFILELRGSRKKF
8387	22288	A	8448	914	729	GLTMDTQKDVQPPKQPMIYICGECHTE NEIKSRDPIRCRECYRIMYKKRTKRLV VFDAR
8388	22289	A	8449	134	392	TCPPFPPEPPSPLTCAVLVPQTRWRGLG SLFRRACCVALLPLQLLLFLLLFLPLP IREEDRSCTLIANNFARSFTLMLRYNGPP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PT
8389	22290	A	8450	37	248	AKITPLLQPGRQEQDSISNKKILRCCLT MLPRLASDSSGFKRSSHFSPLTSWDYRH SPPPLASVPFLLMC
8390	22291	A	8451	367	165	NFFVFLVETGFCCHAGQARLQLLASCDLP VLALQSAGITGVSHCARPISTLKDITKT SHFVPLKISGK
8391	22292	A	8452	2	282	GKRMAGGPENMQLRLDGNRLYITTSMF AWDKHLYPDLIREGSAMLHVDVDTALGG LKLNPYFLVDFWKEPLGPSLAHELRYPG GDCSSDIWI
8392	22293	A	8453	4	163	HHDFHAQSLLANIERIAILVFAACEAAA VLSLLVSIISNTYGLDYLHNLKLLQC
8393	22294	A	8454	374	197	TPEPKQSSHLGLSKCWDYRHEPPHQARN STFDSNHSSLAEDKLLGYFGLSQWQPG YQP
8394	22295	A	8455	343	161	MGMGPSVPGTGYNLLVCRLRPLEKCSI RVGVSVQFSKYHLSRLPLPRKGNSTPCA FWVR
8395	22296	A	8456	1	193	MGFLHVGQAGLKLPTSGDPPTSASQSAG ITGMSHRVQPYVLSICQTLHSHVCICLL IILLTTVL
8396	22297	A	8457	342	263	WLRPVVPALWEAEAGGSLELRSSRPA
8397	22298	A	8458	101	303	KAAKYLQRLHFCFLNLKKNMLLFNHR MENFKELFGPGTVAHTCNPSTLGGRGW ITRSADRDHPG
8398	22299	A	8459	3	140	YLKHLKMYVCKYLRQGLMLPRLVLNSW AQRILLPWLPKVLGLQV
8399	22300	A	8460	327	248	FPRLVLNSWPKAILMPWLCKVLGLQA
8400	22301	A	8461	327	79	SIPFILAFFIYLSFFFKETGSQSVTHAG VPGIIIAQCGLQLLGGDPDPSASLVVG TTGTYPTPLSVFPNMPSPFILLCMLF
8401	22302	A	8462	365	273	MGFQHVGVGLRWPQVICLPWLPKVLGL QA
8402	22303	A	8463	375	217	QAGLKLTSDDLPPASASQSAGITGVSHH AQPRHHFFKTRFIYIFSSPSSVLS
8403	22304	A	8464	238	354	RGKCFVQAFLYKECSGGQARWLTPVIPE LWEAEVGRWIT
8404	22305	A	8465	367	248	FQMRIHKWLIDLHSPSEIKQITSISIEP GVEVEVTIADI
8405	22306	A	8466	341	153	NMILGWAQWVTPVIPATGEAHWGGLLYP RSSKPAWATQONLLFTKKKKNIIYIYIYI YIYERY
8406	22307	A	8467	368	101	VEMGFRHVGQAGLELLTSSDPPASVSQS AGSSTSLPTADLLTPGWVGVGLVDKNP VTLIAMQRLPAVLEKKSARKNSSENKIV LKRQ
8407	22308	A	8468	362	248	HVGQAGLALLASGDPPTSASQSARIAGV SHRARPEAPL
8408	22309	A	8469	384	196	SARLGLPKFWDYRREPPCPADDMLILMV GILETFSLIFTATMESRNYCVYFKMRNK HIISKTS
8409	22310	A	8470	386	300	LAMLPRLPNSWSQVVLSPPLPNMLGLQ V
8410	22311	A	8471	380	178	PKKNKFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFF AIVYQTLACNNKFLQMERVTRKLRQC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8411	22312	A	8472	3	154	FLVDMGIHHVVSQAGLKLTTSGDLPASASQSPITFFFLFFFEEKQILAQAGG
8412	22313	A	8473	3	162	GLYHVGQAGLKLPLTSGDPLASASQSVRI TGVSHRTRPKIIFKLIFLFFFLVA
8413	22314	A	8474	266	107	LCLFLIEMRFPYVVOAGVKLLSSSHLPS SASQSDRITGVSHCFWPEVFKRGIF
8414	22315	A	8475	361	169	RLPGPSNPPTISASLAAGITGARHHAQLI FVFLVEMGLCQAGKHNFERYSRVLIYSP IVSFTHFI
8415	22316	A	8476	1	154	KKLIPTLMDHGAGFKSSVKEITTAVVEM AREVELEVEPEDGNELLOSARGKT
8416	22317	A	8477	3	193	SHYQSLISSNHGKHCGRPOGPLPRKTI DLCSLDYQLTFPPLLTHDPVKSPSVRNT QELSLIP
8417	22318	A	8478	408	103	TGSRLTLSSRVECSGVITAHCNLELPGS SDPLASASQVAETTGMHHVWLIFLGIF LVKMASHYVAQDDLKLLGSTDPVPSASQ SVGITGISHHAWATICYK
8418	22319	A	8479	59	166	NVNTCLCLHTHTHTHTHTHTHTNYFKE TPIHQYI
8419	22320	A	8480	394	253	FLLLLESSEGFCHVAQAGLKLSSCDLPA LASQSAEISGVSHCAQPLA
8420	22321	A	8481	379	184	CFSLPKCWDFRGVPISPGDFWNFTIKLG VCPFCQGGFELLAPNDVAASGFQNAGIS GINFWAWAL
8421	22322	A	8482	367	170	CGLSSGLGGRSGRESERKKERERERDRE KKKKEGERKREKRESVSSYKDTNSMG SGPHPYSLI
8422	22323	A	8483	324	136	QRSSCLSLPSSWDYRRMPPHLANFCIFC RDGVLPCCPSPWSQMTTSLSLNFLICLV GIILGRG
8423	22324	A	8484	1	57	GERRYGTCTYQGRWLWAFCC
8424	22325	A	8485	35	339	GWLLRFFFWQWKNNGNNLVSLIDGNLSY DTLGYNGILNCHMYILTEGDSOKKKKKK KKKKKKKKKKIDPAGNSKIYNRKIFKT' PRGFFKWALGPLLILFF
8425	22326	A	8486	330	66	RPGVSRFNPWPLIFFLRRVFLCRPGWNA VVQSLLTKISASQVQAIPLGGGGCSEPR SCHCTPAWATTAKLCFKKNGKNFTDIM FSK
8426	22327	A	8487	3	209	CLSLLRSWDAQAPPPHPANFFLMFNFCR VGVLLCCPGLASSDPPPLVVSQSARITGM SHCTWTIFLSFK
8427	22328	A	8488	3	216	GQSITVSTATNSDVGSSNLVSWYQSSN LVSWYQQHPGQAPKLIYEDNKRLSSEK KKKKKKKKKKKKK
8428	22329	A	8489	326	62	PAYFSIGSFLEFLFFFRTECHSVTRLEC SGAI SAHCKLRFPSSNSPASGGGRSE PKSHHFTLAWTTRAKLHLNKNKIKTVKE FLSS
8429	22330	A	8490	2	156	SSAGIGRTGCFIATRIGCOOLKARGEVD ILGIVCQLRLDRWVCGCKQGGQR
8430	22331	A	8491	399	254	KMNKRNTINNKITNKLIIKLKNISFLY FFFFFFFF
8431	22332	A	8492	2	130	FRRVGQAGLELLTSGDLPASASQAGIT GVSHRAQPTFLKSC
8432	22333	A	8493	3	94	HLPAEFTPAVHASLDKFLASVSTVLTSK YR

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EHDRPTALINGHLNSLQSNPLLPDQKVC
8453	22354	A	8514	99	262	MNKRFLLNKKKKKKKKKKKKKKKKGG PFKKNPGGAQIFPGGEKKIFFLKGGL
8454	22355	A	8515	85	2	GWGWAQWLTPVIPVLWEAEAGGSRGQE
8455	22356	A	8516	244	423	VFAVFNFLGWVMDMLINLAVVITLQCAC ISNHHVVHLEYIQFLFANYTSIKLGKKP SKSV
8456	22357	A	8517	3	114	KINGEDKQKILDKCNEIINWLDKNQVCV FFFFFFPI
8457	22358	A	8518	413	91	GGVVRGKISFRGGGFLKKKKKKLLKKKKK WGGGPKEKKKRGGFFFFLLNFFFWGGV KKKKKKKKKKKKKKKKKKKKKKRRK GRKEGREGRRKEGEGRQEIINMTA
8458	22359	A	8519	1	163	SRLPGRSRRRSRGRRRRRRRRRRRRRR SRVLIFFPDQNLDLNIVYIIEDVDAA
8459	22360	A	8520	191	21	RFTTHVDAWATVTVFLIESVFLHVGQAC LELLPSDDLPAASASENARVTGVSHRAWL
8460	22361	A	8521	2	144	AAATSQAWWCMPVVPATWAEVGSALKP GRLQLPLTMIALVHLSYAI
8461	22362	A	8522	90	8	KPTPFLPTLIARTTLLLPISPLILIL
8462	22363	A	8523	305	146	VFRIHSCGIRGSVDVKITDGLLVIRRIE NVPPGPNKNKNPNYAIQSSSIESQ
8463	22364	A	8524	176	2	LAWPFLFLPKCWDYRHEPLQPASLTTFV REWDKIGAWWLTPVIPALWEAEVGRSQ GQ
8464	22365	A	8525	2	200	CLIPSSWDYRHMPPRPANFCIFFFFLGD HVSQVGLKLLTSKDP LAWTSQRAGITGF SHHTKPQGFF
8465	22366	A	8526	2	217	SFSLFPSPSFLLLPPLASLLLPPLPSF SLLFPSPSFLSPPSPSFLLLPSPSIFL HPTFSLHYPPSPSFI
8466	22367	A	8527	2	186	IRGLRPLEKRGIRVGVSFRFSRYHLSRLS FARKGNSPTPCASRVRCPSLLHGLHPL SDKPQ
8467	22368	A	8528	3	153	CLGFLSGWDCRCIPPCLANLKKLFVEMG SLFWPQWILPPWPLKVLGLQV
8468	22369	A	8529	2	388	RTAVHTFILVLQVCVCRHLSLAALTPA HLVCSSHRILSYLSIRGSWDHRCMTTTP GLVISIFFVEMKYRYAVHAGHILLGSSY PASAYQSAEITGVSHWAWPTDSLWQKPH MVIWCISCFLNVLIGTM
8469	22370	A	8530	293	64	YRISIKVSKWFKGWVSFFWIFFFFVFFF SFFFVFFCFMFFLKQYLFIIINIIIL TQALYICTTSKICYSFLYER
8470	22371	A	8531	2	250	SCLGLPSSWDYRGTLPCLANFCIFNRDG VSLCCQGSQTPGSQVIDEAVYSIYAYY ILALLIVYVAQWEVWLKHFCILKYT
8471	22372	A	8532	2	201	FHHVGTGLELLSSGDLPAASQAGIT GVSHCTWPSILYRMNFKNLSAVFIWVI EGNYTNKTCI
8472	22373	A	8533	319	200	TFTFFLQRWGLTMLPRLVSNWAQAICL LQPPKVLELWA
8473	22374	A	8534	160	297	KTETLALVAHACNPSTLGGIGRQVSSAH EFKTIILGNMTPILYTKL
8474	22375	A	8535	333	228	PNRGHYIAIVKSHDFWLLFDDDDIVEVSS FLISYF
8475	22376	A	8536	3	325	PPSSLLPCSWILDCCASNERDSVGVGPS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EPGAGYNLLVCCFLSLLEKRSIRVGVTR FSRCRLSPLSLTRKGNLTPCASQVRRCLALLRLAHSALHPLSCSYCLALP
8476	22377	A	8537	216	5	KLGLVLNLVEFQVKFFFLFFLEILLIE MRSHYVAQAGLELLGSGDLPASASQSAE ITGMSHHALPNYSF
8477	22378	A	8538	136	22	RPRRLVLNPNWPQAILLWPVPKVLGSQV WATCGRRPAS
8478	22379	A	8539	136	22	RPRRLVLNPNWPQAILLWPVPKVLGSQV WATCGRREAS
8479	22380	A	8540	8	319	YIYMSMYMLIYVCIYVSIYICVCIYINS ISFNTYMIYMLIYVYVMCVYICVCVY IYTNISISFNTHITPIKHSVDVHTVSTTRC NLGGRGFCHTWPLPHLAGW
8480	22381	A	8541	331	156	SVNGLLSLPACLPVCLPACLPFLPSFL PSFLSFFLLLLLLQKPVNSLIFSQSLIS
8481	22382	A	8542	72	1	KIGQARWLAPVIPALWEAEAGGSP
8482	22383	A	8543	2	83	QAGVQWRDLGSLQALPPGFMPFSYLG
8483	22384	A	8544	293	2	KTVWHYLVNAPEVEIQAIYSQETCKSMY QETCTRIFIAILFIAPNWKQRQDTMNP GNKENGKVATLDSGFLVRFQSLMRSNCL PLYPFNKFPILLK
8484	22385	A	8545	314	122	LVETGFLHVGRAGLELPTWSDPPTSASQ GAGIAAVSHRGQPVDFKNNISTQIQGRP IICNYKTF
8485	22386	A	8546	316	123	LVKTGFLNVGRAGLEIPTWSDPPTWASQ GAGIAVAVSHRGQPVDFKNSISTQIQGRP IICNYKTF
8486	22387	A	8547	3	247	GIMATERLANYTGGIYAEYQDTTYINHV VSVAGWGISDGTTEYWIWRNSWGEPWVRC FHFLKVI PRKKT SWYSSRLNGSVYV
8487	22388	A	8548	289	25	QRREKFFKNGPPIFFRGPFQIFVVSF PFFPKIGVFFVFFFRFSLVLKGDFFSN FLKINCFEEEEEEEEEEEEEEFIKN RPCL
8488	22389	A	8549	289	2	KKKIGETLCKLCKLCKFLDVT PKAQFIK QKKEKLINWQFIKIKNFRSPKALLRRGK GKPGTGRKRANHISDKGPLCRIQKNS RGRAQWLTLLV
8489	22390	A	8550	290	187	RQENPLNLGGGCSEPRWCHCTAAWVTE QDSINK
8490	22391	A	8551	293	183	RDEGRGISYMLPRLVLNSWPQAILLPQP PKVLELQA
8491	22392	A	8552	364	87	MLPLDFFLGPSLDFCPFCESGSGGIKV PESTTPRASAFLPPGAANLHHLQLVGA PRVPPGFHHVGQDGLDLVDLVLRLPRPP KVLGLQGG
8492	22393	A	8553	57	225	KWQKWPWAGGVAHACNLSTLGGRGGKI ACAEEFKTILENIVRCLSKNKWISFS
8493	22394	A	8554	326	2	KSKRGYSEPLVFSICSARAPRSHSVSQA TVYGHAASTQFPPLNRSSYLSLLSS GDYRHDPPPLAYICISVIGNDVEHLFLC LLSTCISVNRSHVYSTLVPIFGP
8494	22395	A	8555	372	148	YICFLRSSVRQILFTDCSDCSMWVPCN IRLPGSTHWCASASQAGTTGARHHARL IFFVVVFFCIFSIFSRNH
8495	22396	A	8556	422	269	AADQERLHTYQLNYYHFCRWRGLTTFPR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LVSSSWVQAILPTWPHKVLRLQA
8496	22397	A	8557	669	407	AGVKWRNLSTLQPPPRRFKRFSHLSLPS SWDYRCPLPCPANYCIFLVEKEFRHVKG AGLELLTSGDPPAWVSLIAGITGVSHRA HPD
8497	22398	A	8558	195	352	LGLQAGTTASGYSTVILGMLKPRSWAW WPVVPATREAEVGGSLPEGRSKLQ
8498	22399	A	8559	345	219	MLARMISISLPCDPPASASQSAGITGMS HHGWLNLFKSIHL
8499	22400	A	8560	137	2	VKYCLPTRSLIKTVRPLSPSQATASEPT CTYTPRWPEVTEESQKN
8500	22401	A	8561	324	193	RSSGNLPASAAQSARITGVSHRTRPKCI ISKEYVAENNLKSTS
8501	22402	A	8562	326	121	HNHTHTHTKNHKKHQPOHTHTYHTQTD IYVLQAASQKSLILISSLAV
8502	22403	A	8563	3	85	HEHTHTHTHGHHTHTHRHTHTHTLCARM
8503	22404	A	8564	2	153	ARDRHTPPCLTNFSVFWRDGGLAMLPR VSKLWAQAVHPWLLKVLRLQA
8504	22405	A	8565	2	177	ARVGFHYVGQAGLGRITSGDPPASASQS AGITGMSHRARPMSSLTHLIQLDTRWAY AG
8505	22406	A	8566	353	212	AGFRHVGRAGLELVTQDGPRTSACQSSG ITGMSHCAHPEKSTAFLE
8506	22407	A	8567	76	191	ELIFCRDGGGLTVFPKLISNTWPYAVLPL WPPKVLGLQV
8507	22408	A	8568	1	142	GTRGFLHVGQAGLELPTSGDPPALASQG AQMTGVSHCASQKKEFLEW
8508	22409	A	8569	250	95	SASRAPLPLPSSHLPRAAGLSPLCPPR LVSSYRPHVILLPLPPKVLGLQV
8509	22410	A	8570	3	226	HEHTHTHTHTHTHTHTHGHHTHTHTLV LVYSLCEHIWRFIVISRARVCCIYVVVF FECGYADRRVADKWLWIH
8510	22411	A	8571	1	216	GTRGLGVGVSHLVSKNTHHTHTHTHTH THHTATASQLSVFKIWAQFQSLDKGLT YISNSYCSSKFYLYNH
8511	22412	A	8572	356	268	LTMLARLVNFRPQVIPQPWPPKMLGLQ A
8512	22413	A	8573	12	175	RWGFHPVGQAGLELLTSSDLPTLASQKA EITGMSHCARPSFFSFFLSFFFWKHL
8513	22414	A	8574	1	163	GTRTGFFHVGQADLELLTSGDPPVASQ SVGITGVSHRAWPVGLCIALISNEY
8514	22415	A	8575	344	176	EFLVETGFRHIGQAGFELLTLGDQSTSA SQNTEITGVSHAPAGLAIIFKSGNQAFF
8515	22416	A	8576	2	179	ARGILCHSGTFKLDSPSMVAHTCNPST LGSQGGRIACGQEIDTSLKVARPRLYG QIF
8516	22417	A	8577	1	100	GTRGFTMLPRVVSWSAQVILLPWPPKV LELQM
8517	22418	A	8578	3	114	HERHEILSIYLTIIYLSIYLSIYLSIYLI YLPITITRI
8518	22419	A	8579	1	264	GTRPCRTELYRVVESLAKAQETSGEIS KFYLPNCNKNGFYHSRQCETSMDCGAGL CWRVYPWNGKRIPGSPBITGDPNCHIYF NVQN
8519	22420	A	8580	1	245	GTSGTSGILGFYLEREDRLLQIRTDIT LSHGYSTFSLNRCDSRHHMNRMFQMLYQ SPFLGYIQLSHEVLAFGISIYINTE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8520	22421	A	8581	1531	1457	QARNETIARRLWDVSCDLLGLPID
8521	22422	A	8582	191	2	TITSYFSPTPAPGSHYATFCFYKFDYSR YFIKVELWEAETGGSRGQEIETILANTV KPRLSRA
8522	22423	A	8584	2	212	ARAGIYPKEYKSFYKDTCMRMFIAGLGF TIPKTTWTQSKCPSWIDWIKMYRQGPIL SPMLECSGEVSGFK
8523	22424	A	8585	2	192	ARGNSPASSSRVAGITGAHHHARLIFVF FLFVRFFFSFLKTGFKLVAHSNFQPLTL FAPLHFK
8524	22425	A	8586	277	66	PLDFRLGHKRRLPFPKKKKKESKFVCVC VCVCVCVCVKRQCLVTLPRIVSNSWAQA ILLSWPPKILALQV
8525	22426	A	8587	395	286	PHLGLPKCDYRREPPCLAEEVVLKKYVW VTYFSFRR
8526	22427	A	8588	307	177	RYPSTINYSILNRDKIMPKLDRMVYKAR PRVMCLPWPPKVLGL
8527	22428	A	8589	167	349	RNLRELGEFFFFFFFWFFFFFFFVGKFS VFLLVGNLFLFFGGGIFGLSRVMCFKEF RCFS
8528	22429	A	8590	375	240	LLSRFSWFVFRQGLTMLPRLVLNCWA RGILLPWSPKVLGLQA
8529	22430	A	8591	347	215	ETGFPHVGQAGIKLLASSDPPASASQSA QITGMSRRAQPSAKRF
8530	22431	A	8592	340	114	HRTAHCSLYLSGSSDPATSSSQVTGTG KDQHTWLLFKYFCRARVSKINKYKSKINK FYFLNTQTTPSEYGKASPG
8531	22432	A	8593	86	253	LRLCCGLSCSTAKKKKKKKKKPKKKKI KKKNLHPKRGGFEEILFFPKGGKNLF
8532	22433	A	8594	3	135	GFCHVGQVGLLELLTSGDPPALASQNAEI TGVSHRAWPPVLFFF
8533	22434	A	8595	2	274	PRVRTISLLGILVYRSHLISLLCLEGI ILSLFIIATLITLNTSHLLANIVPIAIL VFAACEAAVGLALLVSISNTYGLDYVHN LNLQC
8534	22435	A	8596	3	316	SIPYSWGEKEGIPCMAPPQIQGTSRLND FTALSLHLNTHTHTHTHTHEIQHLPP QGITALILNSLLRHYCPSLAFPSLSPKQ NLTVRHCLSRDTWLATASK
8535	22436	A	8597	385	291	KAPPLFFFFFFFFFFFFFFFFFFFFKPV KKILGV
8536	22437	A	8598	275	369	GVQVLKLLTSGDLPALASQSAEITGVSH RAR
8537	22438	A	8599	98	344	VHYEEFMCVCVCVCVCVCWPRVRGVD MNPVEHPFGGTHQHGPKCTIRRNASA GRKVRMLAALWTVRIGGKTIVTLRKT
8538	22439	A	8600	328	195	THVPPSLAKFVFLVKMGFLHIGQAGLDL STSGDPPALASHVFKR
8539	22440	A	8601	2	214	HVDVVMGTFAILSELHWDMLHVDPENLR LLDSVLNCELANHFDTFTPPVQAYQK VVADVANAHAHYH
8540	22441	A	8602	89	181	GLRHNRLNSGGGGCSEPKLCHCTPAWA TE
8541	22442	A	8603	340	57	KEGHQEMEQAEDGGHGRKAPGTSPWTLG ELPKSARGHTGLFVSYRCRTQFRFKKV LFGGDRNRGLAMLPRVLNNSWPQEIILP QPSKVQGLQK

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8542	22443	A	8604	330	132	TGFLHVGQSGGLKLLTSGDLPTSAFQNA ITGGSHTCTRPFSLFHSYLVLFYGCSSSQ VSLSLIARM
8543	22444	A	8605	546	279	RPGPTVSPRLEICMIMAHCSLDFFPGSG VSPTSASRVARTTSTHHHAWLIFYSSVE TGSHHVAQAGLELLGSSNPPIASQSAG ITAL
8544	22445	A	8606	3	249	NRFNLGSGGCSEPRSHHCTPSWATEQET CITYLEYCFPPVSHNTLVYFKPLNVITR SDYCILGLHASSIGGSDSLIIDCW
8545	22446	A	8607	159	324	VIQYRTNHLHLCEVLVFWFLPYFFLK KTYTGIGQMRWLTPVIPALWEAEAGGS
8546	22447	A	8608	334	179	TGFPHVGQSGGLKLLTSGDLPTSGSQSAG ITGVSHCTWLEVIYFLNISYPS
8547	22448	A	8609	278	202	QQPSTLRQDPFPAKRLHLSEGS DGH
8548	22449	A	8610	236	66	AASTFFLQIKRHLLSGTVAHACNPSTL GGRGIRISRGREFKTS LGNMVRPRVYK
8549	22450	A	8611	29	177	GKQVMALHCFIFHHFFRRSLAMLRLV SNSWVQEILPPWPLKVLQLQA
8550	22451	A	8612	1	215	HTSRTLFLVHLRLKFNFKYLIEWGLSMLP RLVLNSWAQAVLPWPSKVLGITGMSHC TWLYLHLSTDLLKLC
8551	22452	A	8613	3	91	LRHGNCLDPGEGGCSEPRSCHCTPAWVT E
8552	22453	A	8614	2	167	FTISLLGILVDRSLTHHNNIKPSFTRE NTLMFIHLSFILSTRKQLAIQHLSRLE
8553	22454	A	8615	2	281	FCILVETGFHCVAHAGLQLLSSGNPPAS ASQSVGITGMSHCTSPNLSLLTQSKSFC LLIQHNPNYAFINSQLTFSILFLLSYFI FYDSLFLLF
8554	22455	A	8616	282	182	GQAWLTPVIPALWEAEVGGLEPRSSR PAWST
8555	22456	A	8617	379	207	SNQTTKKYINFFFVEMRSHYVAQGLKF LGSSNPPTSASQSASITGISHYVWPISP S
8556	22457	A	8618	705	483	DKSFALVARAGVQWHHLGSLQPLPPCFK QFSYLSLPSSWDYRHAPRPANFCILSR DGVSPCWPGWSRTPDLR
8557	22458	A	8619	359	220	RQSLTMLPRLVSNWSAQAILPPWLSRL GLQALAPIPGKSYNEKTP
8558	22459	A	8620	3	186	HEVSWVKRKQDEWIEFDDDTVSIVAPED ILRLSAGGDCHIAVLLYGPRRVQILEE ESEQ
8559	22460	A	8621	1	116	GTSFCRDGGLTVLAQLGSSFWPQRI LPPWPKVVELQA
8560	22461	A	8622	369	188	MYSLEMGFTGNHAGLELLASGDLSALA SESAGITCMSLRYRTRFSFKRATCGDL SLQS
8561	22462	A	8623	202	22	YILGFYFMPVICYQERKKDKKNWEVT TMSFVGICMELGAILSLKLMQEQT KYHIFSQV
8562	22463	A	8624	387	315	SNLGGGCGSELRLCHCTPAWATE
8563	22464	A	8625	2	135	TRDLCSLVYLLTFPPLSHDPAKSPSV RNTQELSIKKKKKGRPF
8564	22465	A	8626	3	232	HASAFEEPVIYIKSRQKRKESNPPKLV SSQPHGLKKKKKKKKKKRGRGLKKKKK KHKKFKKKQKKYNFGRGAF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8565	22466	A	8627	97	373	QHGFLLKKKKKKKKKKKKGGPPLLKKPLG GPNFTGDGKKKKFFPKKGGIKKPPGEFLK KNLFLGGKKNGKNPPKKNLPLGEKKNFK GKKGKNPP
8566	22467	A	8628	2	188	RYGCPPPYHTFEFPVYIKSRQKRKEWNP PKLVSSQPHGLHDFKKKKKKGA AVLKD PSGGPS
8567	22468	A	8629	287	68	GEEGRTOQGERNNGGGSERKEGEEHEAR RTGRGEGGGGEAKGRPRSARRRGSRG SKSQTPSRHLPAHIITN
8568	22469	A	8630	364	136	VSLLLGLEYSGTITAHYSLNFFLLFIVET GSHYVAQTGLKLLGSSNPPTS DSQTFEI TGVSHGAQPKVQFWSKNLDT
8569	22470	A	8631	355	70	LFPPRFFPFSPSLSPLEFFSPKGFNF REFFPIFSPPKRVLSKNSPGGFYKPLL RGKIFTFPPPVKFGPPRGLFKGPPPPFF FFLFFFFFFLVI
8570	22471	A	8632	2	266	AFTISLLGILVYRSHLISLLCLEGIIL SLVI IATVITLNTSHSLANIVPIAILVF AACEAAVGLALLGSISNTYGLDYGHNLN LLQC
8571	22472	A	8633	1	186	LTHHINNIIKPSFTRENTLMFIHLSPIIL LKKKKKKKKKKKKKKKKKKKKGGALKKK PGGGQN
8572	22473	A	8634	2	80	VLEIAVALIQAYVFTLLVSLYL RDNT
8573	22474	A	8635	713	333	EGPPPPRSKKKGTQGGKDDPPSPPEPKT PGNPQGRKTGPPPPGPRYTGP RPSSGP TRGGGSRSSSSNTNAPGEKIFFSKNPGR KIFPPRAILVFFSPFPLKNFFFSRLLI FLGGCAPFFPPPK
8574	22475	A	8636	389	1	FIFSFLFLIIFFFLNINFFFIYFSSLSF FFFLNFNLLKHTPPIILFFFSLSPIFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFGTKKELY LLRARGCKQYKNQKLIWYLT
8575	22476	A	8637	2	192	VRTLGLRDTAIPGRLYQTFTATRPVY YGQWYEICGANHSFMPIVLELLALTIFE IGPEFTL
8576	22477	A	8638	1	87	PTRPLEIAVALIQAYVFTLLVSVYLHDN T
8577	22478	A	8639	2	132	INLASTLIIFTILILLTILEIAVALIQA YGVTLVSLYLHDNT
8578	22479	A	8640	2	113	LEFFIAEYTNIIINTLTITIFLGTTYDA LSPELYTTY
8579	22480	A	8641	375	22	FIFISPLAYLFFLPFPFFFIPLCFFFF IPLFFFLFSLFSLIFFLFSLILIFPPS LFFFFFFPFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFCWLPHRVMIKVGISVSVSKKI
8580	22481	A	8642	180	34	WFISDSLWLGMAHTCNPSTLVGGGWI TCGRSRSPVPKRTPSQTCAPI
8581	22482	A	8643	338	133	NLPLGLFYSLQKKKKKPLRPGTLGAPK GNFQGA PLFGKFAFFFFFFFFFFFFFFF FFFYGFFFFLKF
8582	22483	A	8644	156	287	LTYPKIPPLCSQKKKKKKKKKKKKKK KKKKKGAFKKNPWGAQI
8583	22484	A	8645	1	325	LHHCHTHNFVNKVCVIRKKKKGKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKREKKKKKKKKKKGGGPKKKPPGGPK FSGGGKKKLFPPQGGYKKPPGGFLGKTL FLGGEKMGENPPKKIKPLGEKKIF
8584	22485	A	8646	370	3	PVRASRLCLPKQAWAMAGAPPPASLPP CSLISDCCASNQRDSVGAGPSEPGAGYN LVMHCFLSPSEKHSIWGVTRFSRCCPS PLSLTRKGNLTPCASQVRQCLALLRLV QGAGTHRTRG
8585	22486	A	8647	341	88	KKKKIFSPPIKRGPPSVYFICPPPPFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF PIWHKLCGDL
8586	22487	A	8648	1	108	PTRPRTRGVASVLYFTTILILIPTISLI ENKILKWA
8587	22488	A	8649	3	96	EICGANHSFMPIVLELIPLKIFEIGPVF TL
8588	22489	A	8650	457	297	SPSFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFLFYFALF FIYLI IKDNYMFQC
8589	22490	A	8651	84	352	YEKTDVKIISILFNTDYMLEYNVLHILG QIKMLLISKKKKKKKKKKKKKKKKKINK FFWGGLILTLGIVLYSPLEALKISPSF GFLEK
8590	22491	A	8652	2	111	NNIKPSFTRENTLMFIHLSPIILLLSLNP DIITGFSS
8591	22492	A	8653	1	305	RQQQQQQQLRNLRDFLVYNRMTELCFQ RCVPSLHHRALDAEEELHSCAGKLIH SNHRLMAAYVQLMPALVQRR IADYEAS AVPGVAEQPGVSPSGS
8592	22493	A	8654	129	268	LSEVLYLFPPKKRLIILCLFFRNPGSS NLQKITKEPIIDYFDVQD
8593	22494	A	8655	281	117	CTITLSFINTLQAYI IWL VVFSEVCLYV SLSIYLSIYLSIYVFERYIKISPHL
8594	22495	A	8656	3	177	DLHAHKLGVDPGNLNLSHCLLETLAGH LPGEFTPAGHAFLDKFLDEVSTVLTYYK R
8595	22496	A	8657	3	270	RRRGRAHCSLDLLGSRNPPASASRVAVT TGRHLAWLIVGGFLFFVLRDVLVRFH ATDKDIPKTGQFTKERGLMDLQPHMAGK ASQS
8596	22497	A	8658	107	11	QEHTKPTPFLPTLIALTTL LLPISPFI LIIL
8597	22498	A	8659	21	136	VPIEHDPVPNSRAEL LKMFGIDRDATA QAVRGLITKA
8598	22499	A	8660	1	395	LVTALYSLYIFTTQWGS LTHHISNLEK KKKGKGGKKRGGALFKGIFGGSHFFGV WELLFFFLKGGIKKTILGLGKTLFFGG GLLGAPLPRKIKGLREKNFKGELGVKN RVFFFGNFSSLGVYLKKY
8599	22500	A	8661	1	255	RTRGRTRGRTRGLTRGKKKKKKIMKKKK KKKKKKKGGAF LKNPWGGPIFWGLPKF YFLPNKGSFFNLIGDFLKRPFFWGGAYF G
8600	22501	A	8662	136	358	FHIVKGVSIKFKCVILKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKK NKIFFWVGFFYKRVWGYF
8601	22502	A	8663	198	368	LINLVQFTCILGTLLGILFIYFLIRRAI

[illegible]

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFF
8622	22523	A	8684	1	406	LYYFLTKSTTTYLAVPQFPPTPTSPSR AKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKRGGGPKKKTRKGGGQKKKKGR GPEKNRGGGETTPGEKKKKKKGGGGKK KKKKS GGGKNGGKPGRGGGGGR
8623	22524	A	8685	391	265	GRFFFFFLDGVSLLLPRLECSGVILAH NLCLPGPSDSPSSA
8624	22525	A	8686	2	177	DTALYSLYIFTTQWGS LTHINNIPKS FTRENTLMCIHLSPILLLSLNPDIITGF SS
8625	22526	A	8687	479	366	GLPKCWDYRREPPHPAANFCIFSRDGV PCWPGWSCL
8626	22527	A	8688	35	161	SNPPSSAFQVAGTTGVRHHDQLTFFFF FLGGTGILCRGGD
8627	22528	A	8689	1	122	THINNIPKSFTRENTLMFIHLSPILL SLNPDIITGFSS
8628	22529	A	8690	2	152	NIILAFTISLGLILVYRSHLISLLCLE GIILSLFIIATLIYPTPSFSCY
8629	22530	A	8691	541	85	IFLROFLSPRLEYSGVIKHC SLNLLGS SDPPASAFKVAGTTGIRHHAWLIFVFFF AETGFHYVAQGGLELLNLRLPATAFQS AGIIGISHHDLGLIQITTWLQKLSYLQ KKICKDQETGLLHAFHLHPYPMPSSP QLLQGPDIITNG
8630	22531	A	8692	122	38	GRVDHSFMPIVLELIPKIFEIGPVFTL
8631	22532	A	8693	276	77	GVSPCEPVFFFI LGRCPNPAWGVPKGRD FFVLSFFFVVFYILLFFFFFFFFFFFLE SFYCFNGSNK
8632	22533	A	8694	3	70	FMPIVLELIPKIFEIGPVFTL
8633	22534	A	8695	230	3	GSGIPSHPGHPSLPYHLEREWLAKTGIR DTSNSVHLELCLRSQRHGRARWLTPVI PALWEAEAGGSRREQEIEPI
8634	22535	A	8696	401	240	PPPPPPPCGSEPRPPHPSLSPPGSREMF VLALSQESQMTFFFFQLRKKLHLYL
8635	22536	A	8697	103	313	EKKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKGGGPKKKFEAIFGKTP GGVSQGGGPPPLNFFFLNPGPPFF
8636	22537	A	8698	354	110	KKGTLFEVSESFYTTEGVSAKINRIRSI VSVNKVARCIGEIFTDAVQSAFQKEVGG VSDSMVHKY EYAGCVDVKAVCSHGL
8637	22538	A	8699	2	164	FLVETGFLHDGQAGLKLLISGDPPASAS QSAEITGMSPHACNSSTLGGRGGRIT
8638	22539	A	8700	191	371	PPDSRWAIQGGHLELTPTRQDLAQAPR RKLALLEGSFQQAQWLTPVIPALWEAE ASGS
8639	22540	A	8701	2	170	ARAGLYHVGQAGLKPLTSGDPLASASQS VRITGVSHRTRPKIIFKLIFLFFFFFFF
8640	22541	A	8702	31	229	MEKYNVHPHSGILRSHEKQQAALFTIAK RWRQPSYPSIDEWINIMWSSHTVEYYTA MKRNKQLYSQ
8641	22542	A	8703	3	126	LQELRDP TLTFRLLGSPRPVVVETRPVD DPTAPSNLYIQE
8642	22543	A	8704	438	31	SEPCAGYNLLVCRFLSPLEKHNIRVGVT RFSRCHLSPLSLTRKGNLSLTPCTSRVRQ CLALLWLAHSALHPLSCMHCLALPSEM NVPQMEMQKSPIFCIAHAGSCTPELFLF GHLGSTPLTHLLSLRINVLRTSE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8643	22544	A	8705	429	319	PGAI IAHRSI LNLPGSSDEPTSASQVAGN TGVSYCARP
8644	22545	A	8706	426	245	RAATPSPIKLT KKKKKKKKKKKKKKKKK KKKKKKKKKKRGAPLKKTLGGPQINRGK KKIFFFF
8645	22546	A	8707	1	108	KHPRGGSFGYCFALAWAVFPLALVSGI I YIHLRKRE
8646	22547	A	8708	3	146	QTEGHTISALGDGAAWPVQGLIRHFRPE LEERMQRFAQQHQARQAAS
8647	22548	A	8709	2	83	LVLEIAVALIQAYVFTLLVSLYLHDNT
8648	22549	A	8710	1	81	RPLSKTVRFNVLKVTKAAGTKKQFQKF
8649	22550	A	8711	156	4	RPLSFHPGCKKRLFLKKKKKKLCAVAHA CNPSTLGGRGGRIMRSGDRDHPG
8650	22551	A	8712	440	233	TPSYFVLLVERGFMSMLPRIVSLTSGDPP ASAFRSAGITGMSHHAQPERTGRSKAYLP FLEEDLKHIFPF
8651	22552	A	8713	92	302	AMHPTMGPDQDQGTGLYAHTPLPHPHSH THANTLIHSHIYAHASHTIPATCPKGP TQPYLCLLSPHIEL
8652	22553	A	8714	2	166	KKINSFFSQGLTOAKVHGGRPSSSLGPQT PVLKRSSCLSFPSWDYRHEPLYPAN
8653	22554	A	8715	1	129	GFRHVGQADLELLTSGDLPASASQIVRI TGVSPCAQHEFFKSN
8654	22555	A	8716	381	105	RRSLHSHVLNGAQAGVQRDLGSLQPPP PSSLPWPPKVPRLQPLGRHPVWEVRSV SARPPIVWDVRSPSAWLPSLESEERLCL AAPSGK
8655	22556	A	8717	385	125	FFFFLPPAFLLSGXFWFFFFFYIFSSFFF FFFLGSPPPPIFFFFFNLKIFFFFFF FFFFFNNLFFFFFYYYYFFFFF FFF
8656	22557	A	8718	409	264	KTDQRWSSTSSSKIMSQSQVSKGVDFES SEDDDDDPFMNPSSLRNR
8657	22558	A	8719	3	269	KKHVKRVLSHLKASCPSELLHFSWQPQL LELQLMGGSHTHMDQHTHMHPIYT HAHTHTVAKLNLPLWVEMNLLSLGAFO QRLP
8658	22559	A	8720	430	141	LFFFLSFFEDGVLLCHPGWSVVAQSOLT ATSTSKKKKKKATPPGIPKFLIGKSGK PPRVLLIGHWAPKFFFFFNRLAFF
8659	22560	A	8721	386	290	RWGLTMLPRLVLNWLQAILLLWPPKVS GLQA
8660	22561	A	8722	3	157	HEVFLVETVFLHVGQAGLELPTSGDLPT SALWEAEWGGLLEDRSSGPWET
8661	22562	A	8723	493	186	FSPQGGKRAILGLRNLCPPGVKDF SAR PPKEVGNRVPKTKLEFFVLKKKGFP IGRGGFKSRPWESPPRPPQKVGVRQLNP PPGPPFFFDLIWPNRNGS
8662	22563	A	8724	3	186	GGGTPPFPVWGKNGGGTTPPAKTLPPF PSPLFFFSPPSPGEGGSREPLSTPLA CICI
8663	22564	A	8725	370	67	FADPKNFYKGAPPIFFIFLFFILFIYFF FFFFIFFKFLVFLLETGFHHVSEQEDLDL VIHLPPQPKVVGLOAWATTGQFFVFLI ETGLHPVNQDGHNLTL
8664	22565	A	8726	966	652	LGSCLKPPPTGFKRFSCLSLPSSWNYRHA PPCPANFVLEETGFLHVGQVSLELLTS GDPPTLASQSAGITGMSHRDWLQQLIV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NHCYLFYQGHIKTTRSLPP
8665	22566	A	8727	85	425	HMHSFAHELHTFLHTHTNSHTNSQNQSP TYTSKSHTHSYMRFTDSHDSQMQQTHR SLLHMTQLYTCTHTHTHTRTVPLHLHS VKGWLN TKVALGGRTSHGRESHIAGRLL A
8666	22567	A	8728	393	124	LGSSEPQLFQSPSPSGGPPGPKSHWNSWG NANPPVPVPPYIESAPPPPHFPFGAQS SGGQAARLCPCPPFFLKKKKKKAPGSGT GTFSFQ
8667	22568	A	8729	25	217	AVQPIRVQWRRSLQSPQEITILAPSLAK VDMEMTQLTQENADFATRDRYHSSLVN REQLMPHY
8668	22569	A	8730	1	611	PGIFYSALLSLDTSILNQLCFIMHRYRK NLTAACKNELVQKTKSEFNFSKTYQEF NHYLTSVMGCLWTSKPPGKGIYIDPEIL EKTGVAEYKNSLNVVHHPFLSYAVSFL LQTS SSSSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSPSPEERTVNVSSIRGKKWSWYLD YLFSQLGLKLFIRSSVHSSIPRAEG INCNNQY
8669	22570	A	8731	120	378	VEKTOASILGCKCSTPRAALGFRERTLP LRRCPCCGPPEAQMELEKRALGSQAQWL MPVFPALWEAEVGESLEARSFETSLGNI A
8670	22571	A	8732	2	68	VYVCVCVCVCVCVCVCRAKVG
8671	22572	A	8733	382	258	NYHSSLHLETPGLKQSSCLSLPKSWDYR HESPCPALIFNSL
8672	22573	A	8734	479	326	PPLYGFFFFFFFFFFWGGGFFFFFFFYFFF FFFFFFFFFFFFFFFFFFFFQTTF
8673	22574	A	8735	422	2	GRRPPGLYFFFFFPKGKNEFQGRGFLFF FPPKGFFFFFFFPIGFFFSSELGKDWP PKKKVFSQRFPFFFFFFPPLFLFLFFFF FFFFFFFFFFFFFFFFSFFFFFFFFFFFF FFFFFFFFNKQVFIERLLCARHCFRPPAS
8674	22575	A	8736	7	75	IAVALIQAYVFTLLVSLYLHDNT
8675	22576	A	8737	2	176	NFGLLAETGFLYVGHAGLEVRSSGDLPA SASQRAGITGVSTAPGFNRYFYKQTIYK YG
8676	22577	A	8738	408	111	GSSPPPRAGGENFLKKNAGGKNFPGGEG GGGFYPLYPKKFFFSKGFIFWGGGGGK WPPPKKGGFSKKPQKVFTTPQKKKKFF WPPGGNWGPKNF
8677	22578	A	8739	5	249	YEGKKLHMQASPFQRGHPVNHKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK EGALGKKFLAQTSPKGEKQKVFIKY
8678	22579	A	8740	1	226	FFLRQSLSVTQAGVQWCDLSSLQLLAFQ GSSNSPTSASQVAGITGVHHHQLIFIS LVETGFHHVAQAGLELNLQ
8679	22580	A	8741	4	96	DGLIMLPRLVSNWPGILPPWPSKMLG LQV
8680	22581	A	8742	19	112	FGRILLVREKKKKKKKKKKKKKKKKKK GGGPL
8681	22582	A	8743	362	234	KMDQKCLSEVLQRWFPCCCCCCCCCCC CCFSLPFIPEPSRS
8682	22583	A	8744	3	419	LTLRRFQLNLALTAKKKKKKKKNLKKKK KKKKKKKKKKKKGGPLFKNSLGGPIFP GGKFIFFFFWGGFLKPPGDFLKTFFLG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GEIFGPPPPKNTPLGKKKIFKGVGVGKN PPLFLRRKKFFSGGFFKKIFSPGLGF
8683	22584	A	8745	444	1	KKPSKEILYPENSRRFFSPLSPLKFFFS KGFNFWGGGGLPCPPPKERFFSKNPPGG FSPPLKEKIFFFPPVNLGPPRDLFKG APPPPPPPPPFFLWEMFYWLSLSSGSQR LPQQVPTVEPSELGGMGAYFVSKRSTYL QRGWRPER
8684	22585	A	8746	104	222	NKTFCLLKKKKKKKKKKKKKKKKKKK KKKKKNWGGAL
8685	22586	A	8747	403	201	MEKYNVVQPHSGILYSHEKEQAALFFIA KRWRRQPSCLSIDERNIMWSSLTVEYYT AMKRNKQLYSQ
8686	22587	A	8748	1	90	RTRGAVYAALERMGLDGCVEDLRSRLQR GP
8687	22588	A	8749	444	85	SPPPPGLFFFFFFFPKKKTSPPPTKKGFF SPPPPQKFFFLKPPFFLGGLGPNFPPP KKNFFSKNPPRFFFPFKKKNFFFP FFFAPPKFFFLTPPPLFFFFFFF FFFFFFFL
8688	22589	A	8750	2	309	EFFPPYWEFLKINACMFSPKKKKKKKK KKKKKKKKRGPPLKKTGGPQIPRGGK KKIPPLKGGQKKPPRGFLEKNPLFGGGP FGPPPPKINPPEKKKNF
8689	22590	A	8751	3	76	TASVSEGGGLQGITMKDSDEEEEG
8690	22591	A	8752	433	145	SFFFFFFFFSFFFGKKSSFFFTPL
8691	22592	A	8753	2	124	GHLLMHLIGSATLAISTINLPSTLIIFT ILIKKKKKGRPF
8692	22593	A	8754	80	201	FINANSKKKKKKKKKKKKKKKKKKKK KKKKGGGLLKKTGGGAQF
8693	22594	A	8755	415	1	IYFPTPEKFGPPKETLKKCAPFFFFFKQ KPPFFGPGGKQKGGFGLQTLPPGKKKI SRPNPPRKRGFKDAPPPPGKFVFLKKKG VFPGGQGGFKTPTPRDLAPPAPLNPAL FFFFLQSLSLSLRLECSGTILAHAS
8694	22595	A	8756	3	136	FTATRPGVYVGQCSEICANHSFMPIVL ELIPLKIFEIGPVFTL
8695	22596	A	8757	80	326	KKFSLGSQGRAGVFPRLGLKLTAL NSGAKGTPFLFPEPRKRGGPPAPGWE GIFCPHFPPMGQKGEGLWHTGEGPH
8696	22597	A	8758	1	164	SLISSTQGHKQCRRPQGPLRKTDRDPCS HVYLLTFPPLLSYDPAKSPSLRNTQE
8697	22598	A	8759	431	79	FFFFFFIFLKKVSTQSPPPQFYFFFLKT FFLFQPLLKEGGSWGGRGDKPPPLAPFK KWGVFFFFSFFCCFVFFFLPFFFL FFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFPRCVLTRL
8698	22599	A	8760	60	194	ARPTCPATAVTQKKKKKKKKKKKKKK KKKKKKGGVLLKKKQGGKY
8699	22600	A	8761	383	38	CASMTFPKKKKKKKKKKKKKKKKKK KKKK
8700	22601	A	8762	399	164	HITVKSLLVPMDDPPKKKKKKKKKKKK KKKKGGGFKKNLWGGQKLTGEKKKIFFF LKGGKKKPLGIF
8701	22602	A	8763	353	48	NFFFKVFFFLKDFSHKGAPPKGGPPKK TPPRKFFFLKIKPLFFIAFFFFWSLFG FFLIFSLFFFFFFFFFFFFFFFFFFFF FFIVFTITLMHFKIYLH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8702	22603	A	8764	2	93	FAMLPGLVSNWPEAICLPWPPKLLGLQMM
8703	22604	A	8765	398	63	PPPPVFFFFSGGFFFWGGGGQKSPPRER CFFFKMHPGFFFIIPPFVGGKVVFFVLEGV VCPLGFFFLSGGAFFFFFFFFFFFFFFFFF FFFFFFFFGGFFFFFFFFFGFSPSVSHL
8704	22605	A	8766	3	83	ILEIAGALIQAYVFTLLVSLYLHDNT
8705	22606	A	8767	450	306	QKKKKRRNKPEGLGTVAHACNPSTLGG RGRWITQPGQQEGNFISKY
8706	22607	A	8768	1	111	WSIALVAQAGAPGFKQFSCGLPKSWDY RHEPPCPGL
8707	22608	A	8769	385	261	FLAEMGFCRVGQAGFKLLNSGDPFASAS QSAGITGVIAPVL
8708	22609	A	8770	3	293	SLGSKPLGLSLSPVKWFRIFGKERNKV WGKGGTDRNQSSSAFKHLQRGDSDPKQ NKIKACSSKFYLRRCVKRSFLLIKKKKK KKKKKKKKKKKKKK
8709	22610	A	8771	2	281	CVCVCVCARVYIYIVYIYIYTYMCVY MYICIYIHVYIHVYTCVYVYIRIHMYIC ICVCIYTCIYTYIYTHYKHSVYYLHNF YINPKLLQS
8710	22611	A	8772	295	161	THTHTHTHTHTHTHTHTHTHTHTHTHTH LAQLLGNCCIKAAISILYIL
8711	22612	A	8773	1	318	FFFFVRWSFTLVAQARVQWRDLGSLQPL PPGFKQFSCLSLLSSWDFRHTPPCLANF VFLVETGFLHVGQAGLELPTSGDLPALA SRGAGITGVSHHPQPPLCFLFL
8712	22613	A	8774	3	70	FMPIVLELIPKIFEIGVFVFTL
8713	22614	A	8775	369	191	TYKINKIGWAWWCAPLVPAAWKAEVEGL LEPGSLRPASVIQDPHLKKGTYSRVLT THL
8714	22615	A	8776	2	124	GFRHVGRAGLEFLTSGDPLASAFQSAGI TGMNHHVQPIVE
8715	22616	A	8777	1	162	LKYYTADENGKTSRLLPQRPSDECGAGV FMASHFDRHYCGKCCLTYCFIKPEDQ
8716	22617	A	8778	346	138	YNSPPYKEKTIPLQARVNFPGPPRDSLKR PPFFFFFFKRQSLTMLPRLVLNSWAHGI LLPWPPKVQVLQA
8717	22618	A	8779	2	117	LNLDTTAVQVRNYPRIRESYKVSFLSAL EETKKNLNTQ
8718	22619	A	8780	2	97	WDLTMLPRLVSNWAQVILPSWPPKVLG LLA
8719	22620	A	8781	403	276	IISTVFQRGSCPIPSRKEVCSEPRRLQ KDSLTFPHTVYKH
8720	22621	A	8782	2	119	QAGLELLTSSDLPASATQSAGITGMSQR ARPHFQCKNVP
8721	22622	A	8783	245	101	ELQFKMRSGWRRSQPISWGLTLVPRLLS NSWAQVILLTWPPKVLGIQA
8722	22623	A	8784	2	124	AKLEKKKKKTGRAKRRMQYNRRFVNVP TFGKKKGPNANS
8723	22624	A	8785	3	355	VGPSEPGAGYNLLVCRLLRPLEKHGIRV GVTGFSRCHLSWLPLARKGNSPTPCASW VRHELALLRLTVCGLHPLSCTHCLTSPS EMNPVPQLEMOKSPVFCVAHAGSCRLEL FLFGH
8724	22625	A	8786	238	9	PVKLGAGPPQAPFWLRKNAPLIKPFKFG PIGSLQIPLFFFLRQSLTLPPRLECSAT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						WLTESSTSWVHAILLPQPE
8725	22626	A	8787	336	10	CLSLPSSWDHRRLLPPHPASFCIS
8726	22627	A	8788	1	147	IFYLLETGFHYVGQAGLELLTSGDSPAS ASQSAGITGVNHHALPEIHVF
8727	22628	A	8789	3	130	DLEEGIQTLMGRLEDGSRRTGQILKLDH SSEFSKTRELYPVF
8728	22629	A	8790	206	3	VPPSGPIKKGDKKKNLYLIFLIKNVENK KLRKGVSPALIPFFFFFFVFLLETGFHH VGQAGLELLTS
8729	22630	A	8791	124	390	RAGAQSNNLMPPPSGVKAIFFPNFPKKW GNGTPPPAPLIFGGLKKGVSPCGPGGS EPPAPGGPSPLAPPKGNGRDLPPPP DKFLN
8730	22631	A	8793	2	301	HEERERERERERERERERERERERERER ERERERDALFAFFPPRGARPPPEIERGV FVGAGSVREIYPTLSIFFSPPAHRCRE LRSRCVSHSLHLISRA
8731	22632	A	8794	1	285	ARGERERERERERERERERERERERERE RERERERERERERERERERERGAPPP PLFFLGRGGALRAHAISPPPF LGAPPYI YIFFHMRARPPHYLCAQRETRPAL
8732	22633	A	8795	1	321	ARGERERERERERERERERERERERVS RIPRGDLRDQFPPLARSDFSFGSADH FGRGVFNKVSVDPPTHRVSSSLGGV ERDLLTSLGGGTYPWKNMCATGEDQ
8733	22634	A	8796	2	140	HEERERERERERERERERERERERERER ERERERERERERESLPPAGCAKAGAGW E
8734	22635	A	8797	2	223	SARERERERERERERERERERERVS RNLSRGGGVPPPLQNVRIHSGGPARGT LHHIKKKTSLTDVGLAQ
8735	22636	A	8798	1	176	ARGEREREREREREREREREREKISF LGGGRGTQFAIERGVIFCGRRYTGRV RN
8736	22637	A	8799	335	27	PPTKFFFFFFLVEMGFCCIAQGGLELLS SSSLPASAYQSAKIIGVSHHAWSVF
8737	22638	A	8800	342	191	STSLSLPKCWDYRREPPCANLSYFFKD PFSKCNPLRLRYWGLGLQHRNFG
8738	22639	A	8801	104	332	AVPLTMVKIQPLWKRVVRFHNKSKLELP CDPAISLLSMYPKEMKSLCQRDVCTPRL STGPLTIAGMWNPPKRSSMD
8739	22640	A	8802	563	258	PFLNLETRS WYVAQARVQWLTGTVT YSLDLLASSHPPISASGVAGITDACC AQ LTLPLKLGGLLGLGGGVGYPSYF GLEGFHNDCSRVRVLCMWSYQ
8740	22641	A	8803	2	199	ARGLLVRRFLSPSEKSRVGVTRFSRC RPSPLSLTRKGNLTPCASQVRQCLALL RLAHGACTH
8741	22642	A	8804	266	108	KLVVSKCVALPPSFSSSCSSHIGCACFP FTFHYDCKFPQASQAMLPQAVEP
8742	22643	A	8805	1	140	KVVWFKRPGVYGGQCSEICGANHSFMP I VLELIPLKIFEIGPVFTL
8743	22644	A	8806	2	90	SSAAAEENNDKKEEAETEDDMEFGLF D
8744	22645	A	8807	229	34	KKKIFFFFPGFFWPPQKFFFKAPPPFF F FFFFFFFF FFFFLDLFIYLIILSYTK LISIRAAPI
8745	22646	A	8808	43	173	NADSGHAQWLTPGMPALWEAEAGGSQDQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EIETILAGAGKPRLY
8746	22647	A	8809	259	134	IYMI FKNKFFNRDRGLPMLHRLVLNWAQ VILLSWPPKVLGL
8747	22648	A	8810	391	193	VLPKIPGIQFPPPCRFKKRPRPRFKKPP PKRKKISFSNPPKIWPQGYFKRGPPRL FYFFFFVVL
8748	22649	A	8811	304	3	TTPPTNIFCFLFFIFIFLWYFIFIFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF QCFIGHDDQKMMVHTHTQTSSHLLQGG NPQGGKQSPGWVLWCA
8749	22650	A	8812	395	268	FLVETGFHHVQGAGLELPASSDLPALTS QSAGITGVSHHGWS
8750	22651	A	8813	782	1174	LSRLFYFCVLFCLYMKTTQLPYFRGLVC LFVLRQGLTLSSRLECSGMIAACCSLNV PGSTDSPTSASRVVRTGVRHHTQLIFV CFVEMWFHYVAQAGLEPLGSSSPALSS QGAGITDVSHHTPLELCF
8751	22652	A	8814	95	236	ATMPGLKNIYFLKNKDKGLTMLPSLVLK SWARVILLPWPVKVLGLQT
8752	22653	A	8815	381	58	SCLLFPPFWGARGGGPPRAGGSNPPGPP GLTFPPPKPKNYWARGGGPFIPPPREG WAGGFFLPRRGRVPLAPGSNNLELGPLP SPPGYQKKTFFSKKKKKEKKKKR
8753	22654	A	8817	441	158	FFFFLRTDGYLTMLPRLVSNWPQAILL PQPPKMLGL
8754	22655	A	8818	415	342	RLVLDSWAQEILLPWPVKVLGLQV
8755	22656	A	8819	400	171	NFFFPPGVKFLGGGGPQFPFPQKRGFFQ KTPGGFFKPPPKKKKFFPPPKIGFPQ GIFKKAPPPPPPPPPPPPPPP
8756	22657	A	8820	2	268	INIILAFITISLLGILVYRSHLMSSLLCL EGIILSLFIATLITLNTSHLLANIVPI AILVFAACEKKKKGGAVLKDPPWGGQSLR VLAR
8757	22658	A	8821	2	258	LCLPNQAWAMAGSPPASLLPCLISDC CASNQSDSVGVGPSEPGVGYSLVRRFL SPSEKRSIRVGVTFRSSWVRWLRTVIPAT
8758	22659	A	8822	250	456	GGGDKFGLIETFPFPGKPFLLNLLSGW ELGPLAPPFKFCFFKGRGFPLPRFVF VANLLLTCKKRD
8759	22660	A	8823	492	376	QENCLNPGGRICSELRSCLCTPAWATER ACLKKQNKTNQ
8760	22661	A	8824	1	116	LTPLPSPAPSVDNLKTPPEWVCSLFF HPQRMII SRN
8761	22662	A	8825	2	191	FLVETGFHHFGRAGLKLNSGGALTSFAF QRAGITGVITGVSHCFEVNRVWTGTQYF LCYILKS
8762	22663	A	8826	393	75	PRFFPPPPPKIFFPPPPFFFLGGFPPI PPPPKNFFPKPPPGFFPPPLKKKIFF PPPPFSPPNFFPPPPPPPPPPPPFF FFFFFFFFFFFFFFFFFFFFSI
8763	22664	A	8827	81	380	KIITKHNIARTNPYTFCTIMNYLKKKKKK KKKKKKKKKKKKKKKKKKGGGPFLLK NPGGGQNNPGGKKNFFFFGGGKKNPPG FFKKKPPFGGKFGAPPPPKN
8764	22665	A	8828	354	13	TKPKTPPLTKGPRRGFLAPRVPGGGGPI TPPPQNLGEGKTLARKKVFPGRPAKP RPPRKNKGFEMRPLKKNPGPWKFLGFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LANPPGFGPKKKPENQTHKKKCQRRKPRF
8765	22666	A	8829	1	215	KHSTTHSHCPRTIKLKKKKKKKKKKKKKKKKKKKKKKKKKKGGPPFKKTLLGGPPFSPGGKKKFFFLGGL
8766	22667	A	8830	1	127	ILFFWQRRGLALLHRLVSNWSAQVILPPRPPRVLGLQVIYFK
8767	22668	A	8831	264	55	FFFXFFXFFFFFFFFFLEVFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFWCSCS YVLIFIQPFIKSFH
8768	22669	A	8832	399	85	PPQKNFFFPQAPKISGGGGPQIAPPQKK GSFQKTPGGFFIPPQKKKKNYFPFPPGKM GPPQGGFFKRPPPLFFFFFFFFFFFFFH NRHLFKVKHLQNSFHLVQLRL
8769	22670	A	8833	47	288	NCLYRTKKKKKKKKKKPKYKKKTLRGPN FPPAGPPAPLPLSGGEKKPSRGLLRPP TLGGAAGPPPPPKLTPLRKKKIF
8770	22671	A	8834	1	146	INILAFITISLGLVYRSHLISLLCL EGIILSLFIATLITPSTLC
8771	22672	A	8835	2	79	EDPKTSPKPKIITQTRRPGLPSPVSN
8772	22673	A	8836	1	156	PTRTIITPILLTLFLITQLKILNTNYH LPPSPKPIKKKKKKKKKKGGGP
8773	22674	A	8837	152	292	AKTFNFYKVEFINVFFNGLCLLIKNL PKKKKKKKKKKKKKKKKK
8774	22675	A	8838	1	122	VASNSIHPKAKENTAPHTHTHTHTHT HTHTHTHLFMAIFK
8775	22676	A	8839	2	106	HVGQAGLELLTSGDLPTSASQSVGITGV SHRAWP
8776	22677	A	8840	364	224	APLCGRQICDCDCTYPSPTYIHTHTHT HTHTHTHTHS
8777	22678	A	8841	266	1	NSLSVEFLILFPPYNYSKQCICSHQNC LNFVVIKCVNTPHPNFLNLRMPLLAKRG AHACDPNTFGGGGRWITRSVDRDHPGQH NETP
8778	22679	A	8842	343	52	KTGFRHVGQPGELLASSDLPASASQSA ITGVSHRVRPGLHILDNSSFLDTSFADI FSVLYLKAGIASLLHTYIHFLPLRLDLL LVSSLTVSFPTAV
8779	22680	A	8843	256	35	LFIFSLSLQYIFCVCGVCVFMSLCFLV CAWGHVQLHVCSCVRMCVENDVCVCGW VQMCFCIKNFQKEVYQI
8780	22681	A	8844	333	11	PPIKKKAPPPKGRAFFFFFLKKKKGGPP PPQKKTGGGGPKKRGVKKPPPGFFPGF FGPLFFWGPPPLPPFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFISTKNLF
8781	22682	A	8845	15	288	RCGLTVLPMVSDCWAQVILLAQPPRVL GLQAGASASTPITSVNCQGAITYPEVGT TGSTIIAAASSGGEFDSVLQNDICMCF L TQQHF
8782	22683	A	8846	1	397	ECAHHTQLIFLFLISSLHHVQAGLKL PISSDPPTSASQSAGTTAVSHHA
8783	22684	A	8847	1	179	ARERERERERERERERERERERERER ERERERERERERERERERERERERER GGGPQFPFGGLTQGGGG
8784	22685	A	8848	2	233	HEERERERDRERQRERERERDRERER ERETFFSSGGGPKETTLFFETGAPKEG YQNMHARLIPSAVPFKKRG
8785	22686	A	8849	2	180	HEERERERERERERERERERERERER

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predict-ed end nucle-otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ERERERERERERERDFVFFYRWGEHTDRQYCSELFPGWCHCPM
8786	22687	A	8850	2	79	PEERERERERERERERERERERERERERERE
8787	22688	A	8851	1	178	ARGERARLIFARGEKKKHTGGGPPLFYLYLI
8788	22689	A	8852	3	76	TRRERERERERERERERERERERERESP A
8789	22690	A	8853	5	227	EERERERERERERERERERERERERERERERDFFFFFLEKKYLFSPIGELKGRGGGSLTPLLTKGWNPCPPPH
8790	22691	A	8854	1	189	ARGERBRHR SRLFPRESVCVARAGGASSPPRG
8791	22692	A	8855	2	271	HEEREREREREREREREREREREREREREREREREERPGEKYCIRVP PQKILSPACDSL LYVT HNLCVSHSTPRGERYVALFNSETRCF
8792	22693	A	8856	2	309	HEQQQQQQQLRNLRDLFLLVYNRMTELCFQR CVPSLHHRALDAEEEA CLHS CAGKL IH SNHRLMAAYVOLMPALVQRRIANYEAA SAVPRVAEQPGVSPSGS
8793	22694	A	8857	44	203	GYSTCVGMHAHTHIHTDTHTHAHTYIHQC LIQIGLCT FATCTS QVNKS SMAEL
8794	22695	A	8858	329	182	I IFVCLVERGLHYVGQAGPELKASDDL PALASQS AGTS GVSHCVSKMS
8795	22696	A	8859	1	175	GLTLPPRLGCHATITTAHYSNLNLPSSNPPTS ASQVAGTT HS RPCE ITQTAL QRGH D
8796	22697	A	8860	3	350	HEATGLRSNIKNGLDHFLPLGTPTPLIP ILAMIE TILLVQPIALAVRLTANITAGHL LMRLNGSATLAISTISLPSTLIIFTI LILLTILETAGALIQA VF TLVLGYLR DNA
8797	22698	A	8861	139	3	TFKEADIKGGGPPHLASF CIFI GRDGVSWCWPGWSRTPD LKR STRA
8798	22699	A	8862	3	134	SPTPPPSSKPSSI PRKSSVDLNQVSMLS PAALS PASSSQRHES
8799	22700	A	8863	346	219	RLVFPCLDNFLNFRCRYSCLTMLPGLVSN SWAQVI FL PP PKD
8800	22701	A	8864	1	147	GTRFFF FERGI DHVQGAGIQLLTLGD PPT PASQRAEITGV SHHTWP NFIF
8801	22702	A	8865	267	132	KKKFWPFFFFFFL RDGVS LL LR LV SNCWAQEILL WP PKLL GLQV
8802	22703	A	8866	343	215	LAQGLKTPIPKRVPPHTQKKKFCSERPTR IQTD RS CWV SPLS
8803	22704	A	8867	1	242	GTSKKIDKLDYIELKCFTAKETISR VKRPVEWEKIFANS SPEGLISRINKBAKK LN SSAIAAHNCNP ST LGGQVR RT
8804	22705	A	8868	1	219	GTRRP TWATWQNPA ST KKKKN S FF FE TE SR TVPQAGGQGG NLGSLSLP PGL KR FS CL SMPGA PK QS GLMG
8805	22706	A	8869	1	181	ATGGII LLLL DVVS LAYESHLLLEG AKSES AEEL KKRA QE LE GK LNFL TKIHE MLQP GDQDQ
8806	22707	A	8870	1	255	AAAPP NAPG GP PGQPAPSA AAP PPPPAHALGGMDAE LIDE EA LTSLELELG LHR VR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predict-ed end nucle-otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ELPELFLGQSEFDCFSDLGSAPPAGSVS C
8807	22708	A	8871	383	233	ATTFFNPNGFLFVRLFVLVQWPDHEPPGF KQSSHSFLSPSSWDYRHPPPPP
8808	22709	A	8872	211	294	AXKKKKKKKKKKKKKKKKKKKNIIWGG
8809	22710	A	8873	398	100	QKERPPPGFPFKPGPPQKRGGKGAPPKD GEHYFFWVLEKSTGFPPKTKRVYYPSPV YPHPAPQKEGFPGGSPPPRPIASPFQG KKKEKKSYIEKENLF
8810	22711	A	8874	3	214	DANVLGIIVYRSHLISSLLCLEGIILSL FIATLITLNTHSLLEKKKKKKKKKKKK KGGAFKKNPGBAQI
8811	22712	A	8875	2	254	PRVRPEGRNRTPQSWFQANPMACMTFSK KKKKKKKKKKKKKKKKKKKRGGGFIKKM GGGNFREKEKKNFLLIRGKIKTGGDF
8812	22713	A	8876	2	135	TINLPSTLIIFTLILLTILEIAVALIQ AYVFTLLVSLYLHDNT
8813	22714	A	8877	2	296	LARGAEVLGYGSHSRGRVPALVGQGAG RLFTEHPGSSPATLAITYPTPEGTSVAVS ISAPPKARSRPYPPSRSCHNLFLAGSSV LVPPGPVHRWGRP
8814	22715	A	8878	164	29	RKIGPARWLTPVIPALWETEAGGSRGQE IEIILANTVKPGACEVL
8815	22716	A	8879	381	219	GKMTTEEVEHMLVAGHEDSNGCINYEGR R
8816	22717	A	8880	2	156	ANGNSFATRLSNIFVIGNGNKPWISLPR GKGIRLTVAERDKRLATKQSSG
8817	22718	A	8881	3	402	SGFNIEYAAGPFAFFIAEYTNIIINT LTTTIFLGTTYDALSPELYTTYFKKKKK KGGRRPFFFFFFLKKKKIPPPKKKNFGKK GETLKGRGGAPIFQPKKILSPKKKKKK RGGAFKKSLGGAKFNGGGRN
8818	22719	A	8882	1	406	RYSTPSEGEVGERYSTPPGETLERYSTP PGETLERYSTPPGETLERYSTPPGETLE RYSTPPGETLERYSTPPGEALERYSIPT GGPNPTGTFTKYPSKKKKGGGRFKEPLG GPREFGVGRVKVFSWGGVILNAR
8819	22720	A	8883	484	307	KKILNRRVRWLTPVIPTLWETEAGSSRG QEMETILGNTVKPPASASQSAEIKGMRI IIF
8820	22721	A	8884	1	131	GSLTHHINNIIKPSFTRENTLMVIHLSFI VLLSLNPDITTFSS
8821	22722	A	8885	406	106	KGGAGPKIAPPKKKAISPPIPPFFFWPPP VFLKGPPPPSPFNFFPPPVFFFGRGLFF FFFFFFFFCETVVLPFRPSNLVFTLPHVF AWLIPIDQYLFISHSC
8822	22723	A	8886	425	325	SSTHTHTHTHTHTERSHLLAFEPSAG ELWMAM
8823	22724	A	8887	394	278	VVCVCMCVICYICIYPCWLPCWHMCLELY KVFKGIMKGV
8824	22725	A	8888	2	86	YSRTAAALIQAIVFTLLVSLYLHDSAY
8825	22726	A	8889	400	62	FLYLKSFPPPPPERGVFSLPPQKFFFS KALNFLGGGGPKFPKKRKFFFKYPRV FLYPPHKKKNIYFPDDFGPPRVFFKA PPPHFFFFFFFFFFTTTTTRLEWVQ
8826	22727	A	8890	3	100	SLEPGTSGLGFSCLTLPSSEDYRHEPP CPAN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8827	22728	A	8891	32	142	VRPTRPGQVASVLYFTTILILIPTISLI ENKILKWA
8828	22729	A	8892	3	382	TPHNPLSRPSYEPKPASTPSRAPKKKKK KNPKKKKKKKKKKKKKRGGALLKKT LGGPKLPGGKKKNFFFFRGGKKKPPGDF LKKTLFLGGGNIAPPPPKKNPWGKKKI FWGEGGKKNFFFG
8829	22730	A	8893	368	199	KKKRISPPSRKRAPQGDFLRPTPIKNI YYLSFFFLILYIFFFFFFFFFIFFF
8830	22731	A	8894	3	136	TINLPSTLIIFTILILQFILEIAGALIQ AYVFTLLVSLYLHDNT
8831	22732	A	8895	1	144	TATINLPSTLIIFTILILFILEIAGAL IQAYGFTLLVSLYLHDYPYN
8832	22733	A	8896	153	375	PQKKKKKKKKKKKKKKKKKKRWGGGF LKNSSGAPIFGGGKFFFLGGGFKTP RGFFGKNPFFWGGKKKN
8833	22734	A	8897	332	400	WLTPVIPXLWDAEAGGSFEVRS
8834	22735	A	8898	215	359	TELVNPAVLFCLPCSSGHLLCAIHAK RVTIMPKDIQLARRIRGERA
8835	22736	A	8899	414	73	PRLLCFHKKAWAMAGALPPALLPPYSLI SDCCASNQRDSVGVGPSEPGVGNLVVR RFLSLSEKRSIRVGVTRFSRCCPSPLSL TRKGNSLTPCTSRRLRQCLPLWLHAGAR TH
8836	22737	A	8900	374	88	VSPSPPLKIFFSPKAFNFWGGVGPHEPP PQKRVLPQKPPGGFFSPPLKKKKFSFPP PVKLGPPKGSFKGPPPPPPPPPPFFGL DFMYTGSSNVW
8837	22738	A	8901	433	56	PEGPPPPPGFYPGKRGFFFTPLVVFGGP KRDPPPRGKKNPSWRSGGQTPRFRDP LLKAFFPGGPPQRLGKAQGFWFFFGPK KGKTQTGPPFFFKLGDWPCKKPPPG GAPRLGPPKKKFL
8838	22739	A	8902	3	73	IAVALIQAYVFTLLVSLYLHDNT
8839	22740	A	8903	3	149	PNLSYIIGKDTWVEHWPEEDECQDEENQ KQCQDLGAFTESMVVFGCPN
8840	22741	A	8904	351	137	FPPEFFAAPKSGILFFSKTWMEVEVLF LSQLMLGQKTQYCMFSLINGRLIIPAG SLKGDHHPPLGLLEG
8841	22742	A	8905	142	5	KIFLQKKKKKGLGTVAHACNPSTLGGQ GGWIMRSRDQDHPGQQW
8842	22743	A	8906	367	244	HVPQARAKFFCIFSRDGVSPYWPWSRT PDLMICLFFIVEL
8843	22744	A	8907	146	248	SQILGRLRQENCLNLGNGCSEPRWCHF LAWAKE
8844	22745	A	8908	2	197	AAASTHHARLFLCVCLFAYLLVEMEFHH VAQAGTELLDSSNPPPLASQNAGIIGMS HHTQPQYIC
8845	22746	A	8909	1	127	KKTRLERAQWLTPVIPAFWNAEAGTLL ARSLRRLPWPNNVL
8846	22747	A	8910	368	280	LTMLRLVLNSWAQAILLTWPPKVLGLQ A
8847	22748	A	8911	355	211	QQQNLHLFWPGTVAHTRNSSTLGGQGM ITGAYEFETTLGNTARPHLY
8848	22749	A	8912	325	190	KKKKKKGGGPGQKKKNPPPPPTSKKKK KKKKKKKKKKKKKKKKKK
8849	22750	A	8913	1	411	VNVPAPRGAYRGRQASFSGGGLHPVPA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						YRPLCLPNQTTNSAMAGAPPLASLPPCS LISDCCASNKRDSMGVGPSETGTGYNLL VCHFLSPLEKCSIRVGVTFRSRLSPL SLTKKGNLSLTPCTSRVRCLALLRL
8850	22751	A	8914	258	9	GAIPCLHCETNPSTHISSTQELQTPPEQL PGVPLELPPPGSCFKCRKSGHWAKECQ PGIPPKPCPICAGPHWKLDCTGPRL
8851	22752	A	8915	326	42	EKIHRYFCYSFFVFLVEMGFYFVGQAS LKLASSDLPASPSQSARVKAMSHCVRP VLVIFKNKILQNTENSTKIYVPPPNQ ILTFCHFCFK
8852	22753	A	8917	3	106	GLELPTSGDLPASASQNAAGITGISHHAR PIMTYS
8853	22754	A	8918	320	171	AASTDGSYKCLCLPGYVPSDKPNYCTP LNTALNLEKCPGLPHLSGSS
8854	22755	A	8919	1	201	VKPSDRYHLMPIFTAAYPHQNSTYNVPV STRMVMAEEFKQKRLSLCSDLYRKDLR TIVDPVVSCAT
8855	22756	A	8920	3	182	LLRPLEKRGIRVGVSFRSRYHLSRLPFA RKGNSTPCASRVRRCPSLHLHLPLSD KPQ
8856	22757	A	8921	142	1	SCHPGWSAVVRPQLLRLRYENCLSLGG SGCSELGSCHTPAWTTEG
8857	22758	A	8922	1	117	LFFNYAWGWSTLLSRLSLNSWVHVILT PWPPKELGLQA
8858	22759	A	8923	357	121	LGAFSDGLAHLNKGTFATLSELECDK LHVDLENFRLLGNVLVCVLAHHFGKEFT PFVQAAAYQKVAGVANALAHKYH
8859	22760	A	8924	343	133	LFFNFNFLETRLREWLIFVFSVETGFPI KRAGLKLQASSDPPARGSQSAEISGMSH YAWPCKSNRAFKCS
8860	22761	A	8925	321	44	PDSGGSPASASQVAGTTGACHDAWLMFI FNMDININIPPSAKRDKLSMDKINEIIF SLLINRISSFQIMYFLCSSRIESRKRWL KQTGRKKE
8861	22762	A	8926	335	106	HFVFLIETGPHRVGHAGLELLTSTDPPA LAYKSSGITGVSYRSFTKLHLACVCLC ITYTLGLVLSFTPGSWEKKT
8862	22763	A	8927	2	160	LSRVPPRSANLSISVFAEKRCFTMLPR PISNSWAQGILLPSQAPKVLGLQA
8863	22764	A	8928	3	140	RVITEEEKNFKAFASLRMARANARLFGI RAKRAKEAAEQDVEKKK
8864	22765	A	8929	126	59	NSGGGGCNELRSCHCTPAWATE
8865	22766	A	8930	3	104	KNMACYCRIPACIAGERRYGTCTYQGR LWAFCC
8866	22767	A	8931	311	112	MENYLSKMQQELEKNITRELKEAAAELE SGSIASPLGSTDESNLNQLVWKASREY VQVLKKNYMI
8867	22768	A	8932	345	134	GGGSSPWFPFWRPRRADSLRVGVLP GPGGAPFFLNPLIGWGGGARLWFQLI LLRVRPENSFDPPGR
8868	22769	A	8933	262	39	RPRRPHPGNFFFFFNSGSHYVAQGLEL LDSSDPTLPSQSAGTTGMSYQAWPLDHT FENRDCVLLHCSSPVSNT
8869	22770	A	8934	84	22	TPAWVWWLTVPVLPALWEAKAG
8870	22771	A	8935	277	111	ERIINHAAGSHGVSGIFMKYDLSSLMVT VIEEHMPFWQFFVRLCGIVGGIFSSTG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8871	22772	A	8936	2	106	DSAIPIRRLECLKEDVQRQEREKELQHR YAEFVF
8872	22773	A	8937	1	193	LMWDFSPSGLDGAQFQGYWYYNXYINV KKGSISGFTMVLGYMLFIYCLSYKELK HERLCKYH
8873	22774	A	8938	240	69	DSGNQLKRSPSGRARWLTPVIPALWEAE VGESLEVRNIYILQNMNIGNIHLIK
8874	22775	A	8939	329	177	RWNLAAMLPRVLNSWAQATCPSWPLKML GLEAEPSPARTNFKVTSPLRH
8875	22776	A	8940	358	120	HPSNFFVFLVMGFHHVQPGLELFPAR YVPTLAFRSGGITGISHCAWPKEWALPR KASPGLSGRGSPHCATCSSKAW
8876	22777	A	8941	333	104	PHVYSNGHICLSILTEDWSPALSVQSVCLSIISMLSSCKEKRRPDNSFYVRTCNK NPKKTKWWYHGKQFEFVITF
8877	22778	A	8942	1	241	APLVAFTQVNLEDKGGLSKLVEAIRINF NDRYDEICHHWGGNVLGPKSGTRIAKLK KAKARELATNWIKCTLLSFLYIKR
8878	22779	A	8943	1	240	APLVAFTQVNLEDKGGLSKLVEAIRINY NDRYDEICHHWGGNVLGPKSVTRIAKLK KAKARELATNWIKCTLLSFLYIKR
8879	22780	A	8944	306	150	AASTLCPRLECSGAIMAHCSLNLGSGD PPASASQVGARGSLPEGRWRLQ
8880	22781	A	8945	284	2	GKSRSPDLCTSGFTGSTHFTLLICWV PRYVATCPPIGLNFVFIKTWWSHYIVQA DLKLMVSSNPPVSASQSAGNTGMSHTW LENRLLTTKK
8881	22782	A	8946	1	226	WSFALFAQAGLEFLTSGDPPASASLSAG ITGMSHHAQPAVSLNSIFSASTFCATSS YCAKMEKELKFMLIVDAA
8882	22783	A	8947	363	96	NTAPGYMPLLSIPFLVLSKAVFLFLGFMFTAALLIIAQRWEQPKASTDEWINKMW HMHTMEHYSTCCGVHAAVNISIQISEWN CWEW
8883	22784	A	8948	1	208	GRVGQPGRLRLTSGDLPASASQSAGVAG VSHRAQPTPALNCVLTCWVLQHYIKHNH GKRSEYFTIFNDM
8884	22785	A	8949	69	298	SRGHQRVADAALLSFPDVICLGLMLWGS SSIVCILHRHKRRVQHIHRTSVSPTSSP ESGATKTILLEQERTSRPS
8885	22786	A	8951	2	201	LYDLLNMRISLPLPSLVCIHSHTHEHT YTHIHTHAHTYTHTHSHWVLSLKQKMKV KHRPRLSVWI
8886	22787	A	8952	1	285	GASPPASLPPCSLISDCCASNQRDSVGV GPSEPGAGYNLVRRVLSPEKRSIRVG VTRFSRCRPSPLSLTRKGNLSLTPCASRV RQCLTLLWLWH
8887	22788	A	8953	341	256	LGLGGGGCSEPRWHHRTPAWVTERDFIS L
8888	22789	A	8954	227	43	ILFFIGKHTHTHTHTHTHTHTRAKCLFP PARFPTSPNSTTNCFTPEPAANPRGLV RAGLG
8889	22790	A	8955	310	79	RPRRPGLMERVNVFIFSLRESFYKIRI TNQAQCCMPIVPVTQETEAGRSLEPKSL RLAWAIQQNSISKNNNNFF
8890	22791	A	8956	374	198	FFFFLPNRHGLAMLRPMVLHWQAVLPQ PPKVLGLQG
8891	22792	A	8957	138	10	RPRRPRLCQAQWLMPITIPALWESVAGGL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LEARSLRPAWFFNT
8892	22793	A	8958	354	216	AGPRVFPGGEGGFRPPPPGSGPPQGPBK GGESGGKPPPAHWVFF
8893	22794	A	8959	364	223	LQAARSKKKKKKKKKKKKKKKRGGGK
8894	22795	A	8960	259	11	FEALKDPSNNLQSLFSFIVTLVVAHVY EKLSTLTSLAARRGLAMLPRLASNSRTQ TILLPWPSKVLRLQARATEPGLGLLL
8895	22796	A	8961	334	213	AASTKNFERMEWGLTTLFMLVLNSWPQV ILLPWPPEMRL
8896	22797	A	8962	260	3	KGGFFPIPFIGIKPGFFSPALIFPKVF IFSQNFVFLKKIFFFFVETVSSHVVK AGLELLASSNPFAFTSQSAGMTGMSHHA W
8897	22798	A	8963	425	248	ADEWIHKMRHIHMIYYLAIKRNEMLIH ATAGMHLENILSEKDHMYDSIYMKCLAW ANL
8898	22799	A	8964	1	118	GKLMELHGEGSSSGKATGDETGAVERA DGYEPPVQESV
8899	22800	A	8965	2	130	GRVGPRMALNSWAQVIHLPPPKVLGLQ VAMKRKIMILTSY
8900	22801	A	8966	119	364	LGWYLIETQICCSPLGADPFQQMISP LRDGLSTVLPLVLNSWPQVFLPPQTRK VLGLQAEVTAPGHIIFMIIMINTFK
8901	22802	A	8967	238	333	TRCLRLPLRLVLSNWTQALLLPSPPKVL GLQV
8902	22803	A	8968	297	169	NPPPHIYKFFFIENIFFFFFFFFF FFFFFFFMSKILIF
8903	22804	A	8969	2	212	RVRPRDRPLVRVRVGRNKDGAETTPSPG LLPAHLTFPLDYHLNQPFIFGLRDTDTG ALLFIGKNMDPRGP
8904	22805	A	8970	242	357	TLDIKSFKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKII
8905	22806	A	8971	191	265	ILMPXKKKKKKKKKKKKKKKKKKKKR
8906	22807	A	8972	398	97	MFLYNRIWFFSPHPPLRFFFSRATIF LGGGAPHFPPPKGGFSKKPPGVFLSPP QKEKIFSPPPLFLAPPKDFKSPPPFF FFFFFFFVSTGSSVS
8907	22808	A	8973	370	265	YNSSLPSWDYRHVPPCPDNFCIFSRGW SQTPDLR
8908	22809	A	8974	3	119	GLKLLTSSDPPASASKTAGITGVSHHTQ TIFVFSSHKS
8909	22810	A	8975	1	110	VAQAGFKLVSSANLPTLASQSARVTGVS HRARSMKQ
8910	22811	A	8976	3	152	WNQPKYPSTGEWMEKMWIYTKLVQPM HGPHVAQDGFEGSPTQIHKLS
8911	22812	A	8977	375	193	FQDLPLGSTSNISFFKRWSPAMVRLIS NSWPQEILLPQTPKVLGITGMSHCTWPG GHISI
8912	22813	A	8978	2	395	RAALPTQASAMAGAPPASLPPLSSD CCASNERESVGVGPSEPGAGYNLLVCYL LRLEKRSIRVGVTFRSRLSLTR KGNSLTPCASRVQCLALLWLTLALYP LSCTHCQTLPEMNLVPQL
8913	22814	A	8979	120	19	ARVQWHDHGSTATLNSWPQVILLPWPBK VLGLQA
8914	22815	A	8980	204	48	LNRDKGLTMLARFVRNSWPQAIPLPWP KVLGLQALATAPCQMSFLRAPLS

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8915	22816	A	8981	335	221	FFFLFLFFCMITSHCSVNVLGASDSPTS VSHIAGTIGT
8916	22817	A	8982	360	150	LSHMPLLFVSLYPDHRAFMQVIFFFET ESPSVTRLECSGAILAHNCNCLPGSSDS PASASYAGYSFYL
8917	22818	A	8983	346	116	GQGRGVETESCSVTQAGVQWCDHHSLLS LELLGSSDPSTSASPVGTGTGGHYHTSS HFLFSVSSSYFPTPVCLAYR
8918	22819	A	8984	350	263	LPMLPRLVSNAPQATFLLWPPKVLELQ A
8919	22820	A	8985	3	159	EEYNLLVCRLLSPLEKCSIGVRVTQFSR CHVSPLSLTRKGNSLTPCASWVR
8920	22821	A	8986	2	253	KHVVGELKNDLSICGTLHSVDRYLNIKL TNISVIDSEKYPHMLSVKNCFIQGSVVR YMLPADEVHKQLLQDAARKEPLQQKQ
8921	22822	A	8987	2	115	GARIVGHLTHALKQGEYGLASICNGGGG ASAMLIQKL
8922	22823	A	8988	3	159	GFYHIGQAGLKLMSGDLPASASQGAGI TGLSHCAQAGIFFFLPYDIFTVF
8923	22824	A	8989	1	123	SHYVAQAGPKLLGSSNPPASASRSAGIT GVSHHAWPPSLFL
8924	22825	A	8990	462	303	LARTPSRPTRPPTRPPTRPPTSPTRPP FMLSVDCLLLY
8925	22826	A	8991	382	178	PPFFFYFFFFSFFFFFQKGFKGF PQKFFFFFGGKPKVKNFQKFFLRAGKG GEKKPPQNKVF
8926	22827	A	8992	532	432	RDAGLTMLPRLVSNWAQVLLLPGPVKV LTLQV
8927	22828	A	8993	418	172	KKGKKKKKNIFLIFFNYFFLIFFFIFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFGGAWSLFRGGDSGEVKGTDSMS RQCFQGF
8928	22829	A	8994	2	722	AVRLNISYPPQNLTMTVFQDGTASTTL RNGSALSLEGGQSLHLVCAVDSNPPARI SWTWGSLTSPSQSSNLGVLELPRVHV DEGEFTCRAQNPLGSQHISLSLSLQNEY TGKMRPISGVMLGAFGGAGATALVFLSF CIIFVVVRSRKKARPVAVGVDGTGMED ANAVRGASQGPLIESPADDSPPHHAPP ALATPSPEEGEIQYASLSFHKARPQYPO EQEAIGYEYSEINIPK
8929	22830	A	8995	498	323	EPKAELNEGDIADVHIKREEGWFKGTLQ RNAKTGLLPGSFVENI
8930	22831	A	8996	21	511	LIIDGVEAYALNASGVVNIIVFDPKGWA LFRSFKAVKEKLDTRRGSNSELETAVKD LGKAVSYKMGYGDVAIVVYSGQYVENG VKNFLPDNTMVLGNTQARGLRTYGCID ADAQREGINASARYPKNWVTTGDPAREF TMIQSAPLMLLADPDEFVSVQLA
8931	22832	A	8997	178	306	GAINATNWPPFNNVGMGKTLGFNLMAL KQIPFSPVGEKTKRR
8932	22833	A	8998	351	211	SIQSLRMQPVPCYISGRHHHYHSHHHIH HHHYSSYFLKYPQYEYLRPL
8933	22834	A	8999	1	381	FRLFKEALMELCSIEGTSDDQLFFVFGF FFFGKEASFGPQGGREGGKFKLMEPLAK GVKGISCCKPPHPCLNPPKPRGGESSP PEGPKKTGAPGPAKGLFFLTGKNPWP GPGKTRKKAFFPKNF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8934	22835	A	9000	173	399	IKSEWAAKKKKKKKKKKKKKKKKKKKKKK KKIFFFGGGRFFFWGGDYFWGGGGVKK KGGGKKNPGPQKKNNGGGKK
8935	22836	A	9001	2	81	EFTPAVHASLDKFLASVSTVLTSKYR
8936	22837	A	9002	3	835	DAVRANDDLKENIAIVERNNLLQAELE ELRAVVEQTERSRKLAEQELIETSERVQ LLHSQNTSLINQKKKMDADLSQLQTEVE EAVQECRNAEEKAKKAITDAAMMAEELK KEQDTS AHLERMKKNMEQTIKDLQHRLD EABQIALKGGKKQLQKLEARVRELENEL EABQKRNAKSVKGMKRSERRIKELTYQT EEDRKNNLLRLQDLVDKLQKVKAYKRQA EEAEQANTNLSKFRKVQHELDEAERA DIAESQVNKLRAKSRDITGKGLNEE
8937	22838	A	9003	429	280	RGFRGHKFLEPPGFGFPFIMGPSPPF GSPPOKNFPLQPKPLGFKPPP
8938	22839	A	9004	2	108	LSAYQGTPLPANILDWQALNYEIRGYVI IKPLVWV
8939	22840	A	9005	3	158	SSTQGHKHCGRPQGGLPRKTRDLCSPVY LLTFSPLLSYDPVTSPSPRNTQE
8940	22841	A	9006	3	370	LLLTGLNRLTDLYSLYIPTTTQWGS LT HHINNIRPSFTRENTLMFIHLCPILLLS LSPDIITGIFSYTRHYVNSSTYLETNER GGSYKNRLGGPESKGLRIKDDSLCWGPL HDT SAYYENK
8941	22842	A	9007	363	76	KLFNVGGGGGLDKPPPPPKKFFFKNGLF FFYPLKKKNFFFPRELLWGPFRFFIKT PPPYFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFVMIS
8942	22843	A	9008	1	87	KMLKKPKFELGKLMELHGGSSSGKATG D
8943	22844	A	9009	420	3	RFYFPKPRKRGGGGVFFFPKKKKFFFL NPPPPFFFPKKKKKNIFPPRKGGGRGS KVQTMGPPLFFFFFFFFFFFFFLFFFF FFFFFFFFFFFFFFFFFLRETSSNNV LAYQIENSLLKLDLQRQCLPLPGRV
8944	22845	A	9010	2	74	LHRLGGPEAGLGEYLFERLTLKHD
8945	22846	A	9011	33	132	IDERCNSARAPLSLAGPHPGMGDASNH MGQM
8946	22847	A	9012	83	607	RRSGTPCGYNVTSQNGTIYSPGFPDEYP ILKDCIWLITVPPGHGVYINFTLLQTEA VNDYIAVWDGPDQNSPQLGVFSGNTALE TAYSSTNQVLLKFHSDFSNGGFFVLNFH AFQLKKCQPPPAVPQAEMLTEDDDFEIA ITGEGKPTRMPQSRKKSCHIIISVLISAK LNRAFL
8947	22848	A	9013	483	364	PPPPPPFLNPAPGIFFPPLGGIGARPP PPSFFFFFFFFF
8948	22849	A	9014	74	180	LLSTYVGRLSARPKLKAFLASPEYVNL P INGNGKQ
8949	22850	A	9015	488	317	HVGQAGLVLLTSGDPPTSASQSTGITGV SHRAQPLRSFSFVLSLLQKRIVLC
8950	22851	A	9016	149	13	DERGGLOAVAHTCNPSTLGGRGGWITRL GDGDHPSCRILAGDASQ
8951	22852	A	9017	20	107	FDSTADSDQVNPIQGLASKWDYEKNEWK K
8952	22853	A	9018	448	239	VDHQQVIWNRERISNSQNGIVKEIKGAD TFIFGHTPAVKPLKFAQMYIDTGAVFC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GNLTLLIQVQGECA
8953	22854	A	9019	3	209	CPPLSPGCTNSARAEPVHALPDALNNLR THEGSGDGPSSSVWDNRPEDVYPQGIY VISAPSIYAREA
8954	22855	A	9020	504	20	NYAQMSTYSTARASANESWAYFMGRKRKFV ASRQASQMFLCWLEEAIVRRVVTLP SKARFSFQEARSAWGNCDWIGSGRMAIDGLK EVQEAVMLEAGLSTYEKECAKRGDDYQ EIFAQQVRETMERRAAGLKPPAWAAAAAF ESGLRQSTEEEEKSDSRPAAGS
8955	22856	A	9021	3	168	LPRLEAAARIRHEERERERERERERERE RERERERERERERERERAPPPTLCET
8956	22857	A	9022	2	89	LCSLVYLLTFPPLLSCDPAKSPSARNTQ E
8957	22858	A	9023	508	371	FFCRDKVLATLPRLLANAWPQVIFLPQP PKVLRQLQPCTTPSLKDL
8958	22859	A	9024	2	170	RTHSAGRPHYQCNCQCEKAFRHSSTLVHK RTHVGRETIRNGSLPLSMHPYCGPLAN
8959	22860	A	9025	3	185	PFAATPQGPSPINSPPTKKAKNKNRTK KTKKKKKPPPSKKKGPQKTPKKTMGGPL KTTT
8960	22861	A	9026	104	319	LVFLSKYTPPLLVSLLWIHGLSLLSFLPS LPSFLPSLLTYLLPSFLPSFLTSTVINPL PSLFFLVFKLSQFWT
8961	22862	A	9027	476	364	SLKRLTSGDLPASASQSAVITGVSHRAR PIIYFKYVQ
8962	22863	A	9028	36	154	FLVGQAGLKLTLTSGDLPASGSQSARITA VSHRTWRTHYF
8963	22864	A	9029	2043	1237	WLRTRVAPALPERLGACTQLGPVLPSCQ PYVVCRCQCEYRRQAAQPPHCPAPEGEP GAPQALGDAPSTSVSLTTAVQDYVCPLQ GSHALCTCCFQPMPPDRRAEREQDPRVAP QQCAVCLQPFCHLYWGCTRTGCGCLAP FCELNLGDKCLDGVLLNNSYESDILKNY LATRGLTWKNMLTESLMALQRGVFLSD YRVTDGTVLCYCCGLRSFRELTYQVRQN IPASELPVAVTSRPDCYWRNCRQTQVKA HHAMKFNHICEQTRFKN
8964	22865	A	9030	15	389	IVDHYPCGGIPTSGSVTQAGAQWHNLGP LQPRPLGLEGGSSCLSLICSWGHRHAPPH LARGHFSSEVEQLRSRLQHGAVFVKQRK GTPEDPRQGLRTLISSCILHLVALALWF SLPFGHPRIHMQ
8965	22866	A	9031	3	243	RHSLAFNRFSCLSLPSNWDCHRPSPCPA KFCTFVEMEFHHVGGAGLELLTSGDLPT LASQSAGITGVSHHAWTRCCCCF
8966	22867	A	9032	1	245	PTRPAGIATCICMCMKNHRATRVGILRT THINTVSSYPGPPPYGHDHEMEYCADLP PPYSPTPQGPQRSPPPPYPGNARK
8967	22868	A	9033	46	124	QELMTHGAKSPDGTTRVHNAFLFVTTV
8968	22869	A	9034	235	435	KKKKKKKKKKKKKKRRPFKLGPFKPP LKPGGGLFEAPPFGGPPPPGFFAGGGA PPRGFFKKKKGK
8969	22870	A	9035	333	70	CPYIQIPILKDQVNLSSISSPFSHLIKD LWKTFLISYITELIFVCFVEMMFHHVAQ AGLELLGSSNPPTSTFQSARITGISHHA CLNI
8970	22871	A	9036	297	411	NKTMFSFAATWMQLEVLISKLMQEQKTKY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						CMSSLISGS
8971	22872	A	9037	461	167	NKNYP LLLGGPPFGSPSPENLNGGFPLTP GGGGPINPNSPPPPPPGRRPPFLKKKK KKKKEKETNTYILQDTCRCSAVLPIMQ VKIVMICLIMHRLF
8972	22873	A	9038	466	292	NGCLLEPASWNSLANIFIFCREEGLTML PRPQVILPPLPKVLRLLPPPLSS
8973	22874	A	9039	34	124	GIRNIKFSSLSTFIAHKYYCSSHAAEH VK
8974	22875	A	9040	54	239	RRRRKLRRWGLAMLPRLVSNWHQAILW PPKVLRLQACATTPGLTRRWLHGQIWSP GAGSV
8975	22876	A	9041	469	223	PWARVCVCVCVSVVCACVRVCARASES QTCAAVPSLGPAGAGRPALGCCAVCEDE VGSCPHARPLPRAAVDKAAGRRGLCF
8976	22877	A	9042	491	380	SPGVVAHSYNPSTLDGRGSHITVRKFM TCLATEGAV
8977	22878	A	9043	144	360	IHSHWGYWLDVSLIAAHLAINPDCFMVY YIFSQCTDKLTEKEFIEGTLANKEILRL IQFEPQKVKEKMNA
8978	22879	A	9044	23	263	RWNSDGKGLSRPAWATWPDFVSIKNTON THTTHTPHSPHTPHGQQPFLSPTPFPW PVSSPSPFPFPSHTCLCLLPPGA
8979	22880	A	9045	461	287	PPSLANIYLFYILFIFGRDGVSLFPRLVS NCWAQAILLPWLPKVLGLQGEPPNLALK SL
8980	22881	A	9046	485	6	NNKNSWAWWRVPVLPATREAGAGESLES GRRRLR
8981	22882	A	9047	475	307	LFLRDGSLTVLPRLVSNWFPQAILLPWL LKGLGLQARATLHMACSSCINSTQNILQ
8982	22883	A	9048	483	338	LREGERQREQERERERERERBRDRERAH TTAFTQLLFQYVAIILLPCY
8983	22884	A	9049	680	303	NDLLFGSLYVKQFAASGTGRVTLPEPSE EQVVCLRCFQDLFGDDHNKNGFKMFDSS NYHGQDLLFKDATVRAVPVGEKTTYRGW LGLDYVALEGMSSQQCSGAGRTGPPCR LPWCYSDPFTPEP
8984	22885	A	9050	26	165	AFGYHRVQGAGLELLTSGDPFASASQSA GITGVSHHARSQYFFVYV
8985	22886	A	9051	461	83	HKINLPSHKKKKKKKKKKKKKKKKKKK K
8986	22887	A	9052	475	209	MAAPPKKKKKKKKKKKKKKKKKKKI
8987	22888	A	9053	531	404	SVTQAMQWQKHNSLQGSTLEFRQSSLL SLPTIWDYKHADLS
8988	22889	A	9054	66	416	KKKTNKIKMGGGGLPFPKISPPFLKKTLS WKKGAPKTPPLEMAPFFFPQGGKNSPF KGGKIFFFFPKKTFIKGPPGGEHTPPL GGGPQIFSLPPPQKVPQKNPPPLLRGGL FFTII
8989	22890	A	9055	1	104	ILAVNGETLEGVTHEQAVAILKHQRGTV TLTVLS
8990	22891	A	9056	3	106	LKRWGIAMLTGLVLNSWAQVILPSWPPE VLGLQV
8991	22892	A	9057	1	299	PTRPINIILAFTISLLGILVYRSHLISS LLCLEGIILSLFIATRIYPIAPPLPPL EPEKKKKKKKKKKKKKKKKKKKNTKK RKIKAKRKNLGGGGL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8992	22893	A	9058	482	146	LTSSKKKKKKKKKKKKKKKKKKKK
8993	22894	A	9059	2	290	YFLFAYTILRSVPNKLGGVLAALLSILK KKKRGGPFKRTLGGPKFNRGGQGNIFFL MGGGLKPNLILGRNLSLGGGKNWPNLP PKIKGFRENKNF
8994	22895	A	9060	413	48	PQKKGFFQKNPKGFLKPPPKKKKKKFPF PGKIWPPQKIFKKPPPPPPPPPPPPPPPP PKPPPPPPPPPPPPPPPPPPPPPPPPPP LRSLDVCHLLPPIPTQVPGPTPVLLFST LPDCNHSLL
8995	22896	A	9061	2	274	FTISLLGILVYRSHLISLLCLEGIILS LFIIATLITLNTHSLANIVPIAILVFA ACEAAVGLALLVKKKKKKGRPFKRILGG PQINPG
8996	22897	A	9062	42	255	QEFRTTRERERERERERERERESSGVVR AKFRSNFSAGAIHTIRVMLPPSGIYSN EKSINKCGFALLFF
8997	22898	A	9063	20	413	YALRNSARAGDPHGQLGRDGAVGGRGW LMPREALHPWANVQAWGSPGLFLGAP WPQGGVWLPWLCVMSASSSSINGLPPQ KKKKKKKKKKKKKKKKFWGGGPGPQSPF WGGLKKFGGRFLKRGGEN
8998	22899	A	9064	6	306	ECEHSTTYSHFAGGGGPFVMVGDDADARS KALLGVCVSGSTEAYVLVDPHYWGTPK SPSELQAAGVWGWQEVSAAFDPNSFYNL CLTSLSSQQQRTLD
8999	22900	A	9065	463	126	AHYQLVYTCKVCGTRSSKRISKLAYHOG VVIVTCPCQCNHHIIADNLGWFSDLNK RNIEEILTARGEQVHRVAGEGALELVLE AAGAPTSTAAPAGEDEGPPSPGKTEPS
9000	22901	A	9066	23	244	SCHAGIRHEERERERERERERERERE REREREIYFLALFSQKGRVHGFKTPRG GQKRELLSNRVNTLCTE
9001	22902	A	9068	396	143	KDIQNFQAWWLTPVIPALWEAEAGGSR GQEIETILVNMVKPHLSVLLAKNSSSHC PMCWLAELOWYDLCSFKIFFGILIPG
9002	22903	A	9069	828	99	VDREPVDPVPVCHPDLEERLQAWPAEL PDEFFELTVDDVRRRLAQLKSERKRLLE APLVTKAFREAQIKEKLERYPKVALRVL FPDRYVLQGFFRPSETVGDRLDFVRSHL GNPELSFYLFITPPKTVLDDHTQTLFQG EPLPGRSGCNLGAEEPAGVYLEPGLLEH AISPSAADVLVARYMSRAAGSPSPLEAP DPAPKSEPAEERGALEVPPEPIPGTAQPV KRSLGKVPKWLKLPASKR
9003	22904	A	9070	20	427	DGTRRRERERERERERERERERLYLTEDT LHSLSLEGARSGASVCQSVYPTGASAP HSIINGHKRVLVLCVETEHTFPLAEKDR AFLGDTSVFVGAAPVGGANTGASAGAP PSRGEPKEESGESHEDEMGFGLFV
9004	22905	A	9071	297	126	CSIYDKRIPTFGLGEGVSRQRLTLLLP CLPPALTETPTSSDQSTDATPTLTNNS
9005	22906	A	9072	117	286	VVLRGSEKMFQVQEQINEQYLQCLIKGI FLVKKKKKKKKKKKKKKKKKKKPRPEYIK
9006	22907	A	9073	3	302	PPMETLRQWTTIVHSQEEEEHFEVIKD EVKVVARKHGQPGTPVAIATQLPPRTSA AFPAQQQPLQPLAPTTVLSVSADWNALL QRPNKYIWGLQYLEM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9007	22908	A	9074	437	79	NQKREEEEEEERRKKRRRRRRKKRRKKKK KILRQKKKKRRKAGSREKKKILRHLPEK NKRSKKHYELINALSRLQDTRLIYQKMH FYILAKNNWKIKLKIQVHLQALENKVPR HKWETYA
9008	22909	A	9075	51	185	CRADFMFFHDKIIVYLCSLVYLLTFPPL LSYDPAKSPSARNTQE
9009	22910	A	9076	452	310	QFSRCHLSSLSLDRKGNLSLTPCTSWVRR CLALLRLTLGALHLLSDNPQ
9010	22911	A	9077	438	326	LLHCWWDCKLVQPLWKSVMRFLRDLLE IPFDPTLHF
9011	22912	A	9078	37	169	GIPGFRHAGQRRQLQLLTGDLPTSASHS AGITGTSDRARPPSTF
9012	22913	A	9079	1	408	RKGRLSKEEIERMVOEAEKYKADEVQR ERVSAKNALESYAFNMKSAVEDEGLKGG ISEADKKKVLDDKQCEVISWLDANTLAEK DEFEHKRKELEQVCNPIISGLYQAGGGP GPGGFGAQGPKGSGSGPTIEVD
9013	22914	A	9080	31	168	VRRNPRLEHTVTITAYCSLELLGSSNLP ASASQVARTGLQLLNLQ
9014	22915	A	9081	460	319	YFFVEMGSHYIAWAVLELLGSSNPPASA SQSAEFTDAHKPTDCRPLR
9015	22916	A	9082	465	326	PCVAEFCETHHTHTHTHTHTFKCVGSHL HTNND
9016	22917	A	9083	33	269	PGNSRPISSVRGIIHPPCLANFCFLNVFV EMGSHYVVLAGLILGSSDLSALAVQSGR VTGMSCAWPEIFFLLENWIIIL
9017	22918	A	9084	47	300	DLITSLFLLKQSSLATMNIQTFFKNIFY DLIIKTFLFRFFIFCFYFYFLFFSYGG FFSFFFFFLKGSSFLPRLNGGAKIWNV
9018	22919	A	9085	437	220	NIAIKSLSLSLSLSLCVMCVCVSACVC MCLSLSLFSPSSLSHSLFPPSTPNMDIS HLPILSTQENMLLLQLQ
9019	22920	A	9086	227	23	DCPKANILGLTPRLVSNWPQVILTPWP PKGQSLLCRQGEGRDIWTHPPWLLHPP PQARFPPTHTFH
9020	22921	A	9087	206	326	PHWAQWPTPVIPALWEAEAGKSQGGQFE TSLANTVKPRLY
9021	22922	A	9088	364	123	SRVVLPLKAPGEDTSLPLPASGGSRCSL AWGSIPPIASIPTWPSVLCPCEIFPLL FLLYGDCNLGPTLIPDDLIMRSLP
9022	22923	A	9089	373	205	MPPRLANFCYFSRDWSPYWSGWSQTPC WDYRREPFPFCVRTSYSVQYCACYAGL
9023	22924	A	9090	283	2	REFSFSAVVLAFKIFWKLFSPPFWRVRP EDWFI PGCGPNEPNFPCCPGVGKKGE PRFKKKKKKNFISSQAQWLPVIPAFWE AKAGGSLEP
9024	22925	A	9091	16	261	CPEDLLVGQNVKVEDSDMGDPDRRPMCM FACFYLLVYRRCLAMLPRLYLNSWAQVI LLPQPPASLELLQAHATHPALCLSF
9025	22926	A	9092	17	109	RQGLAMLPRLTNSWTQANLLPWPPKEL GL
9026	22927	A	9093	282	114	KKGGKGALLVFLKTKGRKPPFFFLRQGLA MLLRLVLNSWAQAILLPWPVKVLGLQA
9027	22928	A	9094	205	337	NANLHGRMQRLTPCLPETWEAETGGSQG QEIETILANMVKPCLY
9028	22929	A	9095	62	287	EHSCAKLFCFAFESGPYSVAQAGVQWHD HSLLOSQTPLKQSSCLSFPAAGFYKE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SPSFYKDKSCHHLGKHSGA
9029	22930	A	9096	170	9	AASTGYCIGRFCTKLKIQSGQVRLSP VVPKREAEVGGLLLEARSSRPIWATW
9030	22931	A	9097	2	104	RRPGGRAEPRARVRGDRDPVLLRHYPH IFEECG
9031	22932	A	9098	350	142	LCLSCP KGGYRAMAPWRGNFCSFGKNG GFPMLGRVVLKWPQMGPPLPQPPKRVGFQ GLSPPPGPPFLV
9032	22933	A	9099	494	342	YFYFYFVEMVSHHVTQAGLELLASSNPP ALISQHAVITSGSHHTQPKLYF
9033	22934	A	9100	30	232	GGIMLCHGRACFPFAFCHDCKFPKVFQ PCFLYSLQNCSEFLYKIPSLRSCRLQLAE LLSIYLENPL
9034	22935	A	9101	26	171	RNSRRLRHKNRLSLGGGCGSEPRSCQCT PAWQTARLSLKNKKQQQKKP
9035	22936	A	9102	486	239	HHTCPHQVCVCVCVCVYRVCVCVCVCVY IYMYMCIYIYIYIYIC IYICRERERERE REMWFFHHVAQAGLELLGSRDLPPAS
9036	22937	A	9103	487	344	TGFHHVGGAGIELLTSSDLPASASQSAR ITGVSHHAQPLFMIFCAKC
9037	22938	A	9104	470	221	TPGLKRYTCLSLPKCWDYRCEPHARQGA FLCAFSPLSSQPPWGRPHFHSYETNK VERGKRLPLRSPSTEQGFDFRCVLFQT
9038	22939	A	9105	468	259	YVFFCRDGGLTISSRLVLNSCPQSPCL SLPKCWDYRHEPPCPSCSNLLLMFHFT NVFLIDSECSHFTF
9039	22940	A	9106	466	329	RVAGTTGTHHAWLINIPSVETGFHHVG PQVIQPPRPKALGLQA
9040	22941	A	9107	409	306	AGFELLASSDLPASASQSAEITGVSHHA RPSLIF
9041	22942	A	9108	417	269	MVVAQADMESSEKPEGLFNVIINDSLVQ AYPELKEALYEEIKKAQRGA
9042	22943	A	9109	533	399	RGSLRHETRLNAEARRCSELNSRQCTPA WATERDAVSKKTKQKA
9043	22944	A	9110	16	239	LVHFEVRWNSHEVSLTADSRKSHLIFPQ PNYADTLINQESYEKSEPLLITQDLLET KGEPRQLQVSFFPPKREE
9044	22945	A	9111	68	219	EPHHLANFLQRLVFTMLTLILNSWPGV ILPPGPPTVLGLQDKLPVLLPS
9045	22946	A	9112	192	57	DRVPLCPDWSA VARSWLTAASVSQVKG ILSPQPTCAPPGNST
9046	22947	A	9113	21	201	TIVSVVEFMNLGGGTCGEPRWCHCTPDW GTERDSVSGEKKEDKDVARRHVWGSFYN GPQ
9047	22948	A	9114	2	144	TFTIDRCAKDLFVAKQVGTKLSVNEPLS FSVESILKRPSSAITRVSQ
9048	22949	A	9115	156	316	MILNKKKKKKKKKKKKKKKKKKKKKKKK KGGGPFKKTGGAKITPGWKNYFFFFMG GV
9049	22950	A	9116	1	84	TKPTPFLPTLITLTLLLPISPFLLIIL
9050	22951	A	9117	1	176	HLNLGGGVCSEPRSCHCTPVWATEILSQ KKKKKNGFKFWEPRPQKEGGGGRKKPPG VP
9051	22952	A	9118	1	184	AAAGYPGQQQNFHVSREMFEQRIGLNN SPVNGNSSQMAFPSSQSLYRTSGAFVY DCSKF
9052	22953	A	9119	69	374	IIFS KKKKKKKKKKKKKKKKKKKKKKKP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						WGGPKIFVLRRLVLSFFIRGEKKNTFGDF LKKTTFFWGGGKLGKPPPKKTPWGKKKI FKGERGKKPPFLGGKKK
9053	22954	A	9120	405	93	EFSPLLLLTNQKRGFFPPSPPKIFFFPK RIYFLGGGGPHFPFPQKRGFPQKNQKGF FFSPPKKKYNLPPPGKFCPPQGGFFFP PPLFFFFSFFPFFFRQCQIK
9054	22955	A	9121	2	380	WDYRCPPPHPTNFCIFSGDGVSPHWPGW SWPQVICLPQPPKVLTPWVRDRTRDLE GGDLWYGACLGACLHLGPQAASFGHGIL GPASLLCCIPKHVMDTLPSPGVKLQSCD TGVALRVGEKREGS
9055	22956	A	9122	2	534	DMIREQKIYHKYLAQRREEEKAQEKEFD RILEEDKAKKLAEKDKELRLEKEARRQL VDEVMCTRKLVQEKLOREAKEQEERAM EQKHINESLKELNCEKENFARRQRLAQ EYRKQLQMQLAYQQQSQAEEKEERREF EAGVAANKMCLDKVQEVLSHQVLAQNI HPMPQGMPO
9056	22957	A	9123	389	46	GNFLPPPIFGFFSPFSLKFFFSPKTL IFLGFFFIFFPPPKSFFPKNSPGVFFC PPFKKKNFLFPSPLNFAPRRVFFKPPPP FFFFFFFFFFFFFYRLYFIWVNGLAKV VW
9057	22958	A	9124	422	59	AQOKKKKKKKKKKKKKKKKKKKKKKK K
9058	22959	A	9125	333	168	KGPPCIVVCMVEFHKLEAGSHSVAQAGA QWCDGNLLQTLTLGLKRSPHFSLPSR
9059	22960	A	9126	175	89	KPPPHFFFFFFFFFFFFFFFFFFFFFIFC
9060	22961	A	9127	368	250	CFNYLSRDRGLPLLPGLVLKSWPQAILL PQPPKMVGVOG
9061	22962	A	9128	392	157	FFSPKRLNFGGGGPKMPPPKKVSPPQK PHPGFFSPQKKKKKFFPPPVKMGPPKS FLKSPPPFFFFFLISSIRGLFL
9062	22963	A	9129	396	13	FFFFFFFFFFFFSPRRFFFRGGGSVALSP PKVFFLLNPPPVFFFSPPFKEKTSFFP PPFFCPPPQILFLAPPYFFFFFFFFFLF VFFFLFFFLPLLLGLKTSFLLLLFLF IYLETGSCSVAWARVQ
9063	22964	A	9130	55	180	LLYNKLIPTLKKKKKKKKKKKKKKKK KKKKKEKYEKTKAY
9064	22965	A	9131	2	95	SFVHMEHEKAVLLLSFQNTVDLGIQRE LTV
9065	22966	A	9132	172	404	KKKKKKKKKKKKKKKKKKKKKNWGGGF FKNSWGGPKKRGGGKIFFFSLLGGKKKT LGVFLEKPLFLGGRKMAPP
9066	22967	A	9133	1	125	QPVSYPTTIIGQVAYELYFTTILILIPT MSLIENKILKWAY
9067	22968	A	9134	1	120	QPVSYPTTIIGQVASVLYFTTILILIPT ISLIENKILKWA
9068	22969	A	9135	7	269	IATGQPRLOKLTLDPTLLKRFLLTKKK KKKKKKKKKKKKKKKKKKKGGGHHK KKPPGGPKTYPVKKKIFFFFGKIKKPP WGI
9069	22970	A	9136	1	64	LVSIISNTYGLDYVHNLLNLLQC
9070	22971	A	9137	400	259	SQPLRLRLHKNILNPGGGHYSELGSCHC TPAWDTEQDSIHSWLLSSV
9071	22972	A	9138	3	310	ECFPNSPNMNGHCNLLVQSTSPSISTMP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						CPKYVALEKVFLLNLVWFFYLKYRDNRP GSVAHTCNPSTLGGRGWITGAQEFETS LGNIARPSLIKRRKKYKLF
9072	22973	A	9139	34	142	NCKKLNTHTHTLTHSHTHMLTHSDTFTH THHTTKYK
9073	22974	A	9140	146	2	PPPPPPPEGVSLCGPGWSAVARFRLTASS ASRVHAILPPQPPQQLPTRP
9074	22975	A	9141	3	102	PPASASQSAGVTGMSHHAQPIEPLRCSS HRTT
9075	22976	A	9142	245	51	NREGDLLCCPRWSQTFLKQSCGLGFPKC WEYRRGPPHLYAIMSMRKNILIQMIFY NNPCLLYS
9076	22977	A	9143	2	108	GAKCVSDRIKHAFLIKEQKIIVKVLKAQ AGSQKAK
9077	22978	A	9144	3	200	MGFLHVGQAGLKLPTSGDLPASASQSAG ITGVSHRAWPVSGFFCSEAKECFWEEQL INLDKNSQK
9078	22979	A	9145	405	227	WFFLGFPPLKGLGPPKMFFRAPRVYSPF FPPFFFWPPPPRIIFPPGFKFVFLAG PIW
9079	22980	A	9146	387	220	PLFFVGCFFFFFFFYFFFFFFFFFFF FFFFFFFFFLLGGCERNFIIRKNINN
9080	22981	A	9147	539	220	VINFKHILIKTVIQSLFFFERGSCLP LECNMIMAHCSLNLGSSHPASASQV AGTTGAYQHTQLIFIFFAETGSCYVAQA GLQLLGSSNPPWPPEVLGLQV
9081	22982	A	9148	3	141	GGGGCCEPRWSHYTPAWATSACLKLLK KKRFLKESCLTPLLKA
9082	22983	A	9149	413	240	FIFCRDGGTLMPLGLTSNTWSQVILPPQ PKVLGLQAYHADELPHLATWGLVGLT V
9083	22984	A	9150	395	193	LLFGPCLLNLITQFVSCHLLDIKLQMTL SEGYFPLNIQESPFYRAPLDDPSVRHAR GEILPISLGGP
9084	22985	A	9151	1	77	LVAAILVGGTGWGFKNIRGRSGGA
9085	22986	A	9152	365	181	IVDRPDPCRDAQREVFTLSARYPKIW VPPGDPAREFPFIQSAPVMLLAAPDELV SAQLA
9086	22987	A	9153	373	251	FKKIFFCRDRALNMSPLVSNRTQAIL PPQPLKVLRLQA
9087	22988	A	9154	204	95	DYHWSQPGMVAHACNPSTLRGRGRWITR SGDRDHPG
9088	22989	A	9155	44	280	AEIFGTLMREDGLSLGGGGCKEPKSCHC NPAWATEPDCLRKRRKESPYLLVTPPD SSYSPFFFLLPAPDNNDYFLS
9089	22990	A	9156	2	117	ERLRHENCNLKGRGCSEPGWCHCTPAW ETKQDSISK
9090	22991	A	9157	3	207	HASAHASADAWDYRRVPPCPANFCILYV SHVGKAGLNLTSDDLPTSASQSAGITG VSHHARTPTV
9091	22992	A	9158	117	267	NRVLLCCPDWQTPGLKGSSLSLLSSWD YRHIPPRLAARSSYLGPFGYH
9092	22993	A	9159	415	167	LEFFPIKNXFFFSPPLEFFFFFP XFFFFFPFFFFFFF FFFFFFFFFFFFFFFFFLELKQNF
9093	22994	A	9160	217	41	SSQIHRDRNRMVRQGAHAHACNPSTFGG KGEQITRAQEFKTSANMVKPRLYYKPC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LY
9094	22995	A	9161	341	164	FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFVCF VSVELKKWQNYSFVRIILRVEP
9095	22996	A	9162	190	402	IHTGKHPKCYRNSYSVLFASKKKKKKK KKKKKKGGGFKKKKNLNRGGGEIIFFF WGPKKIFGGGGLKKG
9096	22997	A	9163	108	209	LSVKRCAKNPKKGKVPAGIKEIRTRSHQ DSEDI
9097	22998	A	9164	2	145	KHCGRPRPQGPLPRKTRDLCSLVYLLTF PPLLSYDPAKSPSARNTQE
9098	22999	A	9165	170	402	ISRCHFPSTLSYVKITKTIKAPKSKSK KKKKKKKKKKKKKKKKGGGPFKKKNF LGGGGGEIIFFLGAPKKKRG
9099	23000	A	9166	399	113	WRLRWEDCLSLGGRGCSEPGSCYCTPMW VTEQDQSSGYEGFQRPSSLSKARIPPSVA AERSMCQPACVCNLSVEHLSLYSCLLAQ QGKALYKLLNK
9100	23001	A	9167	3	138	SWITGVCHYAWLIFAFVETGFHRVGQA DLELVTSGDATTLRSH
9101	23002	A	9168	134	301	EKLTSQSHSVTQAGVQRLNVHSLRPPPPR FKRFSCLSLPSSWDYRNLETVLQEETH
9102	23003	A	9169	201	1	GATILRFKTKKKNVFFKKKKKKKKRKKK GKGWSGTESRWNLSEGGSSGLRRRKLQA PAGPQEFEKLA
9103	23004	A	9170	2	191	FVPQPLPLGFKRFSCLSLSGWDYRCTP PHLANFCGFFFLKFFFKKKNFSPR GRGGALI
9104	23005	A	9171	2	191	GGTESCFVAQAAVQGCGLGSLQSPPTGF SETASQTVDPDKVKDPGKLRTMFVAELP KTIVTDS
9105	23006	A	9172	3	143	SWFLYVGQAGLELLTSGDPPALASHSAG ITGVSHRARLQTGIFRAV
9106	23007	A	9173	361	174	VLGIILSMSETEIFNTKCLDQSGTVAHT YNPSTLGGQGGRVIRAQEFETSLGNTGR PHLFKI
9107	23008	A	9174	493	351	LVETGFNVHGQAGLELLTSSDPPASASQ SAGITGVSHLALVLISRKSC
9108	23009	A	9175	1	115	FRKIWIYTYTMEYCIAVKKKEMLSFTITW MNLEDFMLVR
9109	23010	A	9176	286	96	PLFFFNRWGLAICLGSVAIAIHRDHS LQSQTPLGKRSSCLSLSSWDYRRVPPC LANESHY
9110	23011	A	9177	399	237	RNTKWLFFLRSLTLSTGLECSGAISAH CNLRPLGSSDSLNGIFKDLALLDM
9111	23012	A	9178	427	101	GRTGRQGRGAPHISHDGRPGRDAPRFPD VMAAGKRSSLPRWDGGAETLLTFQTG QPGRGAPHIPDDGRPGGDAPHFPDGVVA GQRLQSQHFRPRQAAGRWR
9112	23013	A	9179	193	41	IVFLFIYLFCEFFVGTGFCYVAQAGLKL VSSGPLASAPQHVGITGMSHHT
9113	23014	A	9180	292	119	KITKINKQILNLSYTLDDMDLTDICRIF HPTATEYRFFSRAHGTFFRSGTKNSAWH I
9114	23015	A	9181	3	279	ALSPYSSSECKLGSFNRELSSPSPPGGQ KSEIKVSAGPRPLPRVQGDPSPLPASG GPRCSWACGQITAVSASGVTHPSPLLH VCCVCLI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9115	23016	A	9182	402	238	QMQRHNLWPLQSLPPEVTPFLFCLNLPNNWGYRWPPPPPTNFFFLKGVSLGRPGSV
9116	23017	A	9183	3	207	EFHHVGGDGLLELLTSGDPPASASESAGITGVSHRAQQACRFLHFFEGTCFLSQELS YLKLGRDTIIC
9117	23018	A	9184	3	106	YPHYVKSIVASTFIIISLFPTTIFMCLDQ EVIISN
9118	23019	A	9185	110	248	GVLVGSPRLRTRFHSQQAEGAEIGVVT VVMGDGVLPVCVVLEVDV
9119	23020	A	9186	925	1132	KCPASAWAAHPTSEIRISQGGSQAAVVLV LFFLLKNPGDVIPALWEAEAGGSQGGQF ETSLANMAKPRLY
9120	23021	A	9187	399	292	ASQVAGTTGAHHHARLIFFVFLVETGFH HVSQDENF
9121	23022	A	9188	7	82	PCDPPASVSQSAGITGVSHHAWQIF
9122	23023	A	9189	1	117	LPISLPSFLPSFLPSLPSFLPSFLPSFLPF FFPSSVTPYLK
9123	23024	A	9190	238	46	NKAFRIKAFVSPSNKKFSSFFFLNEMK SHYVDQAGLELLSSGNPSILASQNAKIT GVSHHVRP
9124	23025	A	9191	2	282	LIFYFVDNMLVRAGLELLSSSDLPALAP KVLRFRTGVSHHTRPELYFQRLAPGTL LINSQAAGTNFPIGLSRIKPTQSGHGM LQEVWGTSGLR
9125	23026	A	9192	44	136	CLCVCVCVCVCVCVCSCQKTL MCCFLENF DV
9126	23027	A	9193	469	347	PCPANFVFLVETGFLHVGHAGLKL LISG DLPNSDQKFYVN
9127	23028	A	9194	427	238	PPARPTAFPIEFFVEMVFRYFGKAGLK VLISGDL CASASPGVGITGVSHHAQPK
9128	23029	A	9195	34	178	SLVHVVEFERGRAEWLTPVIPALWEAEA GSGRGQEMETILANTDFWTG
9129	23030	A	9196	22	338	CGPYSMWWSIKRERKEGKKRKKRRRK EQKERERKERKERREGGREGKERGRREG KKRKKKKRKKVGLIGSPCIVFTWQAAYC EESGGVWPGGETEHTQEGLVQ
9130	23031	A	9197	3	91	QGLSLGGGGCSEPGSCHCTPAWATERDS I
9131	23032	A	9198	1	203	RTRGNKSIDDTSNFDDFPESDILQVPVN TTEPDYKSKDWVFLNYTYKRFEGLTQRG SIPTYMKAGKL
9132	23033	A	9199	2	144	PTRTMPCCCCCCCCCCCCRCLFMTGVL FTCCHNQFENHSGCLPRQI
9133	23034	A	9200	1	99	YAAKELVHDIRPTIEMERRRGLWWLVP RLSLE
9134	23035	A	9201	3	149	LNAVQRMWQLKVQELDPAGHKS LCVNE VPSFYVPMVDVNDDFVLLPA
9135	23036	A	9202	284	21	KGPPLFFFFFFLRLQGLVLWHRLEYSGMT TAHCNLELLVSSDPPTLSSQNAETTGV S HCAQPASLILSKPYIGFLHQIQKSLPV TFL
9136	23037	A	9203	1	77	LRLVLNSWRQAILLLWPPKVLGLQA
9137	23038	A	9204	529	340	GVLLWRQAEAGELSLGGGGCSELKVRHC TPAWATRAETPSQKINELIKSMAVELTD DFIT
9138	23039	A	9205	413	241	HPPPELKLFCISLISRWRCHRRPPCP YVFLLAETGFHVGQAGHKHTYCCVSLP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						T
9139	23040	A	9206	33	152	QLQGLESWMERCALPGYPVVFTNLCKY RSWIEETMRDK
9140	23041	A	9207	70	402	HVDWEALGNDPRLVNLGICKLKASGIHE WVHTRTCAHTMHMTHHTCTHCRSPRVV VNLGCTFELPGALKNARAYPHPNATKP MTSESVGIRPTRQVFKAPRAEQHCSTA
9141	23042	A	9208	46	262	GGIPPAAVRGRSWLRDVLRLAAGRR RRGTRRGRGRAGGAGGGRDVRGSRREPA AARTAAEGERA VRGKC
9142	23043	A	9209	15	206	PIEPLSERTNSAGAPPPASLPPCSLISD CCASNQRDSVGVGPSEPGSDMQTSLWA KVPVSKD
9143	23044	A	9210	475	110	NLLAPHLVLSLEKHSIRMGVAQFSRCHL SQLPLARKENSLTPCAGSVRRCLALLRL MLGGLHPLSCTHCPTGPSEMNLVSQLEM QKSPVFCVAHAGSCRLELFLFGHLPL
9144	23045	A	9211	420	132	PPPPNYFGGAGFFPPPPFFLRPPPPFF LPPKKKKLFPFRGPKKLFLLKAPPPSFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFF LVRSHFILTIM
9145	23046	A	9212	353	87	FFFXKQXFFPSLFFFSPPXXFSFYPF* YLKYPLLPPSFFLFFFTPPPPXFFFFF FFFFLPPPPFFFFFFFFFFFFFFFFFFFF FFFFD
9146	23047	A	9213	2	276	FIQLLKRRLCCELGYEVLPHPSYSHDLLP TNYHFFKHLDNFLQRKFHNQQDAESAF QEFAESQSMIFYATGINTLISPWQKCV DCSVSYFD
9147	23048	A	9214	402	276	LSCLSLPSSWDYRCPKPGYFFFFFLF LVKTGFPHLAQAG
9148	23049	A	9215	386	37	GFKKRVCSPPPPPPPPPPPPPPPPGREG FFLQKKKVTCPNPSSNKLTLGLQKKKE IQPALMKKNSISQS
9149	23050	A	9216	1	142	KDFRVQVWNHSSLQPQPPGFKQSSRLS LPKYWDYRHEYLHCQLAP
9150	23051	A	9217	402	181	FFFRXFFFXFFXFFXFFXFFXFFXFFX XXXXXXXXXXFFXFFXFFXFFXFFXFM FQQEKLFIYVNIIVTF
9151	23052	A	9218	2	87	SGSLIFGLIYICMCVCVCVCVCVCVYPC
9152	23053	A	9219	420	271	YYCIFRETGFHHVQGAGLELLTSGEPPA SASQSAGITATAPSPFLTFLLV
9153	23054	A	9220	139	413	SGYHSKTLFQKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKRGGGAFKKK IFFRGGGNNFFFLGPQKNIGGGGLKKR GGGKKPPPPQIFFFVG
9154	23055	A	9221	134	236	LHRWGPAMLPRIILNTWPQVILLPRPPK VLELQA
9155	23056	A	9222	364	280	STHLSLPKYWDYRHEPPCLAKKDAQSFS
9156	23057	A	9223	1	147	TLLPMLESSGTIMAHCSLNYLGSSDPST SASQSARITSVSHCTQPLPF
9157	23058	A	9224	1	208	AGAPPPASLPPCSLISDCCASNQRDSVG VGPSEPGAGYHLVVRRLSQSEKRSIRVG VTRFSSLLSSHA
9158	23059	A	9225	1	145	FQHVQGAGPKLLTSGDLPASASQSAGIT VSNRVRPKTKNFYTGNTRPN
9159	23060	A	9226	396	210	KCWDYRHEPPYPALTNLLFIEMGSYGVA RAGLKLGGSSNPPIASASQSAGVPLSHH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AQPIF
9160	23061	A	9227	2	154	FHHFGQAGLELLTSSDLPTSASQSABIT GMSHHTQPRMVFFSNFSSTAQC
9161	23062	A	9228	1	238	FLLALGIFILHAIYLSIYLSIHPPSMH PSLSIYLSIYLSIYLSIYLSISLSLSLS IYLSIYLSIYLSIYLSIDFLSSAR
9162	23063	A	9229	3	65	RGDLITEPFLPKLLTKVKGS
9163	23064	A	9230	25	188	YERTAWNQAWWYVPIVSATWEAEAGLL EPTSSRLRCVIAVPNSYCTSTWAVS
9164	23065	A	9231	44	232	YDLKFNNHVVFYFLFETEFHSLSKVECN GAISAHNNLCLCDGARLHRRGGKKTCK KQTLPS
9165	23066	A	9232	3	195	FFVGLGSPYVVTGLELLCSGNPPASAS LNARITGMSHQVQPNTRLSFYLGSSIIY GSIHAMI
9166	23067	A	9233	380	244	SVPLAEMGFHHVQGASPELLPPVIHSSQ PKAIGLQARATAPSLH
9167	23068	A	9234	11	101	LLLINTLMFIHLSPILLLSLNPDIITGF EG
9168	23069	A	9235	411	226	FFFFFATNSQGGPTSFWGPRNNAQVAGP LRNKIFTVPVGSPPKIFPSWETPVF
9169	23070	A	9236	404	262	QGLAMLPRLVSNWSWTQAILLPWPPNQSA GGSGVSHHTQPIFISENIH
9170	23071	A	9237	369	152	HAFFVSIWRSFHVSNSTMTVTVMYHNL SIPLDPHFFFRGGGLAMLPRLVSNPWP QAILPPQPPKVLGLQA
9171	23072	A	9238	389	190	RPKKKKKFFPPPGGKGVFFKGAPPYFL NFIFFFFFFFFFFFFFFFFLIYTHNLLIL FLNCDKLYIT
9172	23073	A	9239	330	3	GGMEPPFFPPTGAQWGVFGSLQNSPPEF KQFLCLRLPNVLEYKSIPPCTNFCSFY KNGIFPCWPGWPFKFQKKKISWVWCA LAEAGGSLEPRWRRLQSAKMAPL
9173	23074	A	9240	122	248	KKKKKRGGLTPVIPPLWEAKGGGSRGQK IQTILAGGKAPLY
9174	23075	A	9241	2	286	FFVQTEFHHVAQAALQLVSSRDPPTSAS QSDITGVSHCAQPVIVSCDDQVTLVQR RQVTVTSLIAFCQVAYPKGAKSQWPQSF FFSSPFLFSL
9175	23076	A	9242	2	95	HMKKCSSSLAIREMLIKTTMRFFFFKLI TCY
9176	23077	A	9243	377	293	PLSPRLVLSSWAQMILLPLPPKVLGSQA
9177	23078	A	9244	422	147	KKGGTQGFSPPRVFKRGPRNFFGPPKK KKNPPPPRGKIFFFLKGPSSFFFFFFFF YFFFFFFFFFTHKYFLGLDLLLIYHLS KKNYSFF
9178	23079	A	9245	402	208	TIGRCHHTQLNLKFFVEMGSHYVVQAGL KLLDSTNPPSSAFQSAIGSVNPNYAWTE IMFLYSIPI
9179	23080	A	9246	314	168	EPYHLHFLPPHHYYYCRWGLIVLPLVLS NSWAQVILLPWPPKVQGLQV
9180	23081	A	9247	3	320	VVQAGLKLSSCDQPASASQSAVITGVN HHARPLIFLYEMDYGSRVLIIRKWDND EQSNRTIFLKKDELGNRSACKLYTPMD INVNSGLGWRYRFGMHQCRW
9181	23082	A	9248	22	303	KGSYFSFTYEAQTESCSARLECRGAIS AHCNLRLLDSSNSPASASRVAETTHKKT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LVPERSCTPKERNVIQKGQEESEEMSN HLFTWLPILH
9182	23083	A	9249	13	174	LGLKVRHRLWLI FVLSVTEFFHHLGQAG LELLTSGNPSAGITGVSHCARPTSHS
9183	23084	A	9250	3	141	HVGQTVLRLLTSGDPPTSASESAGITGV SHRPRQIFISLFTICIR
9184	23085	A	9251	56	262	LRIPLTFGGVVKGEEEDRAVMHLRLCGD DSEMSSESLHFIKLPRTVLVDEDARPEKK KKKKKKKKKKKK
9185	23086	A	9252	401	275	PADLFIFIWEDGGLTMSPRLMNSWSQA TLQPWTPKVLGLQV
9186	23087	A	9253	411	258	PKVFKYRCDDPRLAWFLFFVQSLLPRLG LNSWAQAFLLPPWPPRVLLGLQA
9187	23088	A	9255	391	167	GLKILTSGDLPASASQASGNTGMSHCAR PLMSFKIRYFLFTIKMKLKLVLVPPVWSA GVHPPHFSCPIVITNKPRI
9188	23089	A	9256	9	255	FFCRYGGLAVLPRLVSNWTQAILSPWP LKVLGLQACTHHFFLMVNSNAARIKTIE MLLSEVDNFFVALLCPSFTISHFHL
9189	23090	A	9257	487	42	RYFIFLFYFIFKTETGSYYVAQARLRL GSSNPPALAFQSARITAVSHRAQLTCIK YTFLFTHIP
9190	23091	A	9258	1	243	ILSSGGSFISLTAVILIIIFMIGEAFASK RKVLIVEEPSINLEWLYGCPPPYHTFEE PQPKKSEIYSKCFFFSVFVHFGGWG
9191	23092	A	9259	411	2	FFFFSPPVSLSLCVLESPPPPFFFSPP PKKGFFSPPFFFSPPRVFPFVFFFPFPP PFFFFPPLKKNFSPPPPGKIFFFFFRPP PFFFFFLLFFFFFRPFFFSFFFLRWE EVLYFIMCHHISDAYPPNVDNMKE
9192	23093	A	9260	417	219	SVEMGFLHVGQASIKLPTSGDPSASGSQ SAGITGLSHCARPHSQLSIVCCYSVPVQ CLHSLAARY
9193	23094	A	9261	408	172	CENHFRKWGHRGCPPPRVFFVGRDGVY VAQAGLELLDLNSPASASQSNGTGMS HLGQPLLFI LNDVIAVIPLQGSF
9194	23095	A	9262	401	132	HQDNKPAPPGFFFFSPPPKGFFSKPPY FVSPRFFFPFPLNAPLFYFWGPKKKI FFFPFPAIKFFFFKRAPLFFFFFFFFFF
9195	23096	A	9263	393	220	LFLLNKIPFFPPGSGKGGDFGPHNTNPP GVKPIFRPHPEEGGPKGPPRPREFFL GF
9196	23097	A	9264	206	438	FPILKTHFRLGTVAHNTTTLGGPGGR NTCSKFKTSLGTWGDFFHKS ENCLGWG VPNCGPCFWGAQQKSAWSEGL
9197	23098	A	9265	333	48	ALLAGPTPFFFLGKKKTRFGNRLFFFF FFFLNEVLLCNPWIMVVAIHRCDHGT QPPTPGLKRSSCLSLSSSNWYKLPKPLHP AGVRFLDFVS
9198	23099	A	9266	3	275	TGFHHIGQAGLKLTLTLDPPLSASHSAG ITGVSHHAWPMHLESYWRVQYFMPQVL YFWAPSGAQHCAQIIENAIPTLLSRPQE EPASEA
9199	23100	A	9267	49	226	HGPEPCMDADAQREGINVSARYPKNWES TVDPAREFTMIYSAPLMLLADPDEFASV QLA
9200	23101	A	9268	159	236	PRLVLISWPQAILPPWPIKVVLGLQA
9201	23102	A	9269	1	208	IFNYCVFSSGVALAYGIYKQDLPALKEK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PRGVFVDMGHSAYQVSACAFNRGQLKV SIYFFSRRLLVW
9202	23103	A	9270	1	209	IFNFCVFSSVALAYGIYKQDLGALEEK PRNVFVDMGHSAYQVSVCAFNRGKLKV SIYFFSRRLLVW
9203	23104	A	9271	379	263	ESCSVGRLECSGAVPAHCNLCLCLPDSS GSPASSSRLC
9204	23105	A	9272	312	3	FRREGLAALQPWWPNKVSSKKRKKERE RKKERKKERKKEDGATADGISEAE VIRVHPYPVGFGVLSEGDWTEDMRAGR RPHAGESGDTVMLPQAQE
9205	23106	A	9273	405	246	PTKKNKYLHAPPLFHFFFITIPNPFFFF FFFFFFNFFFFKTKGCEFLYFSY
9206	23107	A	9274	2	227	LVE'GFRHIAQAGLQLLSSSYPTSASQ SVGITGVSHQGPSFHFERKSLGLKTLL LCVKVGVRACTALFFQGSS
9207	23108	A	9275	70	304	NLFKASTYPSSEHLHYLPPTPIVYIRKR LDAMAHACNPGLTGDRCGWARTPDLKC SAYRGLSKCDYRHEPPRPVLV
9208	23109	A	9276	2	260	TVFHVHGQAALBLTSGGPALASESAG ITGVSHAQPFLLILVISLFPCNQSFHI SPYRFSTQLNHGFNTVLVPLVINISEI FF
9209	23110	A	9277	406	330	PRVLNSWTQTILLPWPKVLGLDV
9210	23111	A	9278	2	160	ELLTSSDPPASASQSARITGMSHHTRLK YIVVRYSRKSNIPLKHIGIQSFP
9211	23112	A	9279	1	91	GLTVFPRLVWNWSAQMILPPWPCKMLGL QV
9212	23113	A	9280	3	107	LGETGFHHVGRAGLELLNKVMHPPWA RVLGLQA
9213	23114	A	9281	336	234	AHYKLLKIKLEGQAQWLTPVIPTLWEA EAGRS
9214	23115	A	9282	3	241	DREPECWDADAQREGINASARYPKNWVT TGDPAREFTMIHTAPLMLLADPDEIESV QLAQSWPFGATAASLRSPCRKRN
9215	23116	A	9283	404	277	IFFVETRSHHTAQAGLELLGSSDPPYFF QVITEMSLSQRALF
9216	23117	A	9284	399	231	HYVAQASLKLLYSGDPPASAFQSAETAG VSHCTWPTGSLNKIQNINHSRISSM
9217	23118	A	9286	394	231	AAAAAAAAFGERGFFHHVARTVLKLLDSSN PPAVVSQSAGITDVSHDFLISLYRIY
9218	23119	A	9287	420	311	LNFCRDGLAMLRLVLNSWAQAVLSQP PKVMGLHA
9219	23120	A	9288	398	173	LLSEFFYLFFYYYYFILFFLLLLLLLLLLL LMFKALLFSCHYFPAMVTFKFSLSIGSV VRTSGYIMLFSYLCCLKTM
9220	23121	A	9289	270	23	TPEQCRGIKLFYISLILYVRDGVLLCCS GWPVVAIHKCDHSTLQHQIPSLKQASCL SLSSWEYRYAPLHLASANFLKVTVV
9221	23122	A	9290	273	46	HLLNMPLFTETWTERLFLFYILCFVFLV ETGFFYITQAGLKLTTSSDPPAYASQSA EIIGTSHCTRPICYNVNINI
9222	23123	A	9291	424	230	CLPETHSLSLSLSLSLSHTHTHTHTH TIYMNK
9223	23124	A	9292	2	146	NLFLVETRSHHVARASFLLSSSNPPTS ASQSSEITGASHRTWPEVFF
9224	23125	A	9293	393	202	GREERKERERERKERKKERKKERKPER

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PSGSLTYCVREGITAANLGKRRHKASKT LISHKNKN
9225	23126	A	9294	252	193	GFCCCCCCCCYCCSCDKRHPG
9226	23127	A	9295	409	269	SQYFGRLLRRVDCSSGVQDQPGQQGETP SLLKYKIYIHISWAGWHV
9227	23128	A	9296	2	213	FCCGLLIHLIYCKTEYSGQSTVAIHRCN HSVLQPQTLGFKQFSLHLLSSWDYRYS PLCPAYIFNLSIGY
9228	23129	A	9297	169	408	RFAHMHNSPHEERLPPAGIRVRPPQP AASLGPPRMAPSISRPFQMTPTYKHNDP AGQAQWLMPVVPALWEAEAGGSSE
9229	23130	A	9298	199	51	LHPPPPSLSLSLSHTHTHSHTHTHTH TLWLGRPGPAQDVVLVWGNLT
9230	23131	A	9299	1	176	MGSHSLAQARMQWCNQSSLQPPGLKQ PSPFSLPSSWDYRHVPPCLASIFFLKLN YH
9231	23132	A	9300	412	209	MGFHHVQGSGLELLTSGDPPTSASQSAG ITGVSHRNWPHCGFNLVFLMPDDVKHLF MCILAICVSSL
9232	23133	A	9301	195	347	KIKGFRPGATAHAGNPSALGHQGGRTAI AWEFTISMNMGRPCLYRKYKN
9233	23134	A	9302	386	190	GFLFFFFPPPKKEVFPHFILGFPGFFPP PFFFKRAPEFFFWGPKKKKNSPPRALN FFFFKGAPP
9234	23135	A	9303	27	173	SFQLWGHLLKVPRIIRPKRADHLRSGVQDQ PDQHGKTLSELLKKYKISRAN
9235	23136	A	9304	374	121	QWCDHGSLLQPTPGLKQSSCFSLPKRWD YRREPPHPTSLSPYIWAWPCTLCPPPLS ALWKHLIHQKCDGVMVLQVPGRTHNVTIL T
9236	23137	A	9305	70	196	PQVIHPGQAGLELLTSGDLPASASKSAG ITGVSHHAQPISHF
9237	23138	A	9306	378	256	QKWVSICCPGWSQTFGLQESSCLGLPKS WDYRRQPQCLTL
9238	23139	A	9307	206	3	PCHLGWSAVVQSWLTAASNSWPHAILPP QPPKVLGLQASLKLKAGITQVTFSDYN KILNKEIKRGR
9239	23140	A	9308	338	161	HFKKKIYIYIYVYIHTYIYIYTHIYIT HTYTYIYRIYIYIHTYIYMYVYIYIPS LPF
9240	23141	A	9309	503	288	FFLNLDKSQEWLMPVIPTLREAEAGGS LEVRSSRPASSDPPTSASQSAGIIGMRH HARPVVLRENGRIQN
9241	23142	A	9310	418	309	FFCKNGISICCLPKLVNSWPQAILQPQ PPKVQGTIL
9242	23143	A	9311	442	275	VSPPPILGGGFLSPFPKPPPPFFNLKGGP PFPTIPFLIIGKKFCPPPPFFPGLF
9243	23144	A	9312	2	95	HENRLSLGGGGCSELRLCHCTPAWATER DFI
9244	23145	A	9313	318	154	FFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFI FILFIYSLLYVVCVGLGS
9245	23146	A	9314	388	199	EQPKCVHRIKQIWHICALEYYAFAFKKKK VLPYAVIQIKLEDTMLSEINQSWGKYCM IPLIGGI
9246	23147	A	9315	2	97	STPGLKRSSHISLPKYWDYRRGPPGPAS ILF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9247	23148	A	9316	3	235	TMVVNAEGIPIRTTLDNSTTVQYACLLH HLTMKAKSTVRDIDPQNDLTFRLIRSKK HEIMVAPDKEYLLIVIQNPCE
9248	23149	A	9317	253	71	LFFFFFLFFVDTKFHHLAQDGFQLLSSSN SPTSASQSGGITGRSHQAWPYVHLLTLQ KLNY
9249	23150	A	9318	425	95	CLLFCKPKKKKKKKKKKKKKKKKKKKKK KKKGGPIKKKKKQP
9250	23151	A	9319	25	214	VRIDDRPEPCMDADAQREGINSSARYPK NWVTTGDPARECGMIHSAPLMLLADPDE FVSVQLA
9251	23152	A	9320	50	231	GHRPEPGRDADAQREGIIASARYPKNWV TTGDPARECTRIQSAPLMLLADPDEFVS VQLA
9252	23153	A	9321	401	226	QWLFTNMIIGHCSLELLGSPSNPPISASR LAATTGTRHHAQPSKFRNLKGWLCAKRA RT
9253	23154	A	9322	410	159	LGSLQLPPPGSKRFSRLSLPSSWDYRGC SELRLRHCTPAWVTEQDSVPPKKKKQIF RPFPPFSYGESLGVGLRHLCSKPSRRF
9254	23155	A	9323	310	25	KWGG LFFFPKPKRGFFKQVFFCFVPPVF FFPPFFKTGPGDIFLGPLKKKIIFPPPG GKKFFFKRGPPPPPPPPPPPPPPPPPP FSEVECVCCLCR
9255	23156	A	9324	406	289	PGFYHAGQAGLKLTLTSGNPSASASQ SAR ITSISQRT RPH
9256	23157	A	9325	1	116	LHSVLLPFFYFCVCVCVCVCVCVCVKHK YVRAGGAPGR
9257	23158	A	9326	2	158	FIFLFTVGGTLTGIVLANSSLDIVLHDTY YVVAHFHYVLSIGAVFAIIGGFIH
9258	23159	A	9327	3	107	RGCSEPRLRHCTPAWVTEGDCVSKKKKK VPEAWG
9259	23160	A	9328	257	2	GFFSNISASVIIPPPISRKNLFFPFRVY FGPPPKTFKGPPPPPPPPFLSPRLCSCG VIMAQCSLTLPGSSDLPLSASCVMATVS I
9260	23161	A	9329	66	384	GNLCGWMKSMADNPVVRKADWQGIRES LECQPNTGMLKKKKKKKKKKKKKKKKKK KRGGPFLKISWGGPILGGRGKIFFFFFG GGILTPRGVFWKSPFFWGGKKK
9261	23162	A	9330	1	98	IIGQVASVLYFTTILILIPTISLIENKI LKWA
9262	23163	A	9331	33	412	NLFYVMAETILHTHIQLCCQVKLHLSVPR PSLPLLCWNFSLVLHEHSQPASEKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKK FCGGGENFFFFFGGLKKPRGVFGKNT FFWGGEKRP PPPY
9263	23164	A	9332	401	311	PTRPVDLLVDDSVKESLIGYGPTEDSKE FS
9264	23165	A	9333	5730	452	TRSAPRAASWLEDPREVRSVCLSATFFT LSLQKPRLLLFSPSVVHLGVPLSVGVQL QDVPRGQVVKGSVFLRNP SRNNVPCSPK VDFTLSSERDFALLSLQVPLKDAKSCGL HQLLRGPEVOLVAHSPWLKDSLRTNI QGINLLFSSRRGHLFLQTDQPIYNPGQR VRVRFALDQKMRPSTDTITVMVENSHG LRVRKKEVYMPSSI FQDDFVIPDISEPG TWKISARFSDGLESNSSTQFEVKKYVLP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						NFEVKITPGKPYILTVPGHLDQMQLDIQ ARYIYGKPVQGVAYVRFGLLDEDEGKKTTF FRGLESQTKLVNGQSHISLSKAEFQDAL EKLNMGITDLQGLRLYVAAAIIIEYPGGE MEEAELTSWYFVSSPFSLDLSKTKRHLV PGAPFLLQALVREMSGSPASGIPVKVSA TVSSPGSVPEVQDIQQNTDGSQVSIPI IIPQTISELQLSVSAGSPHPAIARLTVA APPSGGPGFLSIERPDSRPPRVGDTLNL NLRAVGSGATFSHYYYMILSRGQIVFMN REPKRTLTSVSVFVDHHLAPSFYFVAFY YHGDHPVANSRLRVDVQAGACEGKLELSV DGAKQYRNGESVKLHLETDSLALVALGA LDOTALYAAGSKSHKPLNMKGKVFAMNSY DLGCGPGGDSALQVFQAAGLAFSDGDQ WTLRKRSLSCPKEKTRKRNVNFKAI NEKLGQYASPTAKRCCQDGVTRLPMMS CEQRAARVQQLDCREPLSCCQFAESLR KKSRLDKGQAGLQRALEILQEEDLIDEDD IPVRSFFPENWLWRVETVDRFQIILTLWL PDSLTTWEIHGLSLSKTKGLCVATPVQL RVFREHHLHLRLPMSVRRFEQLELRPVL YNYLDKNLTVSVHVSPEGLCLAGGGGL AQQVLVPAGSARPVAFSVVPTAAAVSL KVVARGSFEFPVGDAVSKVLQIEKEGAI HREELVYELNPLDHRGRTLEIPGNSDPN MIPDGFNSYVRVTASDPLDTLGSEAL SPGGVASLLRLPRGCGEQTMIYLAPTLA ASRYLDKTEQWSTLPPETKDHAVDLIQK GYMRIQQFRKADGSYAAWLSRDSSTWLT AFVLKVLSLAQEQVGGSPKLEQETSNWL LSQQQADGSFQDPCPVLDRLSMQGLVGN DETVALTAFVTIALHIGLAVFQDEGAEP LKQREASISKANSFLGEKASAGLLGAH AAAITAYALTITKAPVDLLGVAHNNLMA MAQETGDNLYWGSVTGSQSNVSPTPAP RNPSDMPQAPALWIETAYALLHLLH EGKAEMADQAAAWLTRQGSFQGGFRSTQ DTVIALDALSAWIASHTTEERGLNVT SSTGRNGFKSHALQLNNRQIRGLEEELQ FSLGSKINVKVGGNSKGTLLKVLRTYNVL DMKNTTCQDLQIEVTVKGHVEYTMANE DYEDYEYDELPAKDDPDAPLQPVTPQL FEGRRNRRRREAPKVVEEQESRVHYTVC IWRNGKVGLSGMAIADVTLISGFHALRA DLEKLTSLSDRYVSHFETEGPHVLLYFD SVPTSRECVGFQAVQEVVGLVQPASAT LYDYNNPERRCSVFGAPSKSRLATLC SAEVCQCAEGKCPRQRALERGLQDEDEG YRMKFACYPRVEYGFQVKVLRSDSRAA FRLFETKITQVLHFTKDVKAANQMRNF LVRASCRRLRLEPGKEYLIMGMGLDGATY DLECHPQYLLDSNSWIEEMPSERLCRST RQRAACAQLNDFLQEYGTQGCQV
9265	23166	A	9334	46	324	SKYLPFPVITFQHEIWGNTNIQTISDWVL ICCPGWSAVTQSRLLAAASTSWAQAMSSS SCLGLSSSCYYRHTPPCLANFVAFVETK LYTMLPGLS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9266	23167	A	9335	338	178	EVDIAVSHRRKQAFNLCLLKCKPHNNCLNLEGGGSSELKLCYCIPAWATDQSL
9267	23168	A	9336	396	254	KLSTDCTSKETINRHPTWEKIFANYAPNKGPTSTIHSSCLMFPYLF
9268	23169	A	9337	454	359	SSWDYRHAPPCPANFVFLVETIFIQGEIGLL
9269	23170	A	9338	540	328	IKKRGAPRRGVLFFFTRKKKKFSYKKS TKERVSLFVAPGCIQGGKKKKPPTKKK KKKKKKKKKKKKKK
9270	23171	A	9339	21	209	AEEFPDFKLYYKANQNTYRGQWNRTETS EITPDIYLGILVSNWPQVILLPWPPKVLGLQA
9271	23172	A	9340	345	2	KIFFFLIYLFFFNFFFFFFFFFFFFFFFF FFFFLLENRWFLMENFIKGRGHVKGPLG QARDHDISGRWRREQCRASQLPGVRR SLLQVQAGGPVHIRISGLQDARQGPVGA
9272	23173	A	9341	15	252	LERVIRQSAALTDSSFNFILLILFIYLF FETGSPCVSQAGLKLGSRDPPVSASQSARIIGVSHRAQPALTDFFPSISF
9273	23174	A	9342	484	276	RHAPPCQANFFVQTRFCHVAQSGKLIR SRYLFASAFQSVRITCMASHCARPLYFLMFKRLQYLKSPTKS
9274	23175	A	9343	464	326	LVETGPHHVQAGPELLAPCDPPAPASQSAETTGMSHRARPPANFV
9275	23176	A	9344	486	280	SFSHSHSCSLPSSWDYRCTSSHLANFFF KRWGFTILPRLILNSWPQVILLPQSHRHEPLCLETCLKTLNV
9276	23177	A	9345	276	179	DRDFTMLPRLVLNSWPKTILLPLPPKILRLQS
9277	23178	A	9346	45	143	RWNSRQENCLNLGGDCSEPSLCHCPPAWATE
9278	23179	A	9347	229	73	PPPHMIFFFFFFFLFFYYYYYYYYFFFF FFFFFFFFSRLQVSVYCSSVLNKNVD
9279	23180	A	9348	391	139	IPSLKRSSHLSLAKCWDYRHKPPCQVTF SFLNVRIYATKFFLSTPLAASKYWYLV FLLSFSSKYLTLPISFLFLTHNVSSSIF
9280	23181	A	9349	53	191	IYVTYIWIYSEVSHAYNSSTLGGQGGRITGAQEFKTSLVNIAKPLLY
9281	23182	A	9350	373	235	EEGELLEPGVQGCSELSWCHCTPANGTEQDHCVSYNNSNTHNNVNY
9282	23183	A	9351	476	82	YLATYLPYLSIYLPYLPYLPYLYL GSHYIAQAGLKLGLWVGHNGLSCL
9283	23184	A	9352	286	142	ELQFKMRFGWRHSQTISWGLSLLPRLISNSWAQVILLTWPPKVLGIQA
9284	23185	A	9353	3	102	FFETESHVARLEYSGAISAHCTPVIKLYLYT
9285	23186	A	9354	3	270	TAGAPPRPANFCIFSRDGVSPCWPGWSRTPGLRCDPPASASQLGLRLHENCNLG GEGCTGAILAHCTSTLRAQAILQPQPSCPAPQ
9286	23187	A	9355	1	112	GEGSAHCNLCPLGSSNSPASTSQVAGIKGVSHRARN
9287	23188	A	9356	1	63	VALIQAYVFTLLVSLYLHDNP
9288	23189	A	9357	244	140	QRRHHTHSHTYTHTHTHIPNKKIPILTILKCIA
9289	23190	A	9358	464	181	LGAGGMTGILFSLGASMVLGVAQMLAP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KARTRRIQTDDNGKQNTYFSSLDNMVAQ GNVLPVLYGEMRVGSRVVSQEISTADEG DGGQVVVIGR
9290	23191	A	9359	11	469	IDLRCRFRHEERERERERERERERERER ERERERERERERERERGRAPPPPLFFGGG GPPARAHALSPPHLGRPPPLYTYFFSYVR APPTERSARTQREARRALKSVCVVRERE THSLPRARCVCSHPTGCGGAPGARVSL QSAHCFCLCVCGAG
9291	23192	A	9360	22	172	GLSHEERERERERERERERERERERD CPLFCPTGGFILREARVKSGCLCF
9292	23193	A	9361	15	345	PPNRPPAEFTRHLLISLLCLEGIIISL FIIATLITLNTHSLLANIVPIAILVFAA CEAAVGLALLVSIISNTYGLDYVHNQKKK KKTWGGGRAPNSPYGGRNNNRPRAV
9293	23194	A	9362	61	298	SCDSPLQECIHTHTHTHTHTHTHTHT LFSDIKTHTWREWALSLLFLLTEEGGGT LFQGTLLIFGHTLFWDKPLWQKEF
9294	23195	A	9363	430	2	GGAGPPPPCWTQGGPGVPPPTLSPRVNGP SLCSDFPSPKFYKEKRKKGNKTPKRKG KTLLPTETIVLHVSPGCESKPGAGSADR RAPGVRDGGSDASSGTRASELGDGPVR VNFVLGDPEAGRGFSMLGHPPTSGPR TS
9295	23196	A	9364	432	291	GITGLRHHSQILFIFLFLVETGFHHVQGAG LELLIHQHRPSKVLRLQV
9296	23197	A	9365	343	507	GQGLTLVPQVGQVGNLSSQLLPPGLK QSTCLSLPKWDYKCGLPPPASFCFVL
9297	23198	A	9366	417	128	MGWWPGRGAPPFLDEMAAGQRRSSLSRV GSQAEGLLTSHTMGGPAETLLTSQTGWR LGRGCNLGSLEGQGRRLGGGGCNEPSSR HCTPAWAPLSTE
9298	23199	A	9367	500	285	SLPRSWDYRRAPPRPANFLFLVEMGFHH VGKAVLELLTSGVELLTSGDLPASASQS AGITGVSHRAWQIRE
9299	23200	A	9368	1	229	IVDLTTWGIPTHTTHIHYTHIHKYIHTH AYTHHTRHKHIYTYIHTDMVWLSHPN LILNFSSHNPHVSWEGPNGR
9300	23201	A	9369	451	88	KQTNITYTCIYMYVYIYTCIYTYVYIYTR TYTCIYVCVYTCIYVCVYTCIYVCVYTC IYVCVYTCIYVCVYIRVYTCVCIYVYIR VCVYTCIYVYVYIRVYTYICIYTCISTY IQCIYTHIYKVTCKSG
9301	23202	A	9370	1	208	ADETIEQRGGIPKFVHDNYVIRRTAVDR GIPLLTNPFQETKLFABAVQKSRKVDSSK LFHYRQYSAGKAA
9302	23203	A	9371	354	202	PAAQREGITASARYSKNWVTFGDPAREF TMIQSAPLMLLADPDEFVSVQLA
9303	23204	A	9372	1	336	KSLIKYKGYQVAPAELESILLQHPNIFD AGVAGLPDDDAGELPAAVVLEHCKTMT EKEIVDYVASQVTTAKKLGGVVVFDEV PKGLTGKLDARKIREILIKAKKGKSKL
9304	23205	A	9373	2	187	NILVTALYSLYIFTTQWGSLLTHINNI KPSFTRENTLMFIHLSPIILLLSLNPDI TGFSS
9305	23206	A	9374	96	240	ACWLMFVIPALSEAEAGRLVQPRRLRAA WATWQDLISTKKKKKGGPF
9306	23207	A	9375	3	293	STISAFTTSTTSATTSTTSATTSTIS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						APTTSTTLSPPTSTTTSTTTSTTSAPIS SNKLHKKKKKKKKQKKKKRKNDDTKQD TITKIHSGGGSL
9307	23208	A	9376	69	160	EHTHTHTHSHTHSHLPERFCVLN SL
9308	23209	A	9377	336	199	EGITASARYSKNWVTTGDPAREFPMIQS APLMLLADPEFVSVQLA
9309	23210	A	9378	321	128	EPGFTMWASLAPTSSLOVIHRLGLPKCW DHRREPPHPAYHSLYESGPSVQNGEEKG INPIIKMG
9310	23211	A	9379	440	286	SSDPSASASKSAGFTGMSHHTQLTSYS EGECLSYLVFLVLV
9311	23212	A	9380	392	154	KGSSPLSPPISLAGGKPPPRKFFLNFF FFFNDRDRVSPCLPRLVSNWPQAILPPQ PHKALGLQAYATTASFIFLIVTV
9312	23213	A	9381	403	178	GRRHEPCRDADAHLEGIIFSAFYPKNWE TTGDGAREWTMSNSAPLMLLADPEFVS VQLA
9313	23214	A	9382	303	206	DPVSTKICSLQPPPPGFKRFSCSLSPSS WDHR
9314	23215	A	9383	215	116	SNNFVVCCCCCCCCCLRWSLTLPRLH SCGTM
9315	23216	A	9384	2	285	ARHLLMQLSGGATLAISTIDLPLSTLIIF TLILLTILEIAVALIQAYDITLLGSLY LGDNTYKKKRGAAFEETKFTSAGMQSK NFFLGLTNWR
9316	23217	A	9385	12	123	GYENFLPLTLHTQTHAHTHTHTHTHI HSKDPMEY
9317	23218	A	9386	3	230	KCWGYRCEPLRLAPLRCFFTPGGISLTS GPALLSNASALAEVRGQQLCPPTPFLPT LIAALTLLLPISPFLIIL
9318	23219	A	9387	590	396	ARVQWPDLGSLQPPPPGFKRFSCLSLN SWDYKCAPP CRADFCIFSRDGVLSWPG WSQTPYLK
9319	23220	A	9388	224	79	GLGPVGHACPTLWEGEAGGSRGQIEAL PANTVKPRFLKRRKKKKKG
9320	23221	A	9389	249	72	LVYLTIVKKILFPVHIRTFNKIDHMGH KTCLNKLQMTEILQSVFSDYNRIKLEAS NN
9321	23222	A	9390	400	254	LRQPGSTNSPVSASRVAGITGTHHTQI IFVFLVEMVVHACNPSYSGG
9322	23223	A	9391	3	64	PPQKSDPPYKLVFVHLDLIL
9323	23224	A	9392	266	106	LTANFLFLVETGFPHVTRVGLLELSSD LPTLASQRAGITGVNHLQNFWPNGNF
9324	23225	A	9393	430	348	FGKPQPPPKGKSPPPRGNFPPQKAPKG
9325	23226	A	9394	481	311	LSLSEKRSIRVGVTFRSRRCCPSPLSLTG KGNLTPGVSQEIHSPWFGIAYSVCTH
9326	23227	A	9395	3	136	VFPRLVLNSWAQMIILCWPPKVLGLQAC TTRPSHFLPLLNSKYK
9327	23228	A	9396	143	347	NFVFLVETRFHHVQGAGLTLTSSDPAS QSAGITVRPEILTLKRYHFPSGILGTE GMVIMAYLLKV
9328	23229	A	9397	2	231	LELLTSSDLPASASQSAGITRGSHHARP SFTFRCVIHLEFNFMRGAREERLHFYCR WVIRRLTTFGRGYPSPAASD
9329	23230	A	9398	383	200	QHYLNRRLSLAQWMPVVPATQEAFAAGG LLEPRSSSLQCAMMLPVNSHCTLAWATH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						REPHL
9330	23231	A	9399	3	416	GFLHVGQAGLKLTLTSGDLPTSASQSAGI IGVSHRAGCLKSIYLTFFTRKFFVQMSI CDFKVEIEGKIGFISVPISLQSIHIVN NFFFFLETGSFPPGWRWAKFGLIAPLA SGVKGIFLPLPRENLGWRPSPIPPA
9331	23232	A	9400	400	151	FGYPQVFLPPLPKPGGTFGLGPKKN FFFPPLGLKIFSFKRAPPFFVFVRKGLI MLRLVSNWAQVLIIPPPPEVLGLQA
9332	23233	A	9401	324	154	FFFFFFKXXXXLFFFFFFFLFYIFFF FFFXFXKFFFFFFF
9333	23234	A	9402	413	312	PKLVLSNLQALLPRPPKVLGLQARAT ITQPK
9334	23235	A	9403	363	3	FKKKNFCLGGAGVVFYDPPPKKNIF YFPSKKIYFLSPASSSFFFLCFPFIF FFFFFFFFFLENRWFLMENFIKGRGHV KGPLGQARDHDISGRWWRREQCRASQL PGVRPRV
9335	23236	A	9404	401	82	SELPHDPINPTTGYIYPKKMKSVCFTDI CTPMFTTALFSIAKIWNQPKCLSKRITI FMFLVTYSQLFCTHYPIPLYPFPAPLS SSHNYHYTLTYENILLDSTYE
9336	23237	A	9405	382	219	WARWHGFLVPTSPGGEAGGSLEPGKRRV QLTQISPLPSSLGGKVLPLKKKKN
9337	23238	A	9406	3	195	YLYSLVETGFHHVQAGLELLISRDP LASESAEITGMSHSIQPKSAFYIQIPET FWQPAFK
9338	23239	A	9407	371	1	FRRLRLKNRLNLGNGGCSEPRLCCHCIPA WETRAKLGRKKKEERKREKGTMYNKMY KMYLELNLTCPEPASPQMTRQLEVLSS NPSPGTQFICKKQFKFSCCFALRVSIY LLMSVFEYCSC
9339	23240	A	9408	326	229	RQGLTMLPRLVSNWAQVILPPWPPKVL GLQA
9340	23241	A	9409	81	231	LESASFPPGKVAHTCNPTLRGCAGWIA WAQKFKTSLGNNMAKPCLYKIK
9341	23242	A	9410	367	256	HPGWFWLVSVIPTLREAKVGRSLEPRS LRLAWDTWG
9342	23243	A	9411	2	192	VFLVEMGFLHVGQAGLELPISGDPPASQ SAGITGVSHHAQALTFLNIPINPSHPPK ACCSKQL
9343	23244	A	9412	3	83	KNCLNLGGGCGSELRLCHCTLTWATE
9344	23245	A	9413	371	301	EDHPRMVILRLRLRYIVRLVWRMH
9345	23246	A	9414	486	337	AGLELLGSSNLPALTSIAEITGMCHHT WLAYIFVCAFGWVLLDLCLAF
9346	23247	A	9415	378	254	IVAHCSLDLGGSDPLTSASRVAGPTGM CHHVWLIVVFFVC
9347	23248	A	9416	160	309	VVRYSSNEFLFLFLFYLFKSNFTVFCCC YCCCCCWQSLTLPKLECGV
9348	23249	A	9417	162	339	RPSSFCEFLHDSVPELALPMKARFEKSR RSQVSWLMPVIPTFWEAKVGRYQARSLI PA
9349	23250	A	9418	1	147	GGGGCSEPRSCHCTPAWATRVLGLFKK KKKINFLVPPFIFLKSKTGV
9350	23251	A	9419	283	126	KMMYKGQAQWLIPITPAFWEAKERGLLE VRSRPAWATEQDSTATKKNKNF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9351	23252	A	9420	133	3	ELMFSWAWWIMPVIPALWEAEAGGSRGQ EFKTSLPNMVKPRLN
9352	23253	A	9421	3	133	LRGLYSGAGTIRFEAKKNALALWAWDI AGDNCAICRNHIMDL
9353	23254	A	9422	409	291	ILILGGGSCSELRSCHCTPAWATRAKHR LKNKSPINVY
9354	23255	A	9423	1	210	RFFHLGLSKHWDYRCESPHAGTRNEVLI YATIWMNSENIVPNEIIQTORTNIVSFY LYQVGRIGKPIDRR
9355	23256	A	9424	479	306	GVPTNQPWNSNRVKTPSPSTKNIKISWPWW CMPCPNPSCEGQGRRIALNPGRWRLO
9356	23257	A	9425	1	209	GFFLFQGGGHHAGQAGLELLTSGDLPAS ASQSAGITGAGPNQGI FVALESPMESAA LLHLHVVLSSPCS
9357	23258	A	9426	628	433	RQGV AHLPGMECSGTITTHCSLELLGSS DPPASASQSSRLAVVSHCAQPSLLFSVL CLKPIFCCA
9358	23259	A	9427	417	125	FLRQSLTSSPRLEYNGAIPAHCNLCPLG SSDSSILASQSIRITGVNHCTWPDAAVL RQNFFFSEKPPQFYSEGFQQTHIIKSNLL YLKSTKCTCYPYL
9359	23260	A	9428	366	256	SFFYRDRSLATLPRLGNSAWSQAILPPG PKVLRLLA
9360	23261	A	9429	3	140	GFCHVGQAALKLLISSDLPTSPSQSAGI TGVSHCARLTRLFSSHE
9361	23262	A	9430	368	3	VRASQLLCLPTQASAMAGTPPPASLEPC SSISDCCASSEQSGMGVGPSEPGAGYNL VVCSSLRTLEKCSIRVGVPPQFSRCHLSQ LPLARKGNSPTPCASWVRCLTLLQLML RGLYPLSCT
9362	23263	A	9431	3	131	LTMLPRLVSNWSAQGSSHLSPKCDWYR CEPLHSGLDIFLE
9363	23264	A	9432	384	274	LSFAMLPRLVLNSWAQESAHLGLPKCWD YRHEPLGLA
9364	23265	A	9433	431	273	PPPLGYFFIVKMEFPPVVDGFKLLNSS DCSTASPSGRISGVNHSTRPIF
9365	23266	A	9434	211	473	CVCTFFSFLSMHIFFLVGEAESHCVT EAGVQWHDLGSWQPPPPRLKRFSCSLP SSWDNRRVPPYPANFCIFSRTRVNSCWP GWS
9366	23267	A	9435	391	188	LPGSSDSPASASRVAGTTGGCRHTVLLG FEFKDNIRWIKLVEKAHTQYGNIIYICVI KYMPLFYVYHH
9367	23268	A	9436	331	115	SRDRGFAMLPRLVLNSWTQAICSLLDSDQ SAHLSLPKCWNRYRREPLCPASGEILSFI KPSSSKSFHNSTKKRQ
9368	23269	A	9437	3	109	IYGSYSLPACFFPSFLPSFLPSFLPSFP PFFLSFF
9369	23270	A	9438	2	167	ECNGAISGHCNLCLSGSSDSPAPAWATR VKLRLLIKKKKKKNQILFFYPPRKTLF
9370	23271	A	9439	648	310	VCPCILRHPAFLFAKSGNPLESSLLDHS SPTFKLTDRENLRHVKTSHSQSLPTSG FQPGLPDSTLCAWYPTSPKLSPAGWVG GYRAPVGRRGPGSRNSWRLHWTPTISVG D
9371	23272	A	9440	1	170	YEIWF LDVGOAGLELLTSGDLSASGSQS AGTTGMSHHARPLKLFITISVSSNKKVKC
9372	23273	A	9441	133	244	LFGYQTRGLAMLLKLDNSNWPQAVLPPQ

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9395	23296	A	9464	104	336	NHVSQCEEI FLFDEYYIFSRVASMFWV DAELGSDIYLDGKLKNSFLSFLGFFFF FFLGKKVFFFQNGGLGRPGQ
9396	23297	A	9465	410	0	LNLGGGGCSEPRLCPTPAWATE
9397	23298	A	9466	254	61	KKKKDAFFTIPLYPSSQNLFQTMDDP TNISQQLTWTVLPQGFRHSPPTFLDKPF KQTSINFA
9398	23299	A	9467	403	255	PAPQLGGPPMPPMAPPSSWMMPMGCAP AMRLPIGGDI IWL CVPTQISP
9399	23300	A	9468	1	1428	PARFKDLNLAGTAEVGLAGYFMDHTVAF RDL PVRMVCSSSTCYRAETNTGQEPGRGLY RVHHFTKVMFVGVTGPGLQSSQLLEEF LSLQMEILTELGLHFRVLDMPQTQELGLP AYRKFDIEAWMPGRGRFGEVTSASNCTD FQSRRLHIMFQTEAGELQFAHTVNATAC AVPRLLIALLESNQKDGSVLVPPALQS YLGTDRI TAPTHVPLQYIGPNQPRKPG PGQPAGPRVGYKALQPWPAQR LGPVGRP PCRPEGQPLSCCCCGCSCWGLRTRCLAE VVTEVLTVGQVQRGPCTALLHKELCGTE PHGCASTEEKLLLGDFKKQEAGKMRSS QEV RDEEEEEEVAERTHKSEVQEQAIRMQ GHRQLHQEEDEEEEEKERKRGPMETFED LWQRHLENGGDLQKRVAKASDKETAQF QAEKGVRLVGGDRSLWQGAERGGGERR EDLPHHHHHHHQPEAEPRQEKKEASERE
9400	23301	A	9469	265	170	GTESHVSTQAGGQWLNLSSLQPLPPGPK QFS
9401	23302	A	9470	289	110	RDLELASFLSFFPSFLPSFFPSFLPSFL PSFLSFSFLISFFPLPSFFSFISFSLSL FFE
9402	23303	A	9471	67	210	TVTGTQALTHAYNPSTLGGRGQITRGQ DFETTLVPGDLNFSRVLASS
9403	23304	A	9472	2	186	TSLWRQAKNKVEKTKDKTEVLKTHGLL VCTQKSCSFLNKNKAWLGKQANAPARK VEIRC
9404	23305	A	9473	417	265	FLSSFLFFFFFFFFFFFFFFFFFTV
9405	23306	A	9474	430	120	ASQKKKKKNKKKKKKKKKKKKGGAL
9406	23307	A	9475	1	150	PTRPVVQAGFKVLSSGNPPALVSQCFR I TGVSHRARP HLLNLRAPNLPVL
9407	23308	A	9476	404	109	PPPLFFNFPGFFLVEARLHHVGGAGLKL PTTSDQPSASQSAGFTGVSTRAQPTLI TLY
9408	23309	A	9477	391	235	PPFFFFCRDRGLTMLPRLISNSWAQVIL LWSPKMLGLQARATVSGLNKRY S
9409	23310	A	9478	438	277	KRAPFFFFCRDRGLTMLPRLISNSWAQV ILLPWSPKMLGLQARATVSGLNKRY S
9410	23311	A	9479	399	279	PPPPVFKNPPPKKNKGAPKKKNISPPPG RKKYFFFKGPP
9411	23312	A	9480	247	26	LKAGDDSRVTVLGKVHQSPCFSLLLFFIQ VSCRDEGLTVLPRLVLNSRPQAILLPQL PKLLDHRCEPPLANHG
9412	23313	A	9481	2	176	HAPPHPANFLFFEEKESC YVTQVSIKLL DSSNPPALTSQSAGITGENQHGHMPMNCL SG
9413	23314	A	9482	2	178	HAPPHPANFLFFVEKESC YVTQVSIKLL DSSNPPALTSQSAGITGVSHHGQPMNCL SG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9414	23315	A	9483	2	151	GRVGEGLVSLVSLVLDQHPVGTSDHRDA TQLGFQPLMSDLGSTGSTEGA
9415	23316	A	9484	420	325	FFVFLLETGFHHVSDGLDLVICPPRPP NTFV
9416	23317	A	9485	400	104	LEFFLFFFFFFFFFFFFWNPPTFFKKV EGLNFPTLLKLKFNPPPPGPPKKKKEL
9417	23318	A	9486	117	280	SSTNQANNCFFFKKRGAILPRGALNP WAKGILLPWPCKGLKLRGGAIGPGQK
9418	23319	A	9487	76	353	VLWNTLEFCLIIYLDLLFLFFNKEALIR KKKKKKKKKKRGGNKKKKKKTPWQEK AGLFLGDTIIYSRGAVLKNSGGETPRHT PSGGLWPR
9419	23320	A	9488	3	122	HASEDNVFLHCSHSDLGIVLLAGTASLQ DFSFFQKSPPP
9420	23321	A	9489	1	155	PTRPTVCSGAMLAHCNLCPLGSSESILAS ASQVAGTTACTSTPDPIFFFFSL
9421	23322	A	9490	3	212	BTGFHHVGLSGFKLLTSGDLPTSASQSA GITGMCHCVWPQFAYFCLLVLDHLKF TIIMLVLCLLFYD
9422	23323	A	9491	2	163	ETLFRHVGVQVSFEPLTSGDLPASASQSA GITGVSAMPSWMIKFFIAFYSCINC
9423	23324	A	9492	474	296	SQPAGTADCLLPLPPGSCFPTTIPCPAAL VPLPSFSPSARLWPPQSLHQLPLPGTCS SCT
9424	23325	A	9493	7	151	LCAVEFVYMKPPAHEEAKAPSRGFVVRV APWTASSEKGRDDGMGPRA
9425	23326	A	9494	52	363	TTAPSLSVFLFTFTGELFVYWWVGTLE TSFISFFLFFFSFLEKDFSFSPAGREWP NFGLIQPLASGVGGISRPNPPSRWELRA LPPPPGGLGFFFWKKGPPG
9426	23327	A	9495	383	118	WKPRPWVPPGAGVQTPPGPQGETPLFLK KKKKRGRGGPLFGPPSFGGGGEIPLTP APKGQEIYFPPPPPPPGGKKKSLFQKKK KRIR
9427	23328	A	9496	554	419	FFFETKPCSVSQAGVLRDFGSLQPPPS QVQRDSPCPQASQVAND
9428	23329	A	9497	428	281	GSYVQLTFKYFSIYIYVHTLHVLYTH IYVYVHICIKYKEGYITGSVLA
9429	23330	A	9498	144	16	KVKKKVSQCPGIVAHNCNPSTLGGRGGR IAWQEFETLSLQKN
9430	23331	A	9499	2	155	NLALLGSSDPPVSASPVSIGRVHHAQ LIFFFFGKRAWFNPPGGRKGEE
9431	23332	A	9500	2	184	FIYGRDSLTMPLRLVLSNWPQAILPPRP PKVLGFRCEPPHLASLLIFYRDILFTLG LKSV
9432	23333	A	9501	465	153	PHKVFLNKGPFETPQGEISRGWKTTRPP PPRERSRPFHRKGGFGSPPKLRQGPPFV FFSWPPWCPPPKKGARQQKGFFYFPP FFNPPFFFFCLFFIFEIV
9433	23334	A	9502	429	11	CRTLLGADCVCVCVCVCVCVKAFFPI SYSCHLVPSDLPLLGVQFKCVHFGLSF LTCPPSPWPGGAGPGSCYWGCLCL FACKLGARLTQTLGIPASGPGTWATPL GSCASVLRRLPGGSEKTDLKVSVLSG
9434	23335	A	9503	436	202	LEPGGYIFQEGVEKTKFSPLLRENNFFS NFFPPKNNGGGPRIPPPPPPLFKKGV FFIPKFPAPRPKKKFKKKKK
9435	23336	A	9504	3	112	SFDLLSSDPPALASQASGITGVSHSHG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QKVYICNM
9436	23337	A	9505	426	208	VGHNLLVPRFLSPSEKRSIQVGVTRSSR CRLSPLSLTRKGNLSLTPFASRVRLTL LRLARAPTDLRPLSGTP
9437	23338	A	9506	441	189	CPANFFVFLREMGFHHVQGAGLLTSSDP PASASQSAGITGLSHCARPTVGSVDLSL PSGQCTSALTGFMLGSTTVHSNAAARA
9438	23339	A	9507	117	278	NKALLCHPGWNHIKKVNGRLGMETHTCN PTTLGGQGOBFEENSLGNIGRPHLYK
9439	23340	A	9508	3	126	FFVEMGFRCVGRAGLRLLTSGGLPVLAS QGAGITGVSHCI
9440	23341	A	9509	421	134	FLVERRSHHAAQASLEILSSSDSPTSAS QCAGITGMSHCARPKYTFFRLHRHMPM ATPTKLPPTLASASPQVKVCLYPLLPST SKGEIFTLQLY
9441	23342	A	9510	2	200	PQPPTFYPSFLPSTPEPPAFYPRLPST PASRLLPQPPAFYPSACHLLPQPPTFY SLGNRRRLHL
9442	23343	A	9511	414	204	ERDRKKERKKEGRKERERERKKEKKRKK KKERRKEGRKEGRKEASKQRVVIMVD T
9443	23344	A	9512	1	211	FHHVGWAGLGLLTSGDLPASASQSARIT GMSHHARHRHGFDNLSLCALAPSPPTLW RRHRRRGHFTVPEK
9444	23345	A	9513	390	265	VFLVEMGFHHVGOAGLELLTSGDLPPL SQSAGITGVSSQQFS
9445	23346	A	9514	438	180	IGFRHVGHAGLDLPLGLDPLSLASQNA ITGVSHRAWPAMAFVNCHGAGGSVAMRT TRGHSCRHLGIGGFWPASLLQPVL SAGSL
9446	23347	A	9515	126	11	RNLDFFLSLGLAMLSRLVNSWPQVIFQA WPPKALRFQV
9447	23348	A	9516	2	249	FLHVGQAGFVLPTSDDFRPTHPTQSSGI TGVSHRTRPLRCYFLRLNPIPLYVYAY YILFIHSVISGYVGGCTAHYCHPRKVV
9448	23349	A	9517	403	57	PEGALVPQKKKKKKKKKKKKKKKKKK NIKI
9449	23350	A	9518	406	140	PHYNHTFVYNGVRLEDLQHMCLLTWWD REPLASNDFLVGVRLGVGTGEIPSPILT CLKASCLFYSYHSRPPTQSSSVMTVVF FFFS
9450	23351	A	9519	3	75	GIEWMVNCVVRNVHRPPRQRDIT
9451	23352	A	9520	183	6	LLTHLILTSALIGETIMVAPILQKNSGSE RECRLPRLVLNSWPQGILLPWPVKVLS QV
9452	23353	A	9521	89	339	LQCLQKSGKLEPGMTYTKLIDADVNVGN ITSVQFIWKKHLFEDSQNKLGAEMVINT SGKYGYKSTFCSQDIMGNILQNLKPC
9453	23354	A	9522	3	329	PSLMFPWLKLSFPGRPRGRQTYRYQTL ELKKEFLFNPYWTRKRMEVFHALGLTE RQGKIWFQNRMMKGKKENTRDNLPEAQN EEKVEEKGIEEKEKEEKEENRD
9454	23355	A	9523	1	156	AKTSMNVNEIFMAIAKLKPKNEPQNGA NSARGRGVDLTPTQPTRNQCCSN
9455	23356	A	9524	1	272	AKNSARALLGILGYRSHLISLLCLEGI ILSLVIIATLITLNTSHLLANIGPIAIL VFAACEAAVGLALLVISNTYGLDYVHN LNLLQC

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9456	23357	A	9525	1	62	GNDAWVCTNDMFRLALHNFG
9457	23358	A	9526	1	111	GDIHNNENMRQGRDKYKTLRQIRQGNTKQRIDEFEAL
9458	23359	A	9527	427	340	IPIGNIMSCDSHSHHELVMASQALNAIFHD
9459	23360	A	9528	439	27	PRRTDKWLTVEMIQDGHQVSLLSGELTVDQRASIIQFRDQGEKVLIPTNVCARGIDVKQVTIVVTFDLPVKQGEEDPYETYLRRIGRTGRFGKKGLAFNMIEVDELPSPMKIQALFDGRNKQLNAEVPCIQAAEMED
9460	23361	A	9529	1	236	REVLITTNVCARGIDVKQVTIVVNFDPVVKQGEEDPYETYLHSIGRTGRFGKKGLAFNMIEVDELPSLMKIQDHFRRKS
9461	23362	A	9530	437	240	QQVSSARPEPEAGEVSPFVAGVNSNSWAFKYGPGNPKQSGPEPKKQTQVSFLLRRKGEASQPRQ
9462	23363	A	9531	413	260	LFDQVVKVASPSGLRTSTVRYGDPEKLKLEESLRQQAEEKGSALSVRISNV
9463	23364	A	9532	431	260	ASSGQMFSVKQQAAPPVRLPPFGISLFGQGIYDNISPRPPQGIAPPVGGGRGNIPNLG
9464	23365	A	9533	2	134	IHGVCVHMCVCACVCVYACVCVGGYDGRIFLALSSTVPSMVNIM
9465	23366	A	9534	419	53	LLLLTNGDRQTQREKIEACQSYFDAVVGGEQREEKPAPSIFFYCCNLLGVQPGDCVMVGDITLETDIQGGLNAGLKATVWINKNGIVPLKSSPVPHYMVSSVLELPALLQSIDCKVRMST
9466	23367	A	9535	439	109	NCIVIIDSTPYRQWYESHYALPLGRKKGAKVTPPEEEIYKYNRSKKIQKKYDERKKNAKISSLVEEQFOQKVLACIASRPGQCAPADAYVIEGKELEFSLRKIKARKKG
9467	23368	A	9536	1	185	NTSSSHHFTIPCLVLYSTSTHTHIHTHTHTHTHTHVRVFSYIPSDQVKEGCIPAPSVFSW
9468	23369	A	9537	168	280	NENSIRLTSCCCCCCCCCWKSPYNVYNRLRTGFTFP
9469	23370	A	9538	142	324	KIVKMGFPFHAGQAGLELLTSGDTPGSTSQSAGITGVSHRSRARSIFLYPYLPSPVYLPWRRV
9470	23371	A	9539	3	139	YIGGMGQAWWLMPGKPRQNDYLSPGVQDQPGQHSETPSLQKGFKN
9471	23372	A	9540	383	318	MSTQNNIQSYPIGEDEESES
9472	23373	A	9541	372	207	YGLNMCRCQCFRQYAKDIGFIKVGVCRRTPCCLGREGCGGYFFRERQTDSSLEW
9473	23374	A	9542	2	360	ARGDDHRSDDRDKDGLVEEQIERLQEKVESAHSEQKNLFLVIFQRVIMILTEHLVRCETDGTSLTPWYKNCIERLQQIFLQHHQIIQQYMTLENLLFTAELDPHILAVFQQFCALQA
9474	23375	A	9543	379	75	TNLQQFAMSHGSAQVKHGKGVADALTNVAHVDDMPNTLSALSDLHAHKLRLVDPVNFKLISHCLLVTLAAHLPAEFTPAVHASLDEFLASVSTVLTSKYR
9475	23376	A	9544	380	56	RDLSMVRMKSMFAIGFCFTALMGMFNSIFDGRVVAKLPFTPLSYIQGLSHRNLLGDDTTDCSFIFLYILCTMSIRQNIQKILGLAPSRAATKQAGGFLGPPPPSGKFS

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9476	23377	A	9545	304	92	SKSRVTNNTLRSTRKDTMITLNTHSLLA NIVPIAIIVFTACEAAVGLALLVVISNP YGLDYVHNLLNLLQC
9477	23378	A	9546	394	108	KEIDFSLVDVTADDAGNYSYMYQTKSP FWASEPSDQLEILVTVPPGTTSSNYSLG NFVRLGLAAVIVVIMGAFIVEAWYSRNV SPGESEAFKPE
9478	23379	A	9547	1	335	GNAVGLNLHRINFDKYHPGYFEKDMKH YHLHRNQSFCTPVNLDKRLTLFSEQTRL NAAKNKTGTAPIIDAARSVYKVLGKGL LPKQPVIVKAKFFGSLIFCFRIWILID
9479	23380	A	9548	326	188	NFLRMGTVAHASNPISILGGLGGRTAGAQ EFETSLGNITRCPCLYFKK
9480	23381	A	9549	381	152	VTLLISLQLLVVIGVLLVVIARLNINE VEKQWRNLNQLNNAATILVFFTVVINFI TAFGAHKTGFLLAARASRNPL
9481	23382	A	9550	170	65	IHRSKNKWKPHLKDGINNLNGRDYIFSK AIGDAEW
9482	23383	A	9551	544	361	RRLRQENRLNPEGGGCSKPRSCHCTPAW ATEQDSSSKEKKERKNLKGNTVKSVELP LTSHA
9483	23384	A	9552	369	181	GVLGATSGDMQIHTFGSMIIGSITGMVS ELGYKFLTVSTADVMIQTLNLHLFSEMS HQKKSY
9484	23385	A	9553	1	516	SLVHVVEFGQAIARRLKPFGVQRFLYTG RQPRPEEAEEFQAEFVSTPELAAQSDFI VVACSLTPATEGLCNKDFQKMKETAVF INISRGDVVNQDDLYQALASGKIAAAGL DVTSPEPLPTNHPLLLTKNCVILPHIGS ATHRTRNTMSLLAANNLLAGLRGEPMP ELKL
9485	23386	A	9554	386	56	LFPACVLRWQFASDGGDIGFVFLKTKM GEQQSAREMTEVLPSQRNAHMPEDGS LTCIQAGVYVLRFDNTYSRMHAKLSYT VEVLLPDKASEETLQSLKAMRPSPTQ
9486	23387	A	9555	375	150	IVVGKTSFHVSIPLSLFFPGDVLVDLLQ HILKQSKPRILFSPFFHFGNSIHTQPEV ILHQTHEEGTGRGFSFLA
9487	23388	A	9556	3	354	CLPTQASAMVDTPPPALLPPCSLISDCC ASNEQGSVGIGPSEPAGYNFLVCRLLR PLEKHSIRVGVTQFSRCLSPPSLTRKG NSLTPCTSRVRRCLALLQLTLSELPHCP VPSV
9488	23389	A	9557	463	40	PIKVEDPEPVKKPPKEQRSIKEMPFITC DEFNGVPSYMKSRITYNQINDVIKEINK AVISKYKILHQPKKSMNSVTRNLYHRFI DEETKDTKGRYFIVEADIKEFTTLKADK KFHVLLNILRHCRRLLSEVRGGGLTRYVI T
9489	23390	A	9558	338	104	NFKKKKKRRTKKKEIRTEEKGRGANKKT FRGPKKKETRGSNRSPEGKKNHGAKKEG ERRPRKKKKKKKLARYDFTCL
9490	23391	A	9559	1	152	NTCVCVCVYTGFCFHAQVAHELSSSNLP SSASQSAGITGISHHAWPGFGF
9491	23392	A	9560	517	238	SGPGESVPHPWSAVRTRPAKKPGSQCLL QSAFPLWCSSRRTTWAEERKLNTETFGV SGRFLRGRSSRGGRGGRNGTTPRRNPT SHRAGTGRV

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9492	23393	A	9561	709	280	NTSPALTAPCGRPRGIREMQCWARVPAPSSACPAWQLPSLCLRSTVPAPHPSPAHHQPCELSQHHRGGLEPALPGTRQRLCSRTWHRCVRFPLPGAQAEAGELGPAACATGRPLP VSHSTDMEQAPGLTSLHQEPHSTARGGTATH
9493	23394	A	9562	3	130	YRGFCHVGQAGLELLTSGDRITSASQSAEITGVSHRAQPQMS
9494	23395	A	9563	409	160	NPGVKRSPCLSLSSSGGYWSMPPCLAYYKKKKRRFLKDGGLTMLPRLASNSCAQQF SHFGLPQSWDYRHEPLHIAQFFLFSL
9495	23396	A	9564	1	241	GICLGSNIGSGWMTSSLCPYSNTLNQNLSTTKPFPPVPSVGTNCGIEPWSGVT SGLGKMLFLYYYYLLLFQMQTPQS
9496	23397	A	9565	2	215	IHWMMGWMDGWMDGWMSGCVRAVTGPGTSSPHTSTCGHAVCVCVCVCVYTCAHVFLALFGVEKNNYFLWKA
9497	23398	A	9566	244	117	DHQHLNWSVFISFSFKVIKARKNKKGILNPDSSMETSPDEFF
9498	23399	A	9567	414	77	FGGVPPGTLVPPTWLPVRVPPPPAFCLGELSPPPFFWRKGLAPLLNFFFSQGRGFPSPGGKGRPLPRPAGFPGFVAKPPFRPPGFSSTPSDCGGLPFFFFFCKKVF
9499	23400	A	9568	418	198	PPVSLTEIVSKSHKAELVFWMNMPGTLEHPEGDNMYMEFIEVLTEALERVLLVRGGSEVITITYSYPTLNARA
9500	23401	A	9569	549	415	ROENRLNPGGRGCSEPRSCCCIAAWATEGDCLKKINNKKPKEQK
9501	23402	A	9570	546	1	KLECRGAIATAHCSLNLPGPGDPPTSATQAAGTTGTCH
9502	23403	A	9571	415	215	SRLRKKIYIYIMCVVYVYICVYICIVCVYICIVYICVYIYVYIYVYIYVYIYVYIYMHEFITFFSI
9503	23404	A	9572	374	138	LAASAAIQELFKRISEQFTPMFRRKAFLHWYTGEQMDMEFAEASNMNGLVSEYQYQDATAEEEGEFEEAEVEA
9504	23405	A	9573	370	233	GSPFVRVSVHSGVSLSTQVDEGVRSGSKRMVAPPGGRYNITSL
9505	23406	A	9574	3	399	YSSPGPIALALRDPCHAGGSPNSLSLPAQGHPARAQGPQPQGGPSSHLSGDLRPHVAHTRGALHGPAPAPASAPGGSGSGVAASMCSAPRPRAGGTLSVLTAAHPASAGCAHRDAYVCKAPGRAVF
9506	23407	A	9575	314	48	SILPHSDPERCFSTIQPEEGTIHTAAPLDREARAWHNLTVLATELDSSAQASRVQVAIQTLDENDNAPQLAEPYDTFVCDSPAAPGQVSN
9507	23408	A	9576	505	264	IFVVEMEFHHFGQAGRLRLTSGDMPASASQSAGVTDMSHCTRPTDFNFKEPLGAVVTFLLCGMQVGRDELEDDWMAWS
9508	23409	A	9577	508	314	PATWKGCLSNFSSYLTKPADFIEHQVLSWEQVPDGFIFNERFKSFTVVVLNNVAEFVCKYKLL
9509	23410	A	9578	512	1	RMREAI FSPGRLPRGAAPLRGPAGTLVPMPTPGECWLSLSVSAAGEKPKYKCSVCESAFNRKDKLKRHMLIHEPFFKKYKCPFSTHTGCSKEFNRPDKLKAHILSHSGMKLHKCALCSKSFSSRAHLAEHQRAHTGNYKFR

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						CAGCAKGFSSRHKYLKDHRCRLGPPQDKD PV
9510	23411	A	9579	3	487	WDLIYVGRKRMQVEHPEKAVPRVRNLVE ADYSYWTLAYVISLQGARKLLAAEPLSK MLPVDEFLEPVMFDKHPVSEYKAHFSRLN LHAFSVEPLLIYPHTYTGDDGYVSDTET SVVWNNEHVKTWDRAKSQKMREQQALS REAKNSDVLQSPLDAAARDEL
9511	23412	A	9580	1	840	SKYLYDEGEVEEFVFNDEWGAAGGVAVPT LNALERGFSLSAMDWHLTYTDPREIFEVLS WLESCVAEQQRWRGWYTYTDLCLVLEEQ PTWQLALGSLCQRLVLSCLLAVAYVSS VALAVASVAVIHQSLGLSCTPTPGPPDL GLTSRCLLEPCIPSPVQCLPLSLANVSSC LEGSMGLRSLWGSLLASLTTPPLPPDP PAPPTLLHNCCLCQKLQSDSPTCHACLH PNRTVPTALSSPWYHTYGLAPPWPWSPV PLSLPQPQQCSLFSVMEELARLKSFFVFP
9512	23413	A	9581	2	158	IHAGFISVSVDNIIYICMCVCVCVCVC AHMCACISEHITHAPRLPEVFYTP
9513	23414	A	9582	3	144	YTAGVISVSVDNIIYICMCVCVCVCVC AHMSACFSEHITHAPMLP
9514	23415	A	9583	503	3	GKCVCLSAVWGSLLSAFRGSLSVCCLGQ FVCLSAVRGSFSVCCPGQVRVCLSAVRGS VSVCLSAVQGNVSVCLSAVRGSLFVCLL SGAVCLSFCLLSGAVCHLCRAPTPCLSR SLAHRRCVNVCEMTQLISVSYFFCWGW WRHRNNIHLQKCLRILMAYTGQGGP
9515	23416	A	9584	2	1358	AGLDSLHKFQVKIEKEKVYVRASQALQ LQRTKVMACISPSAGYSSSTNVLIIVG AETLRQEGFSDRIVLCTLDRHLSYDRPK LSKSLDTQPEQLALRPKEFFRAYGIEVL TEAQVVTVDVRTKKVVFQDGFKLEYSKL LLAPGSSPKTLSCGKEVENVFTIRTPE DANRVVRLARGRNVVVVGAGFLGMEVAA YLTEKAHSVSVVELEETPFRRFLGERVG RALMKMFENNRVKFYMQTEVSELRGQEG KLKEVVLKSSKVVRADVCVVGIGAVPAT GFLRQSGIGLDSRGFIPVNKMMQTNVPG VFAAGDAVTFPLAWRNNRKNIPHWQMA HAQGRVAAQNMLAQEAEMSTVPYLWTAM FGKSLRYAGYGEFDDVIIQGDLEELKF VAFYTKGDEVIASVMNYDPIVSKVAEV LASGRAIRKREVELFVLHSGTGDMSWLT GKGS
9516	23417	A	9585	360	239	QCRKGLGKLVSFGLGIWSLIDVLLIGV GYVGPVHGSSYV
9517	23418	A	9586	160	1156	MPRLTFAPKGWPHPTSLHPGQVTDQTT WWLFQELPTPSSENSMPPGLSTPTASQEG AGPVDPDSQPTRRQIRLSSPERQLSSL NLTPDPEMEPPPKPPRSCSALARHALES SFVGWGLPVQSPQALVAMEKEEKESPF SEEEEDVPLDSDVEQALQTFAKTSGTM NNYPTWRRTLLRRAKEEEMKRFCKAQT QRRLEIEAALRELEAEGVKLELALRRQ SSSPEQQKLLWVGQLQLVDKKNLSLVAE EAEMLITVQELNLEEKQWQLDQELRGYM NREENLKAADRAEDQVLRKLVLDLVNQ

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						RDALIRFQEEERRLSELALGTGAQG
9518	23419	A	9587	419	130	RRDPHLPRIMGRTRLNRKNAETRINAQL PLTDKGRMARHVLDNSGEWSVTKRQVIL LHTELESLLEYLPLRCGVLTGLAAIASL LYMLTHYLLPYA
9519	23420	A	9588	2	399	FSCEFNMENQCPLVVEPSYPDLVINVG EVTLGEENRKKLQKIQRDQEKERVMAA CALLNSGGGVIRMAKKVEHPVEMGLDLE QSLRELIQSSDLQAFFETKQOGRCFYIF VKSWSGGPFEDRSVKPRHV
9520	23421	A	9589	19	205	LYCLVEWHDLCSLQPLSPGFRQFSCNL LSSWDYRHMPPRPTIKLSSYSIKLIYY LFMLVL
9521	23422	A	9590	500	407	KLTNEVRSVKRSQLFPEFSMCKEKLNT NII
9522	23423	A	9591	727	236	RRSRGLEGREALALCPGDGSHLLCRRTD SSFSSMAFFFTFMAQLVISIIQAVGIPG WGVCGWIATISFFGTNIGSAVVMILPTV MFTVMAVFSFIALSMVHKFYRGSGGSFS KAQEWTGAWKNPHVQQAAQNAAMGAA QGAMNQPTQYSATPNYTSNEM
9523	23424	A	9592	381	278	HPSVYKVASGLKEGLSLFGILNRCHCKW GEKLLR
9524	23425	A	9593	412	156	SQRCLSLGCHEHLANAYATIIICDNGFSA LLGPPLPGWIYDIAQKYDFSFYICGLLY MIGILFLLIQPCIRIIEQSRRKYMGAH V
9525	23426	A	9594	263	50	KHAAPPASLSLSLLHHGQKRACFFFAF CRDCQLLEGSPAMLPVQPAKLLVLLQV CLLCALLIPPSGSR I
9526	23427	A	9595	432	309	GTFSERGPPLEPRSQTVTVDFCQEMTDK CTTDEQPRKDYT
9527	23428	A	9596	457	29	TLLPGWITAQASEGEIGASLPSSLPPLL YLPSPWRCSPGALHTHPACPTGQRSSA LLPSLPQAPPFGCGMTGLRPLPSPSVGC CSAPSPQLLCPTQLPPAPESSEGGCSES RCVANVKYTRDLGDFLEKCTNGEASALE YP
9528	23429	A	9597	864	407	PSRRLSPTGRTTHGSSAACAPPPPRLER RSRTSRPPWGPPhASARTQRACTTWYS RSWACSCSWITSRPSWMTTKRTCMIFST IPTTPRTALWRGLSLWKDAWLLTRLKLA PSSPTSMPTTTCTACSSTWMTGSPAR WASTPMPRSTT
9529	23430	A	9598	421	145	LTQHNGDAAASLTVAEQYVSFAFSLAKD PNTILLPSNPGDVTSMVAQAMGVYALT KAPVPGTPDSLSSGSSRDVQGTDAASLDE ELDRVKMS
9530	23431	A	9599	1013	604	PGRPTRPDICLLLERMEEQVKNVMTFR EELYNIEKAFAFEVERQELLASNKKKWEQA LQAHNAKELEYLNNRMKKVEDYEKQLNR QRIWDCEEYNMIKIKLEQDVQILEQQLO QRKAIYQLNQEKLEYNLAGAEER
9531	23432	A	9600	409	191	HHVGQAGLELMTSSDLPSLASQGAGITG VSHCARTVYGLSIVFFSSHRGFASVRTP PSNENFPDRPISIAHP
9532	23433	A	9601	367	1	PPRYSPPLGGVRRGGVPPGPGVLAPPFPK GKPPFFFKNPNLPRPGGAPYSPPFGGV

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						GRGTSFNPGGQSGSPGQKKPPGPPRRGTG GFFSKKKKKESTKLPVTSHTTHCWFLPE ALDLELDPLY
9533	23434	A	9602	1722	394	GWNGSWNDNLVDTSPDKRDLQDICRRY MEDLKICFYRELNSKTTLKFFVHTSFHG VGHDYVQLAFKVFVGFKPPIPVPEQKDPD PDFSTVKCPNPEEGESVLELSRLAEKE NARVVLATDEPDADRLAAELQENGCKWV FTGNELAAELFGWMMFDCWKKNSRNADV KNVYMLATTVSSKILKALKEGFHFEE TLPGFKWIGSRIIDLLENGKEVLFAFEE SIGFLCGTSLDKDGVSAAVVVAEMASY LETMNITLKQQLVKVYKYGYSKTSY FLCYEPPTIKSIFERLRNFDSPKEYPKF CGTFAILHVRDVTGYSQPNKKSVP VSKNSQMITFTFQNGCVATLRTSGTEPK IKYYAEMCASPDQSDTALLEEELKKLID ALIENFLQPSKNGTSGRSCLGVPPNTV MTLCGAYGNRATRRNCHTLEPCG
9534	23435	A	9603	14	356	DFVERTQYTHQTHTHTSHAVRLSPRP VQSRPEASQTGPTRTKPALGPAHPSPRG APCPDDPGSLRMLGYGSRAHNSRRGRW GHGRCKDQRAMGPHSHMWEALPPGALS SP
9535	23436	A	9604	477	264	LVETGFLCVGQAGLELLTSGDPPTSASQ SAGITGVSHRTWAALSTFTVLCNYHYLF LEVFFHHPKLKLSPH
9536	23437	A	9605	1	378	EGINFSNLRRCVVMVGMFPFNIRSAEL QEKMAAYLDQTLPRAPGQAPPKALVENL CMKAVNQSIGRAIRHQKDFASIVLLDQR YARPPVLAKLPWIRARVEVKATFGPAI AAVQKFHREKSASS
9537	23438	A	9606	417	254	MVSLTQELCPVAMRVAEGHNKMLSNVAE RVTVPNRFIRGALLEQAGQDIQNKLE
9538	23439	A	9607	404	272	PPKFLLESQPIRVVDWWSLGMALMYDMLT GAVGAQLKAACIIGLC
9539	23440	A	9608	409	205	HMNGSLSGDIDGLPKNSLNNISGISNP PGTPRDDGELGGNLFHSFQNDNYSPL PCSWSLFYSLPF
9540	23441	A	9609	449	263	VWICPDPPASASQSAGITGLSHHLPKC WDYRLEPPRPAHCFYFYSFTMRNRNLLS LVKYSR
9541	23442	A	9610	366	75	TPGLKRSSCLSLMSRWGRIEKKRTIIR SVVEAIKEQDGREVDWEYFYGLLFTSEN LNLVHIVCHKKTTTKLTCDSSSIYYPQT RLKRKQPVKRQ
9542	23443	A	9611	1	801	PGYCGSWVFTCGALRQLSGGRDLRSGAR MGNSALRAHVETAQKTGVFQLKDRGLTE FPADLQKLTSNLRITDLSNNKIESLPPL LIGKFTLLKSLSLNNKLTVPDEICNL KKLETSLNNHLRELPSFTGQLSALKT LSLSGNQLGALPPQLCSIRHLDVMDLSK NQIRSI PDSVGELOVIELNLNQNSQI SVKISCCPRLKILRLEENCLELSMLPQS ILSDSQICLLAVEGNLFBIKKLRELEGY DKYMERFTATKKKFA
9543	23444	A	9612	179	329	KGLAFCPPPGRGGGPPPLWPPPPSYKK IFGLKTPKSGALSPPPPPGNF

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9544	23445	A	9613	410	298	PRFTPFSCLSLRSSWDYRCPPRPANFLSLSSVLHGT
9545	23446	A	9614	1	130	NPGSHCVAQAGLQLLSSGNPSASASQSA RITGVSHCAWPNTTI
9546	23447	A	9615	1	146	NTWRLHMVPRLVSNFWAPGILLSWPPKI LGLQKRATTMPGPEIYTSIN
9547	23448	A	9616	552	26	RLSIRNLLTHAFFAEDTGLRVELAEEDD CSNSSLAIRLWVEDPKKLKGKRDNEAI EFSFNLETDTPREAVAYEMVKSGFHESD CKAVAKSIRDRVTPIKKTRKKPAGCLK ERRDSQCKSMGNVFPQPQNTALPLAPAQ QTGAECATEVDQHVRRQLIQREPQQHC SSVTGD
9548	23449	A	9617	420	48	FSQILRASIEFDSPPFWDDISESAKDFIR HLLERDPQKRFTCQALRHLWISGDTAF DRDILGSVSEQIRKNFARTHWKRAFNA SFLRHIRKLGQIPEGEGASEQGMARSH SGLRAGQPPKW
9549	23450	A	9618	190	285	RQGLTMLPWLVSNSWPQVLLPWPLKVL GLQV
9550	23451	A	9619	392	308	SPIKPKIPLSAPRKNTNSVKYRLKFRFG
9551	23452	A	9620	166	23	FCNPISPSSLPSSLPSTFSPFLPCFLT PF LPCFLPPLPFLSFMTLTF
9552	23453	A	9621	49	374	DRRGIRIMAAALFVPLGFSLLGTHGPSG AAGTVFTTA*YLGSKILLTCSLND SATQ VTGHRWLKGRVVLKEDS\LPGRKPEFNV GPHPPNGDKSSFVFPSPPCPRLTF
9553	23454	A	9622	85	472	SHVFPPLRLTLTLHSMVETPRPNHTIY INNLDKIKKDELKKSLEYAIFSQFGHNL DILVSRILNMMGQAFVIFKEVSSATNSL RSMQGFPPFYDKPMRIQYAKTYSYIIAKN KGTFLLSC/DRKLIK*TPQ
9554	23455	A	9623	170	2	IFFFFCFERGS CSA*AGVQWRSYSL* S*TPG\SSNTASATS VAGTTGL\HHHAE
9555	23456	A	9624	2	469	RRLCSDRGLQRSLSGMSAAVTAGKLARA PADPGKAGVPGVAAPGAPAAAPPAKEIP EVLEDPRRRRYVRGRFLGKGGFAKCFE ILADATKEEFAGKIVPKSLLLPYHR*K MFMEIFIHRS LGHQHVL*FHGYF*EHDF MSEELEL\CRPRSFLF
9556	23457	A	9625	661	1393	ASPPPSQTTPAAPGCSAGEVSLA\GLCL QERRLDVAGFSIFIPSRYLDHPQPSKA EQDASIPPGTHEALLQTALSPPPPTRP VSPPPQKAKEAPNTQAQPISSDEAS/RWG RNP*CS*SGSPHQWPLPHLP*GRL*A* PSPCCPG*VG/PVHSPQARRRPITTSIS QRSWKFWPKPTVFRETSGGPWAMP RPSM PSRASISLSPRTSRKQPRPLTLGCCVW HVVHTDGERATCGDVRAHHSR
9557	23458	A	9626	1	286	PTMAKLIALTLMGMEALFWNHQASYQT RLNALREVQPA*LPNCNLVKGF*TGSED F\EILPGLTFISSGLENPWI*RLDP\N SPGKMLMLDLNE
9558	23459	A	9627	173	491	EGPLPLESSSNWQQADLDKKSRELLWKT VYLL*LNIQLPYNPNPILGINPREHT C\HQEMCTRIFIATLFTKAKA*K*PRCP *AREW/IK*/IWNHIIIEHY
9559	23460	A	9628	351	1	VLGDATQSRRGSSRKAGSYLLSRSP/CS

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						EGGGRGGCWAANNLGTMSVASGHGAWVPR ELTS*AWPEPGPAGQREGRRPPPTPCPPT CAHGPPAQF*PRGKAAYPG/CLGLQWPD *SAFNP
9560	23461	A	9629	599	11	KMWR**H*AKSQIRNAIPFTIAHK/RDL KSLKIQLTKEAKDIYENYKIPL/NEIR DVTNKWKNIP\CS*IGYLYSTYKYKCIC LVNIYL
9561	23462	A	9630	226	1	KCDNLGYSTFFFFFFFFFFFFEIGSYFVA QVGV*WHNYSNS/DASAFQVAGTTGVCH HAQLIFNLFVEVGSHYVAQA
9562	23463	A	9631	241	1	VSGCPLPRG*RRPPQPPSTPGTSD HPCTPCR/PALRR*SP**LPCLDLPPAS GPPSTSGNSTGTMQPT*PKLNSSSS
9563	23464	A	9632	201	1027	MTLTAPAGQGQSSQCLWRRPL/PLPPG PDSEEPGSGAAG/PGSSL*SPDLPPAAP PKP*TSS*EMNTVGSTQEGSGLAQTITQ HCPVPPST/RVDILGTCLQFPALCLTS APWLVRMPSPQRSSREIP*RLEAF/SLR TPIPAHSAQPSHQEKEP/PSPR*DHGD* PPP*PPKPTHQTLAQAPRSGQGLARPT LPYPPSPLRVTPRICRVHV*GHLRRPRG PPSSARRPTWDRVGLPWEDLEVVLCR GPAWLLARTSAPFSSLPTHACTGKKTTM PF
9564	23465	A	9633	103	379	YHCITIIVLKCIFFFFFLKPCILSPRL EARGIILGH*NLCLT\SQLLRRLRKSP LTLEGGVCS DPRSPHCSPA WPTKGNFFS KGKKKILD
9565	23466	A	9634	155	405	VPAFRSVTNISISVSFFFFETEPGFVTQ AEMQGLDIGNGQPPCKLSSFA*ASQVM GTTGPRH/HC*ALIFLVKTGFPHVAKTW F
9566	23467	A	9635	4	423	GAMRGDRCRGRGGRFGRGGFRGRFRPF VPHIPLDFYLCEMAFPRVKPAPDETSFS EALLNRNQDLDPNSGEQASILSLVTKMT YEIDNLT VAPGTLDVLEERQQGGPYIK GTMTT*RH/SVADLT VILQILT TWESVA S
9567	23468	A	9637	2	492	GSRAIGFGLAHELERHLIKIWLASIVR* DLA*LMNWSG\SHKDLAGKYRPILEKAI QLSGSEQLQAFKAFESMVNENVSLVIS RQMLTDFCTHLPNLPDSTVKEIYHFTLE KIQPIVISFEEQVASIRQHFASIYEKEE DWRNAAQVLVGIPL*TGQKQYNVDYKLE TYLKIARLYLEDDDPVPAY
9568	23469	A	9638	1	417	VVQGLGLVMGSPSRRLQTKPVITCFKSV LLIYTFIFWITGVILLADGIWGVSLLEN YFSLKDKATIVPFI\LIASGSAIILFG ILLCIFSV*HYPV*LLLVTFLI*LLVFL NKWWISPHFLILTFNYLLFDIIDNSS
9569	23470	A	9639	125	451	IYRKPLKSIRRVGGLHLNKIFFFFFLKQI WGWARGLMPC*HFGRLLKKGDCLTGIGD /SRG/RVDHDPALQPRQSKTSLKINK IGWAQWLMPGIPAPWEG*AGRSFGAGI
9570	23471	A	9640	670	927	GHVLLPRRAGCAQPGTGPAAAPAAVQR LPGGGVQPSGPGGRAGQGGLRG*AGG NPGTGF/GGPHASALLPPSEAPGSLPS

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						QPR
9571	23472	A	9641	115	460	ISWIFLIICVGGFFGGGGGARVPLCHLSP RLECSAIRARCGDFPGSSDP*ASAS* VAGTT/G/SCHHVQLIF
9572	23473	A	9642	1	431	AMRAEVLVYCCRGALASGCVQAFRRY\ WVLIIVDPDNEQANASIIVKLTDSFTE QADQLTAEVGKLLGE*KVDAILCVAGGW AWGNAKFKSLFKNCNCDLMRKQSIWTWTF SHLATMHLKEGGLLTAVAMAVLDGTPG MIGD
9573	23474	A	9643	154	408	IIMNAQSVEEDSILIIPTPDEEEKILRV KL*EDSDGKYGSKI PWNHLPENFRLL FKHVG YLD*SGLY\EILTKF*ILCVLCY Y
9574	23475	A	9644	3	403	YSQFFGGPKLEDPIRPGVFSQPGEHRGH PFQIF*KVGLGNGARPGFPVLGKVKCKD NLKLGQGQCSRVMHPRTSAWAIERDPV LKKKKRQR\EHQCSNEQKHTN
9575	23476	A	9646	3	399	ARAMVLSPADKTNGKAAWGKVG AHAGEY GAEALERMFLCFLT TTKTYFP HFDLSHGS AQVKGHGKKGADSLTNAVAHVDDMPSAL VALSDLHAHKLVEGVPVNCKLLRH*LLVT LGG\HFP AWLTPGGIAFLEKF
9576	23477	A	9647	22	407	APSAWGMCHFTTEEDKATITSLWGKV\NV EDAGGETLGRLLVVYPWTRQFSDSFGNL SCASAIMGIPKVKAHGKKALTS LGDAI* HLDDL*GTFAQLSELHCDKLHVDPENFK LLGNVLVTVLAIHFGKE
9577	23478	A	9648	243	2	QIATTTTLGPGSEGVGKRLDGS SSRHHSQ VESVKH\PRDLAQDA*GHGSAPRPLCPP PAQSWHCLRGPC LAPHPHTLCEPSR
9578	23479	A	9649	283	196	SYFI*IIITTHSLI\ISIPLLFNQIN NNLFSCSPTFSSDPLTPLLILIT*LLP LTIMASQRHLSSEPLSRKKLYLSILISL QISLIITFTATELIIFYIFFETTLIPTL AIITR*GKPTPLIQ
9579	23480	A	9650	10	354	QLRVITRLTVVNN* TSA*SRGVSY*AH \SSDALHL*RELTEQRFIVSVNCAIAHC RHQSASEDHVKLRNEVTEFAQTWDADES AENCDKSLHTLFGDKICTVATLRETYGE MAD
9580	23481	A	9651	2	404	AFGTTKWVTYISVLF LCSSAYS RGVLR DAHKSEAAHRFKDLGEENFKALALIAFA QYLOQCPF\EDHVDLVNEVTEFAKT CVA DESAENWDKI\LHTLFGY*LC AVACFRE T\YGETAAC*AKHEPVEDE\CFLR
9581	23482	A	9652	83	396	NIPGVGGGGVPIPLVWKNISHTQR*RE PYIQSLRSGNWSERM SHMVAR*RQRHIP YYI\LLQAQLSMA\SDPANVMDSVITA GVLVA/SRRARRISKLGHR I
9582	23483	A	9653	67	954	REGNHNTERNCKRPPQDTGPTQ/RPGGP PPEVPWQDASSAPTAAAPVGKLLPS*G PPGSASCQGR*TLGSVHWL*GSPLSPS AGGRALPYGPAQGSQGHWENTGRGTPL PGSRET*GHELT TGVEHQRHKAPREPQA GQPR LCPWVQSLPPT\ARSPSWSQGERP
9583	23484	A	9654	1	252	RPPQLLASDSLPPSRPSPFPPLLSLR PPLSRSLCLSHYLCPPLSLIQQLTSFPD

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						TFSPKSTTSGPPQPEDSPSS*PPTPSP P\PPSLSSLPSSLSSAPPF/YVHSVSP TISAPLYP*YNS*PHFPFPFPRKVQHL ARPSPKTARPPWTIRRI
9584	23485	A	9655	1	394	SLRIYCFVIEVICFLYLL/FIMYSIS*G I*LLMNFTILCIGY*LLQYFFVVKSF YFNFIPIFILFLYLICLLVF*LIFFDL SYF/MCLRLIIFNLFY*LFLLYSICLWN MVLILLISKLF*F*FCGRFALIQ
9585	23486	A	9656	122	371	SPYLLLLQGGVSWIVWLNVSTNSSFL FPETGSHCAVQGGVQWCGRSLQS*TPG /SQS*VAGITGMCHHAS*LEKFFVEMG
9586	23487	A	9657	425	3	KTSMNNSIVPHISIPTLVNGLNVPLKR YRIAE*IKIHQPSICCLQETHPTHKDSH KLKVKGWE*IFHANG/QGVAILISDK/T DFKATTVK/RDKEGHYIIKGLVQQENV TVLNLCAPNLTGALKFIK\QLLLDLRNEI NANT
9587	23488	A	9658	179	373	VHSWLLWGSQS FVLFRLTD*MRLTH/I MKGNNLESKSTSLSVNLQKHPHRNIQN V/AQNIWVSWNS
9588	23489	A	9659	103	373	LKHVLRCLQSERKLHYLFNIDQWGKFY TWDDLYECISSKFTTHFFSF/FFSF* SQGLALSPRLDCSDAIIAHCILEFLGSS HAPTSAS
9589	23490	A	9660	216	424	TDINVTTKTIKPLDENIGITLYDLGLGS GFLDMT*T/AQVANEKIG*WDFIRNLKL TCIGHYHEVKKNPW
9590	23491	A	9661	276	2	PRIGKLPTNMTEPLTIKEMLINLAMRFH LSPVRMAI/IKIKSNRCW*GCREKGI\ IYHYWWECKLVQPL/WKSSLK/FIK*LP IDLSFVPAIPLL
9591	23492	A	9662	239	356	ICIKRRK/WSGTVAHTCNPSLGGQGGR IA*VQEFQPGQQ
9592	23493	A	9663	1	340	RHELMTPHAFGAMKRVTFISLLFLFNLA YSRGVISRDHRSEDAHPKD LV*ETFK ALVMIAFAQHLQQRPFEDHV*LLNE\VT EFAKTCVAEESAENCDSLHTLFGDK*C TV
9593	23494	A	9664	759	1039	KRIPFGRPRRVDHLRSGVRDQPLHDET PS\LKIQKLAGGGICL*SQLRLRLR*E NHLNPGSRGCSEPRSCHCTPAWATE*DS ISKKNKTKIS
9594	23495	A	9665	1	355	ITDLYSMFHFG*VDLATITSLWGKGNEQ KAGR*TLERLLDVYPWTHRFDSFGNLT SASAIMGNPIVKAHGKVLTS LGDAIMH LDD/LKGTFAQLSELHCDTLHVDPENFH ENPCDGS
9595	23496	A	9666	364	3	APNIPPSVTRIPALLAFRSQCCLGSCPL PLATEPVGLLLSMSFQAAPCFTWWVTEA WLTGISWPPDFLISLLCI/HINYNAVIF RKYP RVGAVAHICNPSTLGG*GGWIA* AQEFETSLGN
9596	23497	A	9667	1	357	PISNAMRHLGQEETATITSLWGKVNVED AG*ETLGRLLVIYPWTHRLFDSFGNLS ASAIMGNP*V\KAHVKKALTS LGDAIKH LDDLKGTFAQLIELHCDKLFVDPENFKL LGNVLAT

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9597	23498	A	9668	24	369	APRPDAMGHFTEEDKATITSLWGKGNVE DAGGETLARLLGVYPWTQRLFDSEGNLS SASAIMGNPKVKAHGKKVLTSLGDAI *H LDDLKGTFAQ\LSELH *DKLHVDPENFK LLGK
9598	23499	A	9669	12	365	LLIMDGERK *FLETDSAPCEDAMNTVEM TTKNLE *SINLVDKAVA /SGFERIGFNF EKSSTLGKMPSNSIACCREIFHERKS /S MWQTSFSLSYFKKLROA /PPAATTLDHQ PSALRQDPSP
9599	23500	A	9670	346	2	YPYDPWSLINNMFFLFKRFQNFLLKEGT LTFPFKGFGRDLSLFFWPPYKLFNLKSF L /CKFLEI *RYFFG *IIFFFPPFFFFFL RQSLTSLPRLECNGTISAHCNLCPLD *S NSP
9600	23501	A	9671	121	364	HKKKTAGRVQWPLLVPALWEAKEADCL SSGVQGGPGQHSKTPSLP *PSKSWDYRC TPPHLASFCNFFSFFFGRDGVLLCCPGW P *TPELKQSA /CLGLPKWDY /RARATA PGLLFF \FMLKYVLVKPAVNIANAN *KE LSEPDVKNEICFV
9601	23502	A	9672	437	223	EME /FSLLLPGLECNGTCLAH *NLRLG SSDFPASASPVAGITGVRLHAQLELYFL NLLGFFFFI ISLVVYLS
9602	23503	A	9673	100	338	KSRPSAVANLTPVIPALWEAEAGGSPEL KQFSLSLSSRDHRFATPC /RG *FFIFF VEMEFHCVAQCGFELDSSSPPTSA
9603	23504	A	9674	161	1	SFLWKLCRGAPSCMRCLA \LL *DVSQ LGY /SGVRDPLEEAVCFPSDLKL RAGR
9604	23505	A	9675	304	1	VPPLASQLGDKRRIFFQKKKKKKKNKDK IHIIISITLKKFDKI *YSLIIK \TL *KL GME *TYLNI IKVIYDRPTASIIISGEKL KSFPLKSGR *QECPLL
9605	23506	A	9676	111	346	SKEGSKEGSLEIWGFLVLAFFFPFFFPF SFFFF \ *RQAGRPRLECRSMITAHCNLE LLGSSDPASAS \QVAGTTGPTSP
9606	23507	A	9677	3	349	ARAGRIKDLWLGFLLLLLLLLFPKKTPL FTRDKGGKLTAKKNPHVPKREKKKP PPGTRGKNPPGNPFWGFGPQRFFFGG KTFGGGAHPDPTLG /PSPQS *KRPF GK RGPPP
9607	23508	A	9678	38	368	QASLLKESESERKSPTSLTSLQKLG MIR LCEEGMSKAKAD *RLGLLH /QVSQLVNT KEKLFKEIKSAISVNTLMIRK /RNSLTA DMDKVVVANIEDLSSQNNPLSQSLIHSK A
9608	23509	A	9679	187	345	PFILFFETESYSVA *AEMQWCDLGLSQT PPPG \SSNPPVSALWEARAGGSR SQ
9609	23510	A	9680	192	468	ERTSLFTIHLKLLTITNSAAMSNHV *V FV *T *IFLSLGQMPKSVTAGSNGQSLFR FFK \NCQTLFHGGCAMLH /SHTQLNAIP LFRNLWQHLS
9610	23511	A	9681	141	367	GSWAASPCSCCTMDDFAKESFTVVDYVLL ENCPNMGDYVAPQFMTDNYVRVTQLNW DGVGTQ *KDYI /SSERNL
9611	23512	A	9682	193	3	IFGERR *ILKIYKLTGHVGLRL *SQILR RI /RLNLGGGGCSEPRSCHCTPVWATER DSISEKKEK

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9612	23513	A	9683	1900	1988	NLVHFEHHFSPSLFTSPSLCHIF/CSRD RVSPY*PGWSRSPDL/RYLP/CLDLPKC WDYRRESPCPASSRFLMNFYLYF*NTTLW Q*KTIPLLF*SGDC/S*FF*YNFLAHTS STMVNSGISRNSRPVFKLADKAPSHSPL SILAFGVEFF/NLGSQPPQLK*ASH LNCLSSWDNRHAPCPDNFFFNIL*RWG FPILSRMVLNSW/PLCSLSTASQSSG/ITGVSHCAGPILVF
9613	23514	A	9684	69	358	ILIVKVFFPHTQKPNFVRLSLQSIQOM LLPERKWTQAQKTCVSSENTERCHEKQV ITSHWLGMVAHSCNPSTLGGGGGWIT*G QVFET/SLANTVKP
9614	23515	A	9685	66	344	IGEKLLLTDKHRNWLETE*APGKDSVN IDEMT/TR/DLEYIYN/TDKAVTGERT DFNFKSSIRGQSL*YSII/CAKGSQQKQ QISLVPYFKKLPO
9615	23516	A	9686	269	1	PKIQNGHCKTLPKNPSQSDTKTFPLETS GSSPQPHKLSFCFSAGPTLPSKTQLKIH L\WQGTVPAYNPSTLGSRRGRIT*GQE FKTIQ
9616	23517	A	9687	229	361	DRYYYKSHFKPGAHAHAC*LVLASFFMC YRAIMINK*HLYHRKL/VYQVIRH*KYR D/I*THVTLTTTL*DRYYYKSHFKPGA EAHACNPSNLGG*GG*II*GQEFKTSLAN MA
9617	23518	A	9688	318	46	KLYALNDMASNTCKEYDNLIQYRYKIY KRLIQHD*VEFIPEME/NWFNI*/RKSI NVIIHYIHSWEEKNYMIISLDVADVSDK IKLTFILF
9618	23519	A	9689	168	3	GNSNTMIFFTILYLFYFF/LFFIFDM KSHSVARLECSGVLAHCNV*LPSSNS P
9619	23520	A	9690	192	3	WHKASLSNPQAGCMQPRMALHEAQHTF VNFLKTLWAG\PVAHAYNPNTLRGRGR IT*GQEFK
9620	23521	A	9691	388	1	CRSAGVCWRSTDPVCLGITSSGCRTAE IVACSFVWKLHSGAPARCQPELSCMRC \R*TLL*GVSQSGGTGVRDPLKEAVCP L AELENGARRSTALFRASRQDSLSLLKLR PQLPLLPGALSQIEGI
9621	23522	A	9692	226	3	WFLLPQVKLAITMPRLYFPNLPFFFF* DRV/CTVAQAGVQWRDLSSLLLSLLGSS SSPTSASRLTGIILOHHA
9622	23523	A	9693	305	1	NHAITTVN*FGLIRHLVTKAAFNSGEVD IV/SIKDPLIALNYTVMFHHDSTHGK F RGTVK
9623	23524	A	9694	320	1	PRDPPASASQSAGITGISHQAWPDMILY IENPKDSSKNPLGLINKYSKVAGYKINT QKSAFL*TNNYLKN*P/MRTIPTIAT KKKYLETYLTMEVKDLYTENYKM
9624	23525	A	9695	263	1	VRILLFSESLALSRLCSGVISAHCTL CLPGSRGALSLLSRVDY/Y*VFLVKAGF RHV/GQAGLEFLSSGDETPVSLPDFWDY RCKPR
9625	23526	A	9696	262	359	IRKIKIWSGVVAHTCNPSTLGR*TKA HEGSLYCLRVGKIVSNKVGTRS*FFRTQ K*V/HLFFS*VYHINGSH*SRTSL*IRK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IHKIWSGVVAHTCNPSTLGGRVWIT*GQ
9626	23527	A	9697	166	473	TQDTSQPWKNIWISFGSLKVFENVDIHK LYLELDNRHRSWMTDILFFYF*DGSFT VT\RLECNGAILAHCNLHLPSSNSPAS AS*VAEVGGTLEPRRLRLQ
9627	23528	A	9698	456	59	LFLWKLHLRGAPGYVRCRLA\LLGGASQ LGYSQVDRDPLEEAVCPFSDLKHLHAGRTT TLFKAVRYGHLCLQKFLLPFVRLCPAPT GGVFTVRQASMSCDGLLIV*\VSERH*L PKPQQFWELVPKFVRPGLKSL
9628	23529	A	9699	4	375	VPCSSVTIVSEIAFLMWLSAQLLLVYRN ASDFCMSSLYPETSLSLTKVTQGGAL/H*N G*LT*EQYWKTDQKAVI/CQSTGSS GSSQAREIKGPGAVAHTCNPSTLGGRG RWIT*GQEFETSLA
9629	23530	A	9700	239	361	RNDTFFFFETESNSVA\RLQCTGVTLAH *NLCLPGSSNSPA
9630	23531	A	9701	169	1	IFYWKAIFFETESHVAYAGVQ*SNLGS LQLPSS\GSSDSPISASQEAGTTDAHH
9631	23532	A	9702	37	348	HAKNFDVSLPYTKTHEHFVKEDIWIAN KHVKRCSATLVTKEIPPPQS/TLKWLKH* PPC*QGNRTGSPIP/C/WCEKIVQLW KIV*PFPKKLSIYL/PY/DPPIILLGI
9632	23533	A	9703	16	339	ARLNTFMAAAK*SERKS/RN/SLTLNH KLQMIKLTIEEGLMKAVNGQKRLRLYQ/T SQFANAKDELLMDIISATPATV*MIG*Q NSLIADLEKVRVV*LDDQ/TSHNIHLSH
9633	23534	A	9704	276	2	GISRGGLSKPPFFP*DFPLDYLQSPFC KVKNRS/REFTTKSPLDFPIPLFFFFF EKVSQAISAHCKLHLP*CHSPASASRV AGTTGTRH
9634	23535	A	9705	352	2	CNSRSDFFQLMMNCFRLWAVSPRVECS/ GVITAHCNLNPDSVDPTSTS*VAGTT GHTP\HTWLIIIIIIIVAGIFLFFFLFS FFGRDGVSPCCPSWSQTSEFRQSACL SLPKWDY
9635	23536	A	9706	6	351	TWNSRPRRPLGGQGGRIQDWPKLHGKTR SL/LKKLQKLARRGRASLWSQVLKRLRL TWVDCLSLGG*GCSQP*SH/IHCSPAW
9636	23537	A	9707	76	359	CFLFVCLDFVIFLAYFCN*YLFPPFLISH TFFFLLKKGLIFAPGVNLRDQNKFYFTL FDVFFNIYYC*IFFIF/CLVLLFFIFFF FFYCFVMRFIVL
9637	23538	A	9708	342	3	GEELLLMDEQSKWFLE\TPGENATNIVD LTTKDLEYSISVVDKAAAGFERIGSN*N STLELKTVN/SVPHAR*IFCKRLQSVWQ TSLLPILRN\LP*SPHPLVSAMLIQQS STLK
9638	23539	A	9709	211	350	RQDIALLPRL*SGTITH/CDPQLSGS SEPPTSASLVAGTTGACHYV
9639	23540	A	9710	253	3	VKCFREHMLIRRSATGGKKHIEKGTLI MSFWVYVSQSEH/NLCNHAY\SHIKK VWLGTVDVYNPSTLGGQGGRI*GQEF E
9640	23541	A	9711	80	324	LITLTMASMCSNERKSHTSLTSNQKLEM SKPTEEGMLKAKTS*KLGLFHQT/SQLV KTKKKFLEEIKSTTPLNAPLMRK*NSL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9641	23542	A	9712	246	3	QLAKHGLLFFLFFEMGSH*LRLECSL\TALLSKISAHCNLNLPGP\SDPPTSASQVAGTTGACLLAQLIFKNFVETGSHYVA
9642	23543	A	9713	2	359	AAASTTIKEQDMLKFYFLFYFFETESHPTQVGVQWCNLCSLQPPPP\GPSDSPAWVTEQDSVSKE*KRKKLIKINVYLQVTHP*HSPQHIVRVLSVLN*LNEKINRRVTKSSSKEKDR
9643	23544	A	9714	278	53	KLFRGLNNHRKFQTRCGGLFFFLFIYF*DGA/YALSLECSGTIMAHHSLDILGSSHPPISASLAA\GVVRTCSPSC
9644	23545	A	9715	166	402	TLSLKKNENISRWWHVVVSGVWKAEAR*SLVPRSLRL\HCTPAWA
9645	23546	A	9716	168	1	VDCIIMRRSIAKSPRRKCRGTISARCKLRLSG\SGHSPASAS*EAGVTGVGHDP
9646	23547	A	9717	1	553	TSIRLFFLLSIFFFSRARNRILFKIYCNQVRAKGRGGGWTGCRGHNTMTWPGPQLLLSWGRGMKRQDQGSWGGREGDGTGCI PPPPGSTSRPWTSPSPWPLRLHLFSASGPPGSSSCSP*LFPLTDSQVGRCSGPDNPYPYHLMKVQPLPALLLPKPHRFPPLGQ\PDPPSSPPSP
9647	23548	A	9718	13	364	PENR*RNPLTTLTNHSLIYLPSTPS\GISA**NFGSLGACILQITTLGLFLAMHYSPIRLQLAFSSIAHITRDVNYG*IIRYLHANGASIFFICLFLHIGRGLYYSPLYSQT*NIGIILLAT
9648	23549	A	9719	82	351	GEALEPELMPALSH/HAATLLAPLPTTFFVGTKTIVGQAQW/HQAL*SQHFERP RRVDYLHLFSRNGQNP ISTKNTRISWAWWRVPVIPA
9649	23550	A	9720	179	365	FSLFLASLKAQIIDSKPFFSNTLENI*KYEVINFFLYI\IKLHFMNLTSLCFYCHSVCTILL
9650	23551	A	9721	2	320	PIPPGNESSPPTAQEDMQAANKH/IRRYSTSLAIRET/QL/KTTTREPYAPITMAT TETSANTTCWREYGESGSCYCWVGCKTLR PLCKTVWQFLKKPSM*LAYDPAITLF
9651	23552	A	9722	1	344	PLPTQNWFPQQSFLHYVLLPAVSVLWS SFFFFFWKQILLPPRLBEG/NGQNSG*WKFPLPGPSLFCPSFQTSNGYGPQQAR AIFWKFKIKTGFGHGVTRGLNFLTSGSAPLGS
9652	23553	A	9723	156	3	VTEAYFILFYFETESHV*WHDLSGLKS PPPG\SSNSPASASQVAGTTGALH
9653	23554	A	9724	76	337	YLSIYLSIYLAIVVSIYLPYHPSISIYVSSIYSINHLPLYFYFTHLSSTHSSIIYLLSISILSINYLSSISLSIYLSI*LSIYDSSIHLSIHLSHLYIYLI*YLSIYLSIYLAIVVSI\TIYLSIHLSSMYHLFILSIIYLCIIFLPYI/LSTHSSIIYLSISILSINY/HTSIYLSIYLFVY/HLYIYHPT
9654	23555	A	9725	249	436	ELAG*IQDHP/GQHHKTLSQLQIKNLARRGRHL*SELFRLRQEDHLTPGVRCSE L*SHHSTP
9655	23556	A	9726	177	3	HLN**FSNLIFETESPSVT\RGIISAH RNRLPGSSDSPTSASRVAGTTDT
9656	23557	A	9727	272	233	RKNQRIYQIARKRLNEMARISPLRSMII

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LNVSGLNFPLKRCRLAEWTEKKK\DPIT CCL/QKTHFTG/KDIYRLKIKGWKKIFH ANGSQ*Q
9657	23558	A	9728	368	380	RKGQRIS EIAIKRLNKMARISPLISII LNVSGLNFPLKRYRRAEWTEKKK\DPIT CCL/QKTHFTG/KDIYRLKIKGWKKIFH TNGSQ*RR
9658	23559	A	9729	294	2	KGNLSPKKKKNLKNFKVTPQNFGLKDQK TOGKPTLKVSQNKQKPKFK*NLKGKRPL KLFPPKKKKLNPSRSWFYBKKKK\INKLD GTLVRQINKKRKNQ
9659	23560	A	9730	7	284	SQGLGRLRRENYL*FETESHVARTGVQ WRNLSSLQSPPPG\SSNPASASQVPVI T
9660	23561	A	9731	1	322	RSLKKKKRREKKGKNQPGQHGKTLFLPK TPKI*KIKKIYPG/RGGTHLNSQLLRNL RKENHLNSGGKGCNDPKLGHCI PAQMTK TPFKKKGGAKQNGKLLQLIYGIK
9661	23562	A	9732	168	2	GFYRKSLSLSVWICFKDFFFFFEMVSR SVA*AGVQWHDLGSMRPPPPG\SGDCPA
9662	23563	A	9733	43	317	LKLQPRDTHCIWLSTTSFFIYFFETES CSVAQA*MQWHDLGSLQPPSPG\SGDSP ASASCTGMHHHTWLMKCINSFDVPMPL GLGLNSHI
9663	23564	A	9734	8	296	NVVSACSLNGLVKGRSLCLTLNQIL*MI TLTERFLKAERGQKLGLLHQT/QVVN /AKEIFLNEVSSATPVYEGIRKLNLSI ATMEKACVVWIEDQT
9664	23565	A	9735	3	300	TRPSNSPAALSKCSSRRKT/R/TCLTLN QKLEMIKLSKEGILKAERGQKLGLLHQT A/QVVN/AKEKFLKEVRATPVYEGIR KQNSLIANMEKA*VVWIEDQ
9665	23566	A	9736	352	1	PPFYLLNFPTFFKGPPLIHFFLESFLEN FGFQGAFFKLQNFFAFLSLLNGPFLEN PFFYKFPINC\KFLGQNTFYCPYLGFF* RSFFFFFFFETESRPVA\RLCSCGAIS AHCKLG
9666	23567	A	9737	130	3	KIFFFFFFFFLRQSLSVAQAGVQWC/N* LGSLQPPPAGLKRFLV
9667	23568	A	9738	167	3	ISRSVFCFFETESCSVTQV*EQWRNIG SRRPQPP\GSSNYCASACRVAREFTGLV
9668	23569	A	9739	140	419	INVKYLSRHFFKGNIQSPNKHRAIREI QIS*TDNNKCW*GCGEVQYFIHCCMBE MVHSLWKIVW*LLTGL/HIELSDDPAIL LGGIPPEEMKT
9669	23570	A	9740	93	371	KLCNGYYQESKREPTERN*IFANHKTG CISKTYKELQLNNKNS/NPTQKWAKDL D ISPQTMKQTAKNQVKRCSTSLVIREMQI YTKSIPLHIH
9670	23571	A	9741	1	288	GTRDHLRSGVRDQ\PGQHGETRSLKIQ N*GCGHGGSCSSQ\LTWRLRQVNCLS
9671	23572	A	9742	296	563	FIKHLNSYMLGQNLATKLSEICKLPFYI EK*IQAGYGGTCL*SQLLRRLRHDNCLN LGGGGCSEPKI\HCCTPAWATDGGSVSK KKKSR
9672	23573	A	9743	32	400	DALVPHWSSYPICLDLNLVGIYLFSDR VSLVPRLECSDAIMAQSLDLPLRLR*S SHLSLPRNWLMFVILVETGFCHVA*DGR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KLIGSSNPAL/FLKC/WRNMRKSQL* PLLLGLLSADHSD
9673	23574	A	9744	60	356	HSEVDSIIIPILQGRKQISEVRPQRMCE REGGLFISETLFLCPAPSCS/HFLTPA Q*SYF*KNVSWLGAVGDTCPNSTLGGRG GWI\RGQEIKTILANMV
9674	23575	A	9745	2	446	PMVNVKHVKRCSASLVIRAEQIKTIMRSH CTPNS*M*KTDNTKSW/*GCGATGTPIH C/WMKYKMVQPLWKKAAQQL/KHIHLPI DPINLLLGIS*EK*NHLC/YKKTYVRI IAALF
9675	23576	A	9746	257	1	VWLRLSFPSPFLPILSPSSQGDVCCFL MVF*RDGVSLPIPAQVQWLDRSSLP/P SPGSSSPPASAS*VAGTTGMHLHAEFYA SC
9676	23577	A	9747	148	3	IKLCEQFHK*TIHVLNHK/L/WPGMVAH AYNPSTLGGRGWIT*GQEFDS
9677	23578	A	9748	769	1	YPQLFKIAKKKKSNVPIKSIMVSQYGH *ENKKWVLNKHGATLQ/EGKGNFGDTFK VTLKDKIAVAVKTRQERLPQELKLFLL EAKILKQYNHPSNVKSIGVHTQRRPIYV IKELVPGGDFLSFQRKKNELK\VKFSL DADSGWCISKKCIHRDLAVRNCL/VGE NNVLKISDFGMSRQEDGGVYSSSDLKQI PIKWTAPALNYGRYHSESARSFGILL WETFGLG\VCP*PGMTNQPPQEQVERRY WMSVSWQC
9678	23579	A	9749	607	986	SFSSSSSPEFISYGCDDLPMRDPHFVIT HPAFNLPFLALGMFFSLFSPSPLFYF LPPPPRPPC*HSPP\PPPPLTNSLFVFL PPPPGVPSPPTSPPHLPVPRPPSP TSTHLSPPPPSP
9679	23580	A	9750	313	339	AR*GLSCSG*S*TPGMQSSCLNLPKCW DYRC/RATVPSLCFVF
9680	23581	A	9751	213	453	NLAVNVDEINLFFFLFIVTLASKFCS /HLLVGR*FIQSCHYLFIFDTERSV T\RAEMSATVLAHYNLCPLGSPDSSA
9681	23582	A	9752	368	3	PLSSPRLPFPLFDPSTYIFLISISSIRFL SPPCYFLCVFLSISWGFSLVSQDGSDDL SS*SAFLGLPKCWDYRL*PPHAWRELS FFFS/SFFYLR*GSLSPSLECSGMIIGH CSLDILVSSARA
9682	23583	A	9753	2	335	ARAGFSGGDWNVGMQSTASGLSLFHCPI S*GELFIILYILLKCYITL*IN*LMFGS FYFRDLQHFRLP/TSLVGKKRPGTVAHA YNPNTLRGRGGWITQGGQEFETTLANMVK
9683	23584	A	9754	467	120	SQLFGRPRQTDHLKSGV*DQPG\QHCET PSPLKIQLAGRGWV/CAPIGPRLGRP R*ENGLNSGGEVCSEPRSRHCTPAWVRE RDCLKNQNKTKSGVLFHSPHQCFILISNT SRNLL
9684	23585	A	9755	137	368	DGVYLWTHRPYCGLGSLNFGSVIIVLP* VKAYGWMVLTSLGDAIQPLADPECSF\G QLRELRCMDLHVDPEDFRLLGK
9685	23586	A	9756	172	267	SKSGNKPNDYHLMNGSVRWICIRTV*QLL KRLTTELPGPAVAFGLGVYAREMKAYVH MKTYSLQKMCT*IFIAALFGIVKKWK*A K*LSPDEWISK/M/WCIRTVEYYLTIRE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9686	23587	A	9757	56	318	QFWGFSFFFFFCFIDTETCSVSQAGVQ WHNQSWLTA\P*SDPPAS\AS*VAETTG MCHHDQLIFFFFKQALCPRGWSAMAQSQ LTSSS
9687	23588	A	9758	179	1	KDTRVSRGNTQDTLKP PPPG\SSDSPT SAS*VARIIGVHHNTWLIFCILVEMRFH PRA
9688	23589	A	9759	219	208	NFCNFQMPLYQKILFWVRVSLSPRLEC SGTIITYCSL/RTPKPK*SS*LSLGVQG CSKL
9689	23590	A	9760	133	371	AMAYQLYRNTTLGNSLQESLDELIQ\LR NRVNFGRSLNTRYFCDNVRTFVLNDVEF REVTELI*VDKVKIVSL\DGKQTGF
9690	23591	A	9761	813	3	CGEGWAAGQDQGRMGSLPVPFRAGRL GSLFPAFQVYCSCGTQRSSQSQWHKTE RSLPGNNPAPQDS/ASAPKYQTPGPVLG VQSPLNQQSCHTALSPEASSSAFFHTTP ATLLHQARTLSLTQGSRPITWVLLKMP A*RPRESRH\GR*EWTKRSQARSQEAIN ARPRKALGLSDPAPSLHPSLEDSPKFS LGAPKAPPLPASSPTAQETQQSHISQQP TATGFLGARLCPSPQHCQRGGFPQVTP LLLLGEWGVGEHSFPDVLV
9691	23592	A	9762	96	377	RYHTNMAAQIPESDQIKQTGFHHVQGAG LELLTS\FKEFLGTYNKLTET*FLDCAK DFTTRERKSEETTLSEHCLPKYSTMT\H RISLT\FTDNHI
9692	23593	A	9763	164	399	TDEELLLRDEQ/RKWFLKIESTAGADAV NIVEMTTGDLE*CINLVDKVAARLERTE TNFE/RCSTVRQ/MLSKSIACCTE
9693	23594	A	9764	225	25	KCKITMNST*IE/TVFKDYEHLYVCKL KNLEKTDKVLTIHNFRLRNQ*EPEVLTR AKMYKIYNDIE
9694	23595	A	9765	128	218	FFKDLPDCCFPKWSHCFTLLAVYEGFTF ST*LVIREMQIKTP\I*YHFSNRMVIM KKSININKCWQGRGESKALIHG**ECKTV *PLWKTWVQILKKLIIG
9695	23596	A	9766	194	551	KNFFFFLEMEF/SVLLPRLECNGVISAH RLRLPLSSYSPASSSQVAGDYRACTTTA G*ILYF**RQGFHHVQGAGLELPTSGDP PASASQSAGITGVSHCPQLKKSILHETP KGLTGVT
9696	23597	A	9767	238	3	SFLWKLCPRGAPACLRCLSA\LLGGVS* SGYMGVRDPLEEAVCPFSELEHHAERTT ALFRAVPQGCLSLQKLSAFCSC
9697	23598	A	9768	343	1	RGAAHSRGDCVRFTGFCAPIPVLNHPKP LFPFFV*KSPIERSLLGPPLKRSKNRF PFLR/VPRFFKNHPEFFPKIFLPPFF FFFEMESHSLA\RLSHGAILAHCNLSL PGSC
9698	23599	A	9769	191	2	FRINH*TSH/LRGQKKKKKTNSKAIGRK QITKIRA*LNETOPPESIQRINET*S*F SGKIKLI
9699	23600	A	9770	165	2	GKPPNCFYILNFKKKKGQDVFNRT/WLG VVAHACNASTLGSQGGWIT*AQECKTS
9700	23601	A	9771	97	912	VILSTGCSGGLPGWQSVLHHSLTRCPF SFFLSSPTPEME/FSLLLTRLECNGEIS AHCNLLLLGSSNSPASASGVAGNTGI/C

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GLHAC*AS*FLYFHSVETGFHHVSGGLG LELLTSDD\RPASASQGAGITGVTPRV* PLNSFSRHGLSCFFKETRVLSCCPSWT* TPGLK*SSCLNS*/C*GYRHTPAHPAQ DMVFIFITY/CPFFVFPLL/VYIPRFLF LRWSFTLIVQAGVQWRNLGSLQPPPG\H KQSETPSQI*INKY*LLN*LITFFFSIK
9701	23602	A	9772	3	363	HELRSSANEHVFAFSGFTILGLPGVLL IILYPPLLIRTSIYLISN\RL\VTQQ* LIKLTSLMITIHNSIGRS*SLILGSLI IIATTNLLGLLPYSFTPTTQLSINLAM AIPL*AGAV
9702	23603	A	9773	38	385	YLIILDSPEKGLICGCLCNCMHSSLLDH LNL*SS*MCLYANIHIYVAISCIYFI* F*SI/YIFII*YFHYSIAYVYIY/IYIY MYTHAHIMCI
9703	23604	A	9774	13	1350	DRVSLLLLRLCNGSISAHNRNLGLLGSS DYPASASQVAGTIGVHHTRPTFALFLV ETGFHHVQAGLELPTSGDPPPL\ASQS AGITGVSHCTWPHLSTTGKILSSGTICP GIWQQRWWAFLIL\SLPWL*LWHPCLS IMCLSLFFFLCQ/RCKPLISD
9704	23605	A	9775	376	1	KYFELMYTPVIAICLFNSEVFLNK*QFF NLTSSSGIQNLNRLIISNEVESIIKSLP TVKNLGPDGIAATF\TYKEQLTLILKLF QKHEEARILSNLTSETITLILRKQPK KVPNEHTVKILV
9705	23606	A	9776	192	2	NVYQPPPVFLYPPGVAGGV*PF*SPPVF RVK/LGF*GSLFFFFFFFETKRSVRTL ECSGVILA
9706	23607	A	9777	77	350	WLRKFGSRNSGKLTLYLVVYLOTSFFF FFFKIGV*LSPTLECRGPIWVN*NLCFP G*RDFTLTS*VL\GPRVILEFGFLEKT GFSHVPQL
9707	23608	A	9778	133	325	PRWVRFPYLGDCPTPRVSEMLGLQGVVPS SSPFFVCFT*SCSVAQGVQ/WWCDLG SLQPLPLG
9708	23609	A	9779	145	362	RLAFGSCSTCFPLT*TVLYYLI*FNIF VFEMESLSVS\RLECSGAISAHCNLCTP AWTTERVDAANSRSMN
9709	23610	A	9780	260	1	QKQNEKKRKKIFRNKIQRDYNEQ*YG /NKLDNPEDMNKF*ETRYT*/PNLHQEE IGMLNRPVTNKVL*LVIKIPLTKKSPEP DGFV
9710	23611	A	9781	230	1	SSDSKTGSSVVLVACRFFFFLETGSGSV TQAEVQWHDHSSLQPPPPQPPK*/PGTT GA*STLAS*NAEITGVSHHAR
9711	23612	A	9782	20	322	SOHFGNPKGNPKIFRNLEINFFRLRNAD HMIISTDAQKVFDDKIQLFII*TS*QT* TERIFLNLIKAS*KKPTANIILNG*RLN I\FPKTGETKHIC
9712	23613	A	9783	158	379	LVKIIICNSFQYISFFFFFLETKFCFFP QVEVQGNFG*LNLPPLGLNHFS\ASAS REPEIPGPPHHPG*ILVF
9713	23614	A	9785	54	312	KVDKSTKIGRNQSKMAKNSKNQNASPP KDHNSSPARKQNWTEENELDELTEVGFR WVITNSSKLKEHV*PN/GKETKNLEKRL DQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9714	23615	A	9786	13	613	PGAGWARQHGGV* DQPGQH\KRP SLLK IEKLAGHGGRC LLSPAIGGGLKQ GESLE TGGRDCSEPR LCHC\MPAWGN RNKTL SQ /QNKTR
9715	23616	A	9787	794	164	PSFLFCFFFLRWSL TLSPSLESCV TSP HCNLQLPGLSHSP ATVS*VAGTIG TCHY TKLS*FF\FDDSL *APFLGVVD TETYP DPPSSKGLLPHSG QHQHPPAIS RAWL SC*VLPHLRS/ STSLGQP/ RIW*LSKVE V*RGFTFSPT ONTPTNNNC SIAPGRVD* SLLID*LQWCD HSSLQPQTP VLK\HPPT LASQSAGITG ISHHTRPD
9716	23617	A	9788	256	380	YIFRQAKTQGLPP CALFREAVGENT P*V FAC/PKNVLFYV HP*LPF*I* IYQLKIT F*NYEGMVT/ FVFRFLFETR SHLSRLE CSGTITTHCS LELVGSTNSS SISAS*VDG NTGVRHNASC
9717	23618	A	9789	22	226	TKINSKGNKELN VRAKTIKLEEN IDRN LCDLGLGNCFL D*YCIL*TK INSKGNKE LNVRAKTIKLE ENIDRNLCDL GLGNCFL DMTPNAQT TKGR\IDKL DFIKI* NFWL DT
9718	23619	A	9790	288	2	QVWQE*AETESA IHCWWERKAI QLL*KM RWQFLKMTNV \ELPYGSAI PLVGIHGRE LER*ST*NIM FTAPLFVIGK/ T*NLFKW PSPYEQITK MHSC
9719	23620	A	9791	142	361	PPGEGKRVFP TTEPSPRIP SKAKSVSQG DTCTPMFTA ALFTIARMW NRSKCPSFEE *IKMRCIT T/MECYSA
9720	23621	A	9792	305	346	TYEYTDYGG LIL*LTFFYD HAVLIIFL ICFLFL/YAL FLTLTTEL TKTTGGDA QE IETV*TLPG IILGLIAL PSLRRLYIT D DAPDASLT IKSIGHQWY *TYEYTDY GGL ILNS
9721	23622	A	9793	2	317	SRDRPRVRDR *LFSTNHKID IGTRYLLFF A*AGVLGTAL SLLIRAE LGQPGNLLG ND HIYYVIVTAL AFVIIFFID LPILI\SS F G\SVYVLLIL GVPCTAV FLHSS
9722	23623	A	9794	384	1182	RIGKIKG/LC FLFV*WFLK FFFKMEFL L PRLECN GKI\HCNLL LMGSSNS PTSASQ VAGITG MC*F\VFL IEMRFFH VGQAGLK LLTLGD/ PPRPPK VLGI
9723	23624	A	9795	205	1	GLQIKCTMRY HFAPTKMAI TYFFLKKGK G\NNKCW* GS/GTEIG ILIHCVW ECGMV QLLWKTAD AWADAW
9724	23625	A	9796	307	348	QSARL*EAVCP FSDLQLRT GRTTALFKA VRQGHLSLQ RLLLSF\VCL YPAPRGGAY RGRQASLSC GGLHPVRAS RLLCLPKQAW AMVGAPT PASLPPCSS ISHCCASN QRDS VGYPSSP
9725	23626	A	9797	193	381	ILLI*THILL SMISSPFF FETGSHSS/ V SRLECSGTAS AHCSLDLP GSGGSPTS AF *VAGTTGA
9726	23627	A	9799	153	359	FGTYMCFAD SYQLSYL FVVGTF SWLEEE GV*WCICG SLQPQPP RVK*/FL PSLSLL SSWDYRC APSC
9727	23628	A	9800	2	396	ARAARAARE LEELIKI FFFFFFFF FWGQIL ALMPKGGG GGILTYN PPLPG* NNFPG

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						LTPERTGINGLGPPGRVNFQIFKKKGGF PPGARGV*NPGPRGTPPPGFPKGR\DKA PHFGPL*TFEKVPRPPNFPQ
9728	23629	A	9801	256	347	LYILLNLSLK*LVKELR*NVVLASLIIR YKVTTKRF**FSKPAQSEELQLLTSAPG LNF*RYIIISFFFWIQSFALVA*VGQWQC DQGSPPQLPPGFKRFS/CRSWDYRHEPP R
9729	23630	A	9802	109	401	HLRRPCPTPPFALRTSGDQPLSPEARPD SGLLHSPPLTSPRGLNGQCPPRGSTLNFN P*ASIPASPPPSGQPQASQEPVASEH PPDT*GDPAQPPP\RPQDFWGPATVPRS QAGQWPSPLPSDFSFGAQPVPPT/PP PSTSTQSRWT
9730	23631	A	9803	371	2	PGFPLFSFPEGNGPSKRQTD*IRCLF* DGKVWECSPPKKKKTKRKKAVIF/CV PVQTKCIVVEGGEETLVGDV*V*P*\GS FKHVVAMFPEK/DCLCTLYEASFKTKE RRVDGFVCRVGT
9731	23632	A	9804	188	1	FLFFFFSET*SQSVTHAGVQGLEQSLPP G\SGNSRASASQVAGITSRRKHSWIIFFV FFVETG
9732	23633	A	9805	112	383	VFINIRVFRILFTSFFFKRGFNLSPRVK CNG*TKGHCIPLDLPGRV*SFPFSLTNW DYRCAPPRPNKFFF/SFETGSHSVTQA
9733	23634	A	9806	599	237	FRDRSLTLRLHCHCVITAHCSLKLGLG SSELPAQASPLSSWDYRHSPCLANFLFF VETRSHY/ASRNSLGSSNPT*A/FPKCW DWQV*ATAPSLAYWFSEAKLILRLAL KVSDENICITNF
9734	23635	A	9807	168	2	PQQDVFFFLETGSYSVTKAEVQWCDHG SVQL*PPG\STDPPTSASQEATGTHRA
9735	23636	A	9808	225	3	GPLGYLPPYFPQPLISRG*NPSDFLKIS RVFYGT/HYKFELFLFFETESRSVA\ RLECSGVISAHCKLCLPGS
9736	23637	A	9809	541	3	RQLTGINSRRQFQPQMSNYVIPYMMDM IILKTKKSNNKYWQGCETELLIHCLWE CKMVQLVWKT*QFLNRSDIEFPHDPGI PPL/GYKRKKMKTCLPKKLCVLVEP/RM FTAALFEVAK**KQ/PQTPITR*INIMW RIYTMEYSAIPRKTPLIHPIA*LDTES II*TEKIQSQETTY
9737	23638	A	9810	213	1	FLCVDFVPCNFALKLALVGLFVCLLFG SVTQAGVQWCNL\GSL*PPPPGLSDLPT SAF*VAGTTGVSHH
9738	23639	A	9811	54	388	PARPLPRQ/WDERPNQPTKKKKKRGGRN LPTKKKTQNYSHQNPVAQRNPGKTNQK KPKTNPKKKKGGAL*KKTQRGPKQTGGR K*KISPNGGK*NPCGKLEKNPFSGGE K
9739	23640	A	9812	429	24	RSKGAEFFICPCRSSKFSVLQQRQVRIV FQHPGLGESVAR/CRYSQLLGRLRQ*SH LNWGGRGSSSEPRSCHCIPAWATRASSIF CNFQASSVEVRRSARKKLFSIDILKRHT INWRVSGLLLVDSYFGRLATPVRTQ
9740	23641	A	9813	149	350	CHFPCFHTTL/CE*EPGEDVTGPIGTKE FPAPGRDTGHTHTHTHTHTHTSDPH HLCVWNTLIHFV

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9741	23642	A	9814	66	401	PENKKTIVYRKPIATTIFNCELRNALPLK LETRP*YLLY*LFNIMLEVLASVVRQEK EINLSIFT*DIVIK/MKIPKNLENKLLK LLSPFSKITGYKISIQKLTSSFLYYGFT V
9742	23643	A	9815	82	1	APPARFFFFF*EKFSFPPEVQRG VFCPCNT/CFP*G*KIFFL\KPLKKVGF WPPPPGPKNFYF*KKGGFPFWARGFFI PTPFVPLHPFKKGVKRG*APPARFF FFFFFL*GRVSLCHPGWNA
9743	23644	A	9816	256	2	QHFP*LPIPHIPIQT*QHFPQTRSPFQG PPLCQKPFSSPWGSKVVFILLSFFFFF* DRVSLCHPGWNAVM*SQLTAASNTW\VK *SSHLSLLSS*DYRCVLS
9744	23645	A	9817	53	411	TIYCSNYVYNFVSOHFRSLYS*KNCGLC L*FHLFVLQS*NFMQFHM*FCLKI*VDP IITFEV*FTYI*FF*TYSSVSFTDAYNF VKPHR/VYRGP GAVAHICNPSTLGGQGG WIT*GQEFK
9745	23646	A	9818	100	417	DEHSEKQDEPLQRPRLPFPPTPPSS LLLLNHIGQESGLTHVRLASCLNRGFC FDMKERLCLLPMLCECRGMISDHCSLI/R PG*DKPPASAYQVGETTGTYHRA
9746	23647	A	9819	136	2	IYMGMPGAVAHACNPSTLGGQGG/WWI T*GQEFKTRLANMVKPC
9747	23648	A	9820	257	426	IVPGLFLGTGSCSFTHAGVQ*SNCSVQ S*TPGP\SDPPASASRVAGTTGAHHKAW L
9748	23649	A	9821	151	416	LHKLCLMVMESEGTAKTPSLSPIFNSVGL ILLLLLEYSIDSLC*SVLCCYKEIPEAG* FIKKRGL/WLGVVAHACHLSTLGGRGW ITRSGN
9749	23650	A	9822	50	513	RGDPRVRPRVRIIKLSEEGMWKAEIGRK LDLLHHTISQVNSKEKFLKEMKSATSV NTRMIRE*NSLIADMEKVLVV*DOTSHN IFLVQNIKSKGIGLFKLMRAKRDEES/ AEGKLDASKGRFVRLK/EKRSHLHNMKV QDEASVDIETTASYLKV
9750	23651	A	9823	48	406	LIIVVYTLTRWIGHSAVSYPPLRPYS LRHNEIRPINNPTMASKSSERKSLS LTFHLKIKMIKLSEEGVSKAKTG*KLGL L/R/QTVSQVNNAMKKYLKEIKSATPVN T*MIRKQNNL
9751	23652	A	9824	143	444	WNKKNKNELADMILWCGDKTTFMRKL TRDETKYGIPLALRGHSHFVRDGI\N LDGQVDLS\G*WDGTLHLWDLTSGSTTR RFVNK/TKDVLSADFS
9752	23653	A	9825	297	2	HRSPKTETKIIASIKKKTMITKDLNRQF SKQDKHLTSEYMKRCPTS/LREM*AKTI MRYHLTPIRRAPIKNKNK/NKSKCW*GC GETEILVHCW*ECKMVP
9753	23654	A	9826	175	400	GGKGGKNFSLKGGEKKTNLGIFGKKPIF GGGTNGANPPPKIKGSKEKKNF*VFPP FFPKNFFFP*NL*FLGGWPHLSPPQK* V/CFPKIPKLVSFSPPLREKFFPPLPP* NLGPPGF/SFWGPPLFFFFFFF*RDKF SFYHPGWKAVIAAHFSLELLGSSNPPTS
9754	23655	A	9827	64	622	MFSFFFLFDLILNHLFFCFV*MFSFFLED

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						LILNHLFFCFVIRQQFSFLFF/ISFFFS FFHCNVNTPELCDFSVCIHSDNSFRFLH LF/NF*HMTLCISELR*TLKQSCSYTK IC**FYSVQLSFLTILY**CKS*QALSI ALQNEFLSV\QYHKNNMYITLTIEFSRN KFLSVTFLLFSIFSHNFGISASISIFIL HVYIKNNPIGFVK
9755	23656	A	9828	298	1	MRNCLTDDERKWFPEMASTPGEDAVNTV EMTAKDLE/Y**YINLVDKAASDFEMID SNFERCSTV/NKMLSNTACYRENFHER *GQSVQQTFRVGERV
9756	23657	A	9829	361	1	FLTGTQWGK/DSPFNTWC*DH/WNIHRN LDLYLIPYIKINLKQLTGPNLRAKTIKL PEQNIGENLCDL*LSRERYSTKSITRIR KL/DTLGFIKIKNKCISKDTIRKR*ATD WEKIFANHVLKG
9757	23658	A	9830	402	2	RFHHRFSFVLFGPFAKVAFPIGAKNFIS NHYWAGVFPFWEKKNKIDSLPPFSKNP ILGELKA*F*NFLF*GFQIFF*SLFFCP FGGK*IPGVFSFFFFFLVFFEIGSHSVP \RLKCSGTITAHCSLDLGLSSN
9758	23659	A	9831	2749	3215	FCQ*IKMYVMCICIYNFRVYLCTIYTYL HTHTFTHTHKHTPTQIPEKDS/QCSLSD LKCHSL
9759	23660	A	9832	3	386	KLRIGQLNLSAMAACK*SERKS/R/THL TLNQKLEMIKLSEEGMLKAVIGQKLGLL YQ/TSQVNAKEELLKDIKSATPVA*M IGKQNSLIVDLEKV*VV*IEDQ/TSHNI SLSQSLIQN
9760	23661	A	9833	1	370	RRCRWPPDPSTRTVGRQIGKLVTHRPTVF QERGCPPLTRQAGSHHGGGAFAQVISP TKSISPCGRGGSRL*SQHFGPRMQVDHL R/LGVQDQ/RWPICGQYGETPA\LLKLP KISWAWWLPVIPA
9761	23662	A	9834	125	409	GQENRETWKIVHLV*VLYT*HIKRLNCF SHFI*CYQPTASQAHVHDSNDSSTHV\ N*NSRWPGTVAHACNPSILEG*GGWIT* GQEFETSLANM
9762	23663	A	9835	223	1	PKPQKMGTF*PPMEGS*MGPPHWEKMGP FLKKKEGHPFFFFFFFEMESRSVT\RLC SGA/TISAHCNLCPLGSSNS
9763	23664	A	9836	377	515	FILFLRQVLTLPLRLEYSGAIVAHCSL\ AF*G*SDPPASASRV
9764	23665	A	9837	274	1	AGEWHDQICVFKIPLMKNGLHCARVGQE SWKERNQOV*DRQKQNLSDS*IQT*R/ M/WPGTVAHAYN/PSTLGGQGEWIT*GQ EFETSLANMVK
9765	23666	A	9838	553	114	GAGVKTHPGHKGKTLFFFKFFFQKLPGV GGKTLPSPLSRGLGRENSFHPGGKGSNK QSSPPSPFG/WGKKGGGLPFQKKKKKEK RKKGKKNVAPSEPPLKYSN/WQATWG* RKLLNDTMRVQPTKSRMQKILQDRGPVN GIFTKTGRL
9766	23667	A	9839	36	434	LPFPQCVTEFIIVLISWCYIREDACKNL KHVAITIINVCIYICVVCPSSTLYVYMY MLP/HLSDTLTLN*VTLVEMLSFQCL MFWYHGHI*K*HELDVVAHACNPSTMGG QGGWIT*COEYKTSANMVKPR

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9767	23668	A	9840	268	1	RFPFFFCPLTILFWAPGVVFSNFLGVRA PQPP*IFFPI*KKPSPLIFFFFFEKES RSVS\RLEYSGTISAHCKLCVSGSQHSP ASAS
9768	23669	A	9841	463	86	LYMHFISGLFLLFCWSI/WSVLCQYKN CFDDKVYGLDYGNTSQVFT*NSKLIKLY TLTMYSFLCINQTTIKPSEMIQATKANI DK*NYMKLENFCTAKETVNMKMRQLKKW EKVFSIHIPQEVNI
9769	23670	A	9842	37	400	VHSPFFKFWSLYVSVLKFPCSLYFKFL ALYSIFLQMCQHLLV*AFF*KRGLNSV T\RLECRGAISPNCNLCL/SGSSDNWAS LPRKAEAGNSFT/CR*SQVAGNPISIS TRLNQRKTPFES
9770	23671	A	9843	42	407	NCLSFLITFFFFFLFENKVSFCPQG*G/ RGGPFWPHGTLPPRG*GNNPP*LPGRGE *RGAPPPGYFWLFGKKRGFPL\GQGGG KPPALKEPPPLGPPKGG\NYKRNPFP GNFF*LPYQVV
9771	23672	A	9844	113	379	LGPVVATSLRGRFLGYQLQSKKH*NYP TVR*GCGEMRTSVHCW*ECKTA*PL*KT VWQFLKKLNTGLPFDAETPL/LAETPKE LKA
9772	23673	A	9845	284	528	PLPKTMEIMLDKKQIQITFLFKFKMGHK IAETTRNINKAFPGGTANE\KCTAQWWF KKFCKA*E\SLEDKEA*GHPSEVDTN
9773	23674	A	9846	888	1295	LEQGCNLFHKKH*LGVEVFFVCFRRSF TLVAQAGVKWRDLGSL/HKLPSSLSPS SWDYRPLPRLA/NFFVFLVEMGF\TVL ARMVSI*PRDPPTSASQSAGITGVSHR AGPVAGILMFCRWNTSNKPKGAVFKK
9774	23675	A	9847	88	387	AYRMKIIDRISLSLYTAALWVTLFLFLF LFFFFKTEFCFAPQAGGQ/WGQFKLMDP NPPPPG*K\DFLVSHPRDLGIKGAPPQC GQNFVFYKEKGGWLLTAT
9775	23676	A	9848	298	438	KIPRGAPNFPGGGKTFSPPLGGPIKTPR GALEKKTLE*VRGPWPGFVKKESPRPKK LG*QIFWPPGKKPNPPMG/SLDPPPL ILSRPDP*KKKKKKKKKKGGGPLKNP PGGPKFPRGGKNFPFPRGAYKNTPGGS *EKNPFLGGGKKRKQP
9776	23677	A	9849	251	498	ATIKKMESKKFW*RHGEIGTLIHCYWEF KMW*PFWKTV*QFLK/D/LNMGLPFD SAFQLPDICLGLKTYVHTENCTQMFMAAL F
9777	23678	A	9850	478	37	ESRNKSHLWSINFQKGLR*LNRGKQPL NK*CRHNSISTCKRMKLDPLYTPYIKI\ KSKWTKDLNVRAKTIKSLEENIEVNLHD LG*GNDFLDMTPKAQTK*NID*LDIIK I*NFCGSKDTINKVRRQSTE*EKIFANH VADKLE
9778	23679	A	9851	2	378	RLEGLFLCALFCSIAICMFFFFFFF*K KRGPFQGGDPGGNFRQLDPLPGIKQ FWGP\PPRKAGTGGGPPPGANLGFWGK KRVPHGGQKGFKP/RNPRGSPRPGPKG GVAFVFRPKPPGLEQ
9779	23680	A	9852	229	3	FGPYKIFFKKKGAPCPLENPPVF\HQKL GLGFFFFSFFFF*DGVSFLRLRLKCSAA

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						LLAHYKFLLP*SDSAASAS
9780	23681	A	9853	108	420	GPRVCVRLSLRDDSLLATEDSLAHTEG DPVTASSHSQAPSLSVHPGAALGVVWG TGAIAGTPEPQKPPQLTPGGRPA\PIAP GLTWEPPSHPPQ*RSPPPPP
9781	23682	A	9854	2	256	FFIFPLRYIYCARFQFLSPILYLK* KMD**RRVFQEKWEQAYFFVEV\SPMCLI CNQTLVSKEYN*RGHYETNHGENFD*F TEKMHDENLHLTTTQRP
9782	23683	A	9855	323	3	IIQMANKHRKRH\QSQ**VRVMQKKIIM IHRYIPQWLKTSKSDMIKCCSGYGTTEI FTHYLWECKLLHLLWRMVWL\ILLKFKT DTPHDPAPLLGTYPACEMHMYPR
9783	23684	A	9856	28	385	DGVTOAGTQWGSKFTAA*TA*YQGSTPN AWSFFSPPPVLTTPPPQK\YPPPKKK KIPPPKKK
9784	23685	A	9857	436	518	AANRLNIYRHLIYDKD/EHYRIVGKDD LKNKWCWNWI/ASNKEKNLDSYLPH K/LNSR*IIQLDVKD*IIKLEDNLYLH DLGDRQKFLGRI/PVFTIKKKIGKFDPM LKLSTFVHQTPC*RLNSA
9785	23686	A	9858	153	492	RLAGSDPGVADVSQVLRQEKSPCPSWK AVSQAESSSSSAGVSLVLERLLADWMRP IPIKEENKL\SQSTDNLNFIQKHCHRN TQNSV*PGGVGPPGTCGPFRRQSSP
9786	23687	A	9859	2	419	TTGKLQVSHKSTYSHFSKPTHTTNKD MKRYSPL/AIREMQSKTTG/MRYHFT KYG\NNKCWLGCGETETLIYGW*ECKMV QPLWKAVWHFLK*LNIES/PIY**NYS* YISYSWRKTCITIYDPVILLGLIYPREV KTH
9787	23688	A	9860	88	419	TFFFFFFGFWFLKTKPLFVPLFEGGPI LG*WNPPPRD*KNFS/GPNPPGGGE*RA QPPPPGYFLFFKKK\GVSPWGGGSKPP TPGNPPPGPPKIRVIRGGPPPGGRKHF
9788	23689	A	9861	301	401	KRA*GGQEPKVCFFYNRKVNGSPPK KFKKGRRAAFFGLRANKRGLFVKKGKI WVGKVGEPIT/DPFKEFGGR\LPEKDG LV
9789	23690	A	9862	220	415	KIMGGAQIFRGGGGFFFLGWEKNFNG VSFRRKFFFGGVFLPPPP*HKKNYFSS ORQYISLGGGRKTTPPKNFLLKDTPK LFFSHPSKKKNPPPPRKIWAAPMIF*I PPPIIFFFFFFFFFFFFFFFFFFKN*P/S FFFNFKKPIFKTFLSPPKVFPPPKKK KKNPPISYRRWPLAI
9790	23691	A	9863	116	366	GQEFETSPAMFCFETESCSIA*AVVQWH DLSSLQPLPPG\SGDSPASASRAAGELL EPRIIRLQSVETITPLHSSLGNRVRHL
9791	23692	A	9864	619	295	FFFEMEFSLLLPRLECNCAISAHNRRL PGSSDSPASAGGLL*SQVAGITRLRHHD *LILY/FLVEMRFHRVG*AGLELLTSGD PPSSASQGAGITGMSHAGHYGKIF
9792	23693	A	9865	12	432	IADRRLLFTNHKDIGTLYLLFGA*AGVL STALLIRAELEGQPGNLLGNDHIYNGI GTAHAFGIILVIVIPITIGGFGN*LVTL IIGAPDMAFPRINNISFGLLPSTLILL TSAILEARAGTC*TVYPCLA\GGYSHLG

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						A
9793	23694	A	9866	30	380	LFSTNRRGIGPLYLLFGA*SGVLGPALT LLI*AELGQPGYLLGDDHTYNDIDTAHA FVIILFIVIPIIIGGFGD*LVPLIIGAP DMAFPRIN/NISF*LLPASLLLLLASGI REGRSK
9794	23695	A	9867	256	395	EVLKSEKSFETVCIINNKC/WPGMVAH ACNPMTLGGRGGRIT*GQEF
9795	23696	A	9868	458	2	PKKRFFSQKPPRGFYSAPLKGNKNIFFPP PVNFGPPKDFKGPPLFFFFFFFPP RFFFFFLEKG*KF*NNFFT*NMVFFYIS /CSKKFPFQFVLTPIPF*KVPKPVWFFW DFPIFFKKIFFFFFFCDRVSLCHPGWSA VARSLTASPRV
9796	23697	A	9869	144	425	IPLCSRIYSFGPC*FSLISSSSCLSPFL SIPLCVLS**T**YLFYISMREIYKTR TKGIYPGAQRNSLYTH\FSIEVQSTIKA ERFWPGAVARACNPSTLGRRGGQITWGQ EFE
9797	23698	A	9870	138	401	DLRLKLNLSKNIIRLQGTVESSVLTIKE MQIKAKVRYNLI PVKIKR/SGNDRWW*G CGERGTLRIC**ECKLVQPLKWTVWSFL KKKKK
9798	23699	A	9871	179	441	PSGKGKIGKPPPPPKKIFGNFFFLKKK GVPPGPPGPKPRPLETPPNPPKGGY GGGP\WPPPPIP*FFKGPFKKKGPPWTN RGNP
9799	23700	A	9872	57	435	FTQMRKNLKNNSGNMKK*GSITPLKDHS NFPAPVDPNQNMFEIPGKEFKK/SDY*V TQGDTRERCKPT*VLKTILDMDEKCSKE MDILMKNQSELLEKKTDFRELQNAMESE NNRLDQVEERITELE
9800	23701	A	9873	228	443	FSSKFILISVFLFLFLETGSCSVAQAGV QL*DYSSLQPSQG\SGNPPISASQIAT TAGACLHALLIFVFFV
9801	23702	A	9874	349	2	KKPKKKNFLPPKNFGFFSPFSP*KFFFF LKGFNFFRGFPNFPKKKFFSKNSQL VFFLPPLKKKIF/CFPTPVKFGP/SQRF FLKGPPLFFFFFFFLDRVWLCYPGWSA VARSRIS
9802	23703	A	9875	405	2	KKASRMENVRKKKLEMIKLEEGMLKA NIGQKLSLLAKQQVNAKENLLKEIRSA IPLNTQMIRMQNSLIADMENIL/VVWI/ EDPTNYNIPLSQSLIQSNALT\FNSMKT ERGEEAA*EKFDAISG*FMTFKERS
9803	23704	A	9876	355	394	THPYYSHQEQSP*P/LTGALSALLKTS GLAM*GHFHSITLLILGLLTNTLTIIQ* WRDVTR*SAYQGHHTPPVQKGLRYGIIL FITSEVFFFAGLF*AFYHSSLAPTPQLG GHWPPGTITPLNPLEDPLNTSVLLASG VSIT
9804	23705	A	9877	47	85	TIYIHCIVRIYACEVCVCAYIHCIVP AHLTEQNL\KPARTQSPAPQKNPELPV DLVSI SL DREAQDVELNHRYLGNTRTD VLPKVNTLCRL/NFFPCLPILEELQEL P*LENIPLPFPIDYIYTMRAYICV
9805	23706	A	9878	2	389	GRGQFPPEFFFFWGGSIVPSTPNKKKP LGEVLGGWSNRAPKGWGGGFPPIILAF

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						KPKGPFPGPKFVLKFSNVPPLLFFPKMRG PLPKGGGFLPFFFFFFETKRSVTPQGVQ WCNFGSL*PPP\TGSSNS
9806	23707	A	9879	351	1	FLGPSKNFNPFPQKWPFAPFPKSHRAR VNEIFS/RLSVINF*GLTKPQRLFFSLL NFSS\PIPPFQFPSRLIKEIRFSTFLTP ENSKIKKPLFFF*FFFF*DRVTLCCPGW SAVVQSR
9807	23708	A	9880	123	387	SFLWKLRLPSGAPTCMRCLA\LLGGVSQ LGYTGVRDPLEEAVCPFSELQRHAGKTT ALFRAVRQGCFFFAFY*IELFPCY/CSG RVGG
9808	23709	A	9881	341	659	SFLGRVQWLHACKSQHFGRRLRQVDHLRS GV*DLPGQHDETLSSLKMPK/QKLARHG GMCL*SQLRLRLRQENHLNLGGRGCNEL RSQHCTPAWATEQDSISKTKTKK
9809	23710	A	9882	216	1	PKFFWVLRLDSQIFKPGFGPGQGF/GGFG NPQGGKKPGFWGLG*KKKGFFFFFFF LRDGISFCCPGWSIQW
9810	23711	A	9883	2	244	GRVGAVGRREGENFIKCELP PPPPEGK QQNLCKFLTGFSLPCQDKKP\CFFV*KK KKKKKKKKKKKKKKKKKEKGGGGA
9811	23712	A	9884	310	2	IFLQTLFPNTFENSLSYCIIFSEYSFT **KQ\TNFILSSILLYI*PSGSYISNL *Y*ELFSQNL SYQHFLWI*KKWGLGAVA HTYNPSTLGGQGRWIAWSPG
9812	23713	A	9885	242	358	KTVWLYMNI*MANNHME*CSLPLVIREM *IKTPVTVH\TVGMAAI*NKK*NITR/C W*ACRETAVLVYCWGEFYTQPL*KTVWL YMNIE/IPCDPAIPLLMYLKE*RPGTV AHTCNPR
9813	23714	A	9886	360	2	LLKLGFPPFWAKGKKKRLWVEGPLGKPP GGFCQKLFFSPGGGPKGFSPIIILPKG *PFVWGPFFREVF*KKRFKLKKKFRPTFS /Y/LFFFFFFESHVSVA\RMECSGAILAH CNLCRLGSSD
9814	23715	A	9887	236	347	IKGFFFF*TESHSVT\RECTST/SAHC NLCLPGSSNSP
9815	23716	A	9888	310	3	NFFFFFFETGSCSVTQARVQWSDQ/GSLQ PRSPGL\SDPPTAS*VAGNLKFLSGLC SSL*SLEIS*DTKKSQVQITDDLCTTVV LCLFFEMESHSVVQAGVQWH
9816	23717	A	9889	119	391	APAYWNPHARDSPPFFF*TNFPFPQVG GQWPNSGSPQAPPPG/SPPP/YASASK ISGAPGAPPPGPNFFSFSSPTFFSR DGVSPYEP
9817	23718	A	9890	195	3	DGVSLLLPRLECNGTILTHCCLSPV/SW DYRLP*RL/V*FFFLVEMGFHHVAQA GLELLTSGDHP
9818	23719	A	9891	3	378	RDGERNMLALGTASAKALYSLALSLPR LECSGTIISSHSLNPP/GLKWSSCLSSST SSWDFRPAPPHLAKKTQQ/HATFF*EG ESPYVAQAGFKLLASSPPAFSLPKCWD YKL\DRHAW
9819	23720	A	9892	231	1	PKPFFPKFFSP*N*KPFFQISPAKIQKI RVYQS\HKFFSFFFFFFHGVSLLLPRLE CNGTISAQCNLCLSGSSDSP
9820	23721	A	9893	2	347	APARQENVVCVYVCMVCVIVLHRHC

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						EVLCFYKMLGKKRSIYAY*LVY*YIYIH MCVYIYI/YIYV/YMYIYTYVCIYTH
9821	23722	A	9894	28	382	TAHLEAGATGYRTFLLPAIGLLCLPWVL DDGAGQTAQ*SMLLDHAMLLAHHRAHELF I/DTYYEFEBETYIPKDKYSFLHDSQTS FCFSDSIATPSNMEETQQKSNLELLRIS LLLLIESW
9822	23723	A	9895	93	386	FWKIISHYYFKYFSCSILISPSDLPTIC ICMFHLLKLCQSSEFLHLLFVWLVFET QSHSIKQPECS**LSAA/CHLPSSDPP
9823	23724	A	9896	174	1	TLDWGP RKKNPFFFFFETR SRSVTEAGV Q*HNHGPLQPQAG\SSDSPTSASQADA W
9824	23725	A	9897	251	386	LQRLECSGTI/SAHCNLCLLGSSNPLAS AS*IAGTTGTLTGDDVDST
9825	23726	A	9898	127	393	GHMGTLTGSPATLSILALFFWGGRISTQ LDGINKS\FSLFLYFLRHCSLSRLLE*S GAIITYCRLELLGSGDTPASASQETGTA GTCHT
9826	23727	A	9899	3	334	KLRIGQLNTSAMAAC*KSERKS/R/THL TLNQKLEMIKLRREGLKAVIGQKLGLL YQ/TSQFVNAKEELLKDIKSATPVTA*M IGKQNSLNCLEKSCVVLIQDQTG/HNI FLS
9827	23728	A	9900	356	1	GRKPFSLPKATLLPMGPVLGGRALMG PDSRPGVPVPSCLVLLTPLAPLPLTARE SLCPCPPS*TPQPSVNF/H/GKLARRSP CVVSGRQSLP*AEIVPLHAPPALGDRDE TPSQKKKK
9828	23729	A	9901	118	343	IPYAKEKKKQENVLRFIHVNLCSNWF FETGSHFVTQG*VHWCNLSLQP/PNLQ GSGDPPTSASRAAGATGVQH
9829	23730	A	9902	321	50	SLRTRV*RPPSAPG*NPFCLKPQKIFQG GG\ESPLSQILKRVKQENSYNLGGKGFN *PKLPPCPLTWATKKTSPKKKKKKNYR TWETSVS
9830	23731	A	9903	317	8	NCYDPNSGIVIPLLGILPKSTK\T*VRT KTCT*MLIVALCII*TKKW*SKCLSTDK QVNKI*YIHIMEYYSPIKGRKY*HTLQH /WMNLENIS*KRLDIKKPHII
9831	23732	A	9904	287	3	RGALNGRGGPRGVKSPGFAPFKLQKPP GTFLNPK\QFPFFPNPPF*KKGAFFHFF LPLF*SFRWTEFYSVT\KLECGGAISAH CNLCLSCSSDSRA
9832	23733	A	9905	2	406	PRVRTSSRSRATALFFFFFFFVFFWGKG EIWAPPLKNC/IPPEKFCYFGGAPGAG LPPPPGVIFFSLCRVVKKKKKKGAPPGG VLGKKKKTPFTPKGFTFLTLLGGF*KKSL FGKKTLLWVGGP LLLKNFF*EKFR
9833	23734	A	9906	1	296	IWVGATECIFKNNPTIWHQETHFTCKD TYRLKV/KGWKKI FHTFHTNGNQK*AGI AIVISDKTDFKSKTIKR*KGHY/IMTNG SIQQGDILDWYKSNCSF
9834	23735	A	9907	474	41	FMEYLTLSFIHVLLQ*FIHCFVHLFIHS FFYALMKSLIQ*FIHLYSCF/ICIDLLI SSCIYSFIYALVKSLANSLTHSFIHTFL Q*FVHLFTPLLCISFTHSSIH*PSHSLT FIQLHLFFHALVSGFIWSFIYLFCKINV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FLIDK
9835	23736	A	9908	286	84	LKPPPPFFFFFQANFLCFIRD/GFHHVG QDGLPLLTS*SASHGLPKCWDSCRCEALR EASPLISGPHQTI
9836	23737	A	9909	316	63	DQLLVRSIGFEALMSPIFFQMEF/SLS LPKLECNAGISAHRNFCLLGSSDPPASA AV*/PMANLLKLCASVSYCIELVLNELH WIK
9837	23738	A	9910	370	461	F*F*FLFSETESHVA\QLECSAMISGR CNLRLLGSGDSPATREAGAESLEPRRQ SEPGLCHCTAAW
9838	23739	A	9911	294	28	PGKNSTVQKEPGKWFCEMKFTPGENAVN IV*PTTKDLEY/WINI/DKTVAGCERTD SNFERSSTMGMKML\SNSIAWYTEIFRGR KSQLMGI
9839	23740	A	9912	307	463	CKL*TLSNNDVIVGSLIVT/TCTTLVGV LIMGD/RLCMCGEKEYLGNLGTFLSIL
9840	23741	A	9913	377	28	REMLTVKPLAPSFRRWSRAYRAIFFITP TWVSKSGKVTGPLFFLHIFFGP/CPGL PIFFFIKTKGTRFFFGWFFFERVSLCC PG*MECNAGISAHHKLRLPGRSRYPASA SEFHR
9841	23742	A	9914	384	725	HLTAIRMTVIKDTENSKCERGC\KTLMH SCWEYERVQPLWKTRW*F/LQQVE/LPS PCDPSIP/LLRMPK*LNTD/CKRMC/C IPTSIAALFPVTK/SWKQ
9842	23743	A	9915	187	3	QPHKHLGLDNIYIFFEIGFCSVAQTGVQ *RDHGSLQPRPP\GSRDEPTSGSRVAGR PRQENG
9843	23744	A	9916	15	167	DGVSLSLPRLECNGAILAHCNLR/LPGL K*FSCSLRLPSSWDYRLPPHPAHV
9844	23745	A	9917	345	477	YCSRTSLPL/TLKKGSA*PGAVAHAYNP SILGGRGRWIT*GQEFK
9845	23746	A	9918	460	42	HQRPKVDKTTKMGEKRSRKTGNSKNQSA S/APPKERSSSPAMEQSWTENDFDELRO EGFR*SNYSELKEEVTRTHGKEVKNLEKK LDEWLTRI/SNAEKSLRDLMEITPKA*Q LPPERTNLSS*FNQLEERVSVMEDEINK MK
9846	23747	A	9919	282	21	AAGYLQPSSEFWLHSLGSRRLPISVFPV

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						RGRQAWLSCDGYHPVRPSRLLCLEPTQA
9851	23752	A	9924	254	3	PGGFYFPGFLPPPLGFPKGL*RLWPPC PATFFFLYQISKFPFFFGKYQKNFFFF FFFFPESKSRSVT\RLECNCAISAHYNL
9852	23753	A	9925	309	1	YTPTIMLLGIYSNELKTNVHMKT*I*MF TATLFLIAETWKQPRCSSLSEWI/QQLW YIQT/I/EYYSVVRNIK/LMKTW/MKLK YILQSEKTQSEKTTYI*FQLYDI
9853	23754	A	9926	237	2	RWNFNFTQLILKCIFLRTKFFS*VSK*N FKYFLGFWFFFLRQGLTPVT\RLECSG TISAQCNLRLEPGSTDFSSASAQE
9854	23755	A	9927	244	1	KPQCLWRK*D*WHNTQKLDVEKGKPLIH YWWERKLV*PLWKTVWRLMR/NLKIIELP YDPVPIPLWGNYSKEMK*LCQREDSRA
9855	23756	A	9928	2	644	IVQVDQKIRLNIHCLQETHFKCKYTYRL KVMR*R*VYHVNIHQEKALVAIDGAYFR ARKITRDKERHY/IMIMGSMLQKD
9856	23757	A	9929	1	364	GTSGTRPINNTTVFSKCSSEKRT/R/TH LTLNQKLEMIKLSGGGISKTDMG*NLGL LHQTVSQVNTKEMFLKEIKSATPLNT* MIRHQNSLIAAIGKVLVWIDQ/TQHNT LLSQRLIWNKALT
9857	23758	A	9930	88	374	ILKACGPCPCGNPHPWGPL*GQGGLGLNP SKSPPHPHPRGDPTWGGTPIGDYGPKP KLPHGAGLPKKPCSSGGQNN/PKISGP
9858	23759	A	9931	384	2	LCSPRFFYRKIWGGGQSRLLPPFFWKP GGKDCFSPGVLDPPGEQAGAPCFP*KKI RWG*GAAPVVPPEEG*/VGRAPLTPKI PAPVSFGCSPALPGEGQSETPFFLKKKK KEKSEAMI PPPPGPRA
9859	23760	A	9932	32	359	IFFFLFFF/C*KGGPPVPQAGGQGPKT PPWPPIWAKTKPLSKKKKKKKGAGPP PPFKGGPPPLKKGEGPLLRKFLKKNNG ENFKKKKIWAGGGGNPREPPFPGGAR
9860	23761	A	9933	138	1	TGFFCCC*SFALVAKGGVQWCDLGLSLQP PPPG\SSDSPTYASCSC
9861	23762	A	9934	103	355	LAGQACCS*STSANRCVNHA\PGYANGR CDTITCILVFIRNSWLITPIALITMFCY HVG*VRPQEQAPGNRVSLSDLLL\PPVT C
9862	23763	A	9935	29	363	AWSHNAFLLEFFFKRELAFVQRGERENN FVSLKPPPPG*SPFSAPNPPKGGNKGPP PPQLIFFYF*/GEKGFSPYNPEGPKPP TLGKPGLF*NTKKICPQPRGLKKGQHI W
9863	23764	A	9936	173	363	PKKRPIISLKRAFNSNPGD*QKFLKRGL PPMGSQFKRGNYPYDNLEKLCPGGKNK GSG/YHYGL
9864	23765	A	9937	360	3	NQMRKNQSSKTGICKNQSACPPPKERS SSLAMEQSWMENVFDELREBSR**NYS ELKEEVRTHGKEVKNEK/NLDEWLSRI S/N*EKSLKDLMEKPKAQELHGECPSL SSQFNQLARA
9865	23766	A	9938	194	370	VSNFFFFFETEFCSFAQVGAQQQNF*L KAPPP\NCCLFPT*ASRVGTTGTCHHS WLI
9866	23767	A	9939	426	1	SQEFKVAVSYDLTMHNSNSSETLSQKE KTKQTKTKQKTY*EGRKHIKRCPTPLI

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						IREIQIQTTVRYHFTHIRI/VLLPQKQK KCWCRVEKLPVRC*WECETVQPLWIT VWW/FLKILNIKLPFDLATPVVCIYQME FSC
9867	23768	A	9940	255	16	RVIYNIYIMYILCIYTPSRLLEIGFHH VGQDGLDLTS*SIRLSLPK\CWDYRYE PPCVNIYIYLHIYLIYMSDGVKY
9868	23769	A	9941	206	355	FLQCHTAIKNCRG/WPGAVAHTCNPSTL GG*GGRII*GQEFKTSLTNMVEP
9869	23770	A	9942	3	402	HEELNPRSATSSPALVHVHTIAHVTF AEGCFQHDFFCSQPENRHIPLVFTTASK VRNIFYLLCRGRGILRFFLVCLKIDPAI PLMGIYPK\KSLYHKDTYIHMFLAAEFT VAKIRYQSKCPSTDD*IKKICV
9870	23771	A	9943	79	328	CIKILLKFLCLFCILPPCLNFFLRQSCS VARAGVQW\SLQP*PPRLKHTPTSAS*S AETRGTTHHAHLIFSYNFL*R*VSHVA
9871	23772	A	9944	321	414	VPSWAG\PVAHACNPSTLGGRGGRIT*G QEFE
9872	23773	A	9945	142	480	QEAKSFDSDSTTMEVMDKKQIRVIFL FEFK\MGRKAAETTCNIENAFAPGAAND *QMRWWLEKFKCGEESLEDEECGRPSE VDDDDLRAIIEADPLTTIQEVAKELSID H
9873	23774	A	9946	191	3	FFLPRGGGDSVFKKPKKKNFGPKIFPF CPGFPLAT/INFPQIFFFFFFF*DGVS LCHPGWNAV
9874	23775	A	9947	451	461	K*INK*KVKGW/RKEHHANINQKKVDVT IFISDNMNRKKNKITGDREGRIYIIKQ PIHQENIAILNVYVPNNRVAKYVK*KLI ELKKEIHKFTILVGDFNTILSTDRTR *KVS
9875	23776	A	9948	186	405	NHTLAISLF*PYKP*AILKLGIRKERR LVC*RDICALMFITELVTAAKLWNQPKC PSTDK/WKMWYICTMEYYS
9876	23777	A	9949	18	412	PEFRITITLPEKKNLL*LTN*VSKFSGY NINI*TSVAFF\YSNNKISSETGKIVPF TILSNRMKYLGM/TLTKNMKDLHTENYK MLRKENEYQMGNMGSWILKINIVKISI LHKVIYRVKFLSNFNAILLKK
9877	23778	A	9950	1	396	LAFDGRAERLKTGFHRTQDGLELLTS* SVRLGLLKCWDYWREP/PVPGGLWD
9878	23779	A	9951	307	405	GIRVRR*PQGLRPPNPDALVFKKMWPP PTN\PRGWGGKGWEPPQGPQDPPQAAP GFLPETWRGPWNSLPTRGAWPPNSNLPP WPPAPSRHPAQRAPGPSTAAPPPGGGGE GWDPPGRV
9879	23780	A	9952	2	402	YGRPKEGGSLRFVVLTFPGPKGETPFFL KTQKITGGGGGGP*FPLPRVRQENSFY SRGGGFN*PKRAPCALTWKKQKFFLKK KKNTPOKPKKLPKCRIQY*TQK/SSSLF MGGTPGKRQ
9880	23781	A	9953	249	1070	SSFISRFYFICIYLFETRSHSVTKARVQ CCDYN*LQPQPPGAQEILPLQPP*SAG\ ITGVAENTPQLIFYFFVE/SGGSTHVAP RLALNSWAQNIAL/RLPKVLYFTF
9881	23782	A	9954	75	396	GFKGRKRGPLPLNQLKTLNLSEKGLS KANTGQKLGLL/RPVSQVVPNGKFLRE

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						TKSAF/PIEK*VI*KQNSLIPDMEEVLG V/WKTKKYSHNIPGLSLTQKRVLTLF
9882	23783	A	9955	181	458	RLWNDGLYNIFDLKLQ/SIHV*SLLLLF ILEPESHVS\RLECSGAVTTCCSLNIP GWSDSPQAQFQVAGTTGVCNPAWVPSAF L
9883	23784	A	9956	67	430	LAPRLIYSPIKFQWSFMSVRQIQVQSLA IGNFHNPRLPILICHCYAFHRILLFQMV RNFILYSISISANKQESKICILKYILLYI NLRNWLGTVAHAYN/PSTLGV*GGRIS* AHEFETSQGN
9884	23785	A	9957	77	422	LPLALWASCRPQLCLDTDFIHGPPTSGA ASQFLCFQTMQPPTCSSRLYNL*PALV LDHTTSNVVCFRSP/SFFLLPLPLPPA PLP\FFFFFFFDRVLLCHPGWSAVARFQ LTAAS
9885	23786	A	9958	3	422	LHSSLVTEQDSISKKKKKKKIFLGGTKK GGPSLGGFFFGPPGPFKIVKKKRGALIG FPPFCPKKKPKKPLFFPKPLGKPPRKKG F*IGEPWKT/EGPGFPKKNFVFFSPWG GNFLFPPQKPGGKVGKILLQPKKPPGK G
9886	23787	A	9959	370	2	PFSSWVANFREGDGEKCSVLQGI RFCMF CRYINVTPLVHFPPFISKGTSTFFPLYFF SPEVM/HFP*LPY*FGWALLSRF*/MSL L*LFFSKFFFPSTFFF*RFQFHSSPRLK CNGAISAHCNLCPL
9887	23788	A	9960	256	2	AWEETAPLHSHCLGNQARPWNHRHAP\ P*LIVFVFSVETGFHHVAQAVLELLASS DPPTRFNLLSSWDYRGLSPQPMRSKSAQ EG
9888	23789	A	9961	269	3	HRQACGQVRSPIQCWWACKIAQPSLQIV RSSLK* I*SPYDPVIPLELVIYPRELKT \SLHTKTCT*RFTAALFIARRWKQLKC PSIDE
9889	23790	A	9962	268	324	SGTSLH/WIFS*VGIEITMWLKVDPQTK KISLRSAAAIKYFLQATASIIIRRAI LFNNRLSEQSSITNTTNQYSSLIIMAI AIKVGMAPFHF*VPEVTQGSPTVSGLLV L
9890	23791	A	9963	341	2	ITFLPTKIIRQSNFKTGKRKTDSDNLR HFKREDTQMANKYM*FI*KMQI\KTTMR YYFISKRTTISRKTSNIQC*DTWSPGTF INCLLECKMVRLLWKMTWQFLTVEVHIHL VY
9891	23792	A	9964	250	2	YHPVNLYFKYISPIDV*FGCFIYIFDYP LCSCFSLHPLVYLQ*L/LFFFFFFEASHC VARLECSGVVSAHCNLRPLGSSDSPAS
9892	23793	A	9965	3	334	RTLRRHHIWLIDPSFE*HLSCFHLIAIVN SAAINIPC/HSYV*THF*YS*MYRGRTA GSYAT/SMLNLLRNCSTLLHRNCTF*PF YH/WE*VPISQSCQKLDFFIFLIIAIS EG
9893	23794	A	9966	179	352	NQE*TEILNRPMNSNQIESVIKYLPTRKS HRPHRFTAELYQTY\ILLKLFQKVEGEG LL
9894	23795	A	9967	2	350	THPSINSFIHVFIHASMNSLIHLPTHSF SIYLFKTSFIHLFIHFFSFLFLRPSFT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PVAIYSFIHPFTYSSIH*FIYPCVYSCT DEFTHSFTHAFIQHLFIH*II/IFIYSF ISFLFF
9895	23796	A	9968	228	558	CHQLRQELAIFTSFVILQLFSGHLDVYM QAWAQRDPDKYEYDNK*FIEIKKI IQFTL ISKRMK/YVGINLTR*VKDLHNENYKTL MKEIEEDTSEWKDISCSWNGRINSVKT
9896	23797	A	9969	196	2	DRKVFFRPLFIIFGLKKKIFPLFWFFPS /IRGRG*IFFFFFFFFETESPSRLECS ETISCHCTP
9897	23798	A	9970	245	1	TQCDMCFVIYTHIYISHICYMVYIYIHT RHTGILFTPKREKNSNTCTCATKDNP/ CMTLC*/HKRQTHHTHTHTHTHTHT
9898	23799	A	9971	163	380	NHRRQKKNGR/HNGNKYKTVTKMINSNP PITRNNLVNGLKTPIKRQLSDSIKKQ YPSIYCL*KT/YLKYKD
9899	23800	A	9972	328	1	AKCGFLKKLNIELFNSIPGHSCKT*TM FAAALYIISKYKQSPSCSNDE*MNEIW HILTIIGYSAVKKISWG\RWMNLENIARL SGRQRGHILQDSVDMKSPE*AIPO
9900	23801	A	9973	200	3	MASKCSSERKSHR/SITHNQKLEMIKLS EEGMSKAKIG*KLGLFCQ\VIHVVTAKG KFLKEIKSATP
9901	23802	A	9974	111	517	NLEQPLIKRTIANKPIKKINTTILITIT NVNGLNLT/LTK/RQRWSD*IFKNQDPTMI /C*KKN/HCKYKDTNTLKI*KNIYDA NMLTQIKKKAGVAILI/DKIDFRA/TDI TRAKEGHFIMIKGSVHQEYVTTILNVSAH AS
9902	23803	A	9975	342	3	FLATKKIFFFFVFPPQGGPPVLVAPFF WAFGGGPPKWAPKKKFFGPRGPPFENFF F*GFFFFFFKTGGFFFLRFSKKVFFFFFFF SETESCSVA\RLECSGTISAYCNLCLPG SR
9903	23804	A	9976	13	326	ILDHSNRPSSTLKTNPAGKDVEQKQFL /LCCW*ECKIVNYLGR*L/WQFLTKLNL L*PYDPEILLGLIYQKELKTCIHTVACT *MFIEALFVIAKT*KQPRYSSVG
9904	23805	A	9977	74	396	LAPRTQPLPCSPAPLRQCHTQSLPFPFL LRLIFYFFCFLKTRAHSAQAQAQ*RDH GSLQT*TPTLACTPASA/VARTTGTHHH AWLIVFFL/IEKVSHSLVCDKT
9905	23806	A	9978	287	2	QPHNSSYTQIFTPKIIKTTPPNLKQNN TPIKKTQ*FP/PSTNP/SYPSTHPPT HLFIYPLIHISPPSPTHPRIHPPTYLS IHPSTHPSIHPPSR
9906	23807	A	9979	97	332	GNNDLFLYFFFLETGSHSAQAQVQWC DHSSL*PQPPGSSGPPISTC/RLGLQAC MCHHAWLIFNFFCKGRSLFGLLR
9907	23808	A	9980	168	2	STWLRWDYWKTFFKTSK/WPGTVALTY NPYTLGGQGRHIT*GQEFKTSANLVKS
9908	23809	A	9981	267	1	LKRERR*RRAN/SKTSRRKEIKIRAEI TATENRKPIEK/SNKING*FFEKTDK/I DNPLERLRKKERD*ITKVRNGREDIL*N NDLIKVKKD
9909	23810	A	9982	230	412	CHIYLC/D*PIDGIV*CHIYIYFGHKHT HTYTHHTHTHTHTPTC*VSKILLKKRR TCSVCA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9910	23811	A	9983	229	415	SYVFCHIRFCPLDSLKEIVA/SQVQWC VSVVSTT*VAEAGGSLEPRSLRPDWASQ RDPISK
9911	23812	A	9984	2	288	RGYDSTSSAYTVGHFT*EDKATITRLSG KENVKHAGGETLRRLLDVYP*TORIIDS VGNLNSA\SAMM\GPPRLPKVLGLQAWT TMPGP*KYIHIFF
9912	23813	A	9985	246	3	FLLDYQYCALCCHCFLEFNCGHFNIL LGGVKHTKFPKYS*KFVS/LWDAVAHS CNSSTLSGLGWITRGQEFETSLANMVK
9913	23814	A	9986	342	1	FLNFGLTGFFPKGPPKPLGLRDGALPLD PPQFLGVFKRGAFLLGTQ*FHF\LEGFK FWFWEPKAFFFF/CCETISAHCNLCPL GSSDASAASAWIAGITGAHHYARLSRRL RQQN
9914	23815	A	9987	330	1	NRPLNNLVMASKCSSERKGYTSFVLSRK /LRKMIKLEESMLTVTG*KLGLLCQT /VQVNTKEKFLMEIKSATPGNKGTVTKS NLTADREKV*VIWIKNKNHKLPLSQ
9915	23816	A	9988	209	2	IKGSHFPVLI*YRKIIIFGGVKGGGF YSY\LFFFFEKGYHSVTQLKCSGMILAP CNLCPLGS*DSPTS
9916	23817	A	9989	256	357	QHRWMNTEMLNYLC*IIYVHF/HTHTHT HTHTHTHTHTHTHT
9917	23818	A	9990	263	1	IQIRVFENSHLWPSYVHFPHGHSYLFCS L**AFFRH\G*FVLSVHFLKIFLNLKKI FFETG\SHSVAQACSGMISAHCNLCCLG SSDR
9918	23819	A	9991	3	368	SLDPRRSRLHLAKIVPPRSSLGDRARPC LLKKLELFFETGFCCVAPGVRWC SHGP LQPRIPG\SSNPLTSAT*VAG\IAGMCY HTQLQLAF
9919	23820	A	9992	294	391	SGTVAHACNSSTLGGRGWIT*GQ/ESQ TSLTNM
9920	23821	A	9993	317	3	TDKELLRLRDEQRKCFVEMEFSPGKHAMS NVDMTKDLEYSINLVDKAAVELERADSN FERSSTLGKMLSNSISCYKEIFLERKSQ LM*QIPLLLM/FKKLPQPP*PSA
9921	23822	A	9994	193	395	IFWITCCSSLSVLAASPTFMLWRQLLS LNLNMN*QDHSLSQSLIQSKSATLFSVT AERGDESAEEKLEASRSWFMRFKERSCL HNIKVQGEAARTDR/EAAASYPENLR/V KDEGGYTK*RIFVVDIEAFCKWTMPST FIAREKSI PGFKVSKDRMTARCGRSL
9922	23823	A	9995	82	420	SFLWKLCPRGAAAYVRCVSA\LLEDVSO LGYTGVRDPIEEAVSPFSELKRCRETT AVFTAVRQGHLSLQK\FLLPFVQLCPAH RGGV*RQ*ALLCCGGLSPVQAPLPLCLP TQ
9923	23824	A	9996	376	1	CGRTDAPASTSPYAMTVRFLRPPQCVL DGLHNCPARAPQEONSLGEVDKRGPREQ TR\PATAPPRPLGSPSWICPGDW**CR NSLQGFSLAASVARGRDWALAGLPATVS ARFQEQQKMTV
9924	23825	A	9997	495	982	VOKFLRPNLAPKKHQRKLAPNSLQGRLR SLPSPTVWCTMAPPTGVLSSLLLVTTIA VCLWRMHSWQKNHW*ASFKKTHD*TGLA EP\SCARKQCSSEGRYTSNAVISPNLETT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RIMRVSHTFPVVDCTAACCDLSSCDLAW /WFEGRCYLVSCPHKENCEPKKMG
9925	23826	A	9998	401	341	IASKCSTERV/SRSHTLKQKLERFKL*E KGM/SKNEIGQK*ALLYQ/VSQVNAKE KFLKEIKVD\LHAQMIRK*NSLTADVKK VLVVKIDQTL/PLGHSVIQSKALTLFSS MKAQ*GEEAA*EKS
9926	23827	A	9999	30	393	DTTILKLRQLIIGAVATKHWSEKSLTS LNLNQKLGITIKLTEEGMLKAKKGQKRG L SCQTVGQVMN/SKEKFLKEIKHAIPGNT *MISK*NSL/IADMEKVLVG/WSKVIF *DQTSNIP*SQN
9927	23828	A	10000	133	1420	BQRRLPVTGPVASLQTLCCFLPRRGCSH G*ESAATHPPGPELVLLLQGH*AGYLQ /DFG/PRTATGSPG/PAGVQPGCLVPQ LSRAAAAG*PDPT**GAIFS YHCKALRA TAARHCPPGC*WPG/PAGSPPGTSRPLS HPSSPSPWTVGVSSFLNLVLCP*ASDA QGHACYPGVPALAGQGHDSAGGRLGDP GHHWQQAALHG/DQGP PGHQAAGTQPS AQGLGC*ATHPGEQG*VGYQGLPAG*GR SHPRFPITVRPMGRSCPYATVRPGPGSQ GQTPPGLV\PRGEAGQNP GGAAPGLSCI QEVTGRWWW*GKKPLGHYP PCGAVRCPS S*PHPD TMFKGTGREGCLPPTSPVGVTG QMS\EGSRPCEWTLT MSPWGE*SPRASC AMLHFCPGRVGGYHGC PPLHHMG PQST AGQAGQPHTLDIKAS
9928	23829	A	10001	1818	6682	IKFPEAEEEEIQEVLVLLFRVAEEKENP SRVGN SQREYENQVVLYSICNQLRYRNN L/RHVKKDERGYEEELNYSRDHMLLYP YRLLDIMVKGFSITPFSYTGIMENIMN SGHNFTAADCLRLLGIGRNQYIDLMIQC RSSKKFFRRKTAGDLLPIKPVEIAIEAW WVQAGYITEDDIKICTWPEKCATDKTV DSGPQLSGSLDYNVHSLYKKGFYLDV PMSDDSCIAVAPLEGFVMNRVL/NFDYF ETL LYKIFVSVDEHTNVAELANVLEIDL SLVKNVSMYCR LGFAHKKGQVINLDQL HSSWKNVPSINRLKSTLDP*KMLLSWGG GESRRPVQEASSATDTDTNSQEDPADTA SVRSLSLSAGHTKHIAFLFDSTLTAF LM MGNLSPVQSTGEGEAQRYFDHALTLRNT ILFLRENKDLVAQTAQPDQPNYGFPLDL LRCESLLGLDPATCSRVLNKNYTL LVSM APLTNEIRPVSSCTPQHIGPAIPEVSSV WFKLYIYHVTGQGP PSLLSKGT RLRLK L PDIFQSY\DRLLITSSG\HDPGVVPTSH VLTMLNDALTHSAVLTQGHGLHGIGETV HVPFPFDETELQEDSC\NMGVHKALQIL RNRVDLQHL CGYVTMLNASSQLANRKLS DASDERGKPD LASGSDV\NGSTESFEMV IEEATIDSATKQTS GATTEADWVPLELC FGIP LFSSELNRKVYRKIATHGL*EKR AFKNLLHSSRKLSLQVLNFVHSFQEGAS TLDIHTPEPSFSSLLSQSSFADMGVPLPA KKFN/SLKIVSY
9929	23830	A	10002	439	1135	MAVDFYNFVTKLVVTTGYLRISFLAYKF

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						FSFPFLDSLS/LLSPRLCSGVIPASLQ PLLPGFKRFL/CLSLPSS*GYRRAPPPC PALLYF*VETGFHHVQGAGLELLTSGKL TRLGLPKCWDYR
9930	23831	A	10003	216	572	LTIVSIFTAKQSVTLPIICMLEMRKWL NDTSAF/PII*KVLFPKIFFFFFF*KG VLCPPGGREGAQFGLTKPSPSGLKEIFL PNPPGGWKQRRVPPFAGYFCFFIKRRVS LLWRGLPN
9931	23832	A	10004	3	354	YSNNPKDRKGETGINEKTNNKMVDLSSY TSVITLNF*ML*/D/KIN*KFKVSP*KK PTLCCLLETYFKYGIGGLKVKRWKKI*H ANTIGKKTILVAILITKQTSLS*YPNKE EHIYLIKE
9932	23833	A	10005	187	455	ASTHYSLGVRICIYIPGCIHPGEKSQKC NTCGKNSTQKPELVN/HR*LKGHRCKM* NEGGKTFTRVQSL/ACHKRVYTERKSYK C
9933	23834	A	10006	134	456	IWNPLPGKPCAWKQVTSDLISPDALFIN AAIHSLSFFFFFFFETKFLFVPQVGGPWH NLN*LKLPPKL\SDFLVA*VSKKVGIT GPPHHPGLVIWGFKKKGSPMLPR
9934	23835	A	10007	210	451	CYYTIQTTEQPAANDSMGLIKPHVSILTL NVNNLNTPPKRLGVADWIK/TQDPAFCC LQETSLTCNRTHRFKVG*/WKKIYH
9935	23836	A	10008	169	462	YPCWVDMAKNTSYNKCWQGCGEIRILPH CRWEYKMASPLWK/SQFLNK*NMELP*D LPIPLLDIDPKWKGTGVQTKTCR/RMFI AALFPTSRS
9936	23837	A	10009	490	724	EMPP*FMEKNFLAPGGVTPPGVNTRV NPKTAFDPKRSSSPFLEKSQKPGLIBGL THLKTLLINPLKKDESGEIPVLF
9937	23838	A	10010	306	588	KQFIRAFIEMSWLTPVIPVLWDTKADG SGIRDQPSQHGETPSLLKIEKLAGHGGA GL*/SQLLERLRQENHLNPGGGGCSEPR SCYCIAAWVTE
9938	23839	A	10011	473	53	ISLGQDSTDISTINIPMAFKLSSKRKS HMSFSLNQ/L/EMIRLS/EEAC*KPRS QKLGLLSQS*PSCSKFLKETKSATPVN TQMI*K*NSLITNK\LKEVLMVWIKDQI KHTISLRQSVI*KALPLFNSMKAERGE ESAKC
9939	23840	A	10012	184	455	FWLSLIKPLSSVTQKKINRET\ILLTT KKKKKDCNFLEGGLLIGGSVCRLVYRHY ATLYSVFCVDSSKSERGSVDPTQVFVET *DKCFDY
9940	23841	A	10013	203	453	KEELYISRERKSSTSLLNQSQK*LIKL SEQAMPNANIGDRLKARPLSPNSHLIKT KQKFLKEV/KCATP
9941	23842	A	10014	237	483	TLIRYIILQGLFSYIPFFFFETESRSVA QAGVQW*DLGSLVPGSRHSPSSASQVAG TTGFHY/HAWLIFCLFCATGS
9942	23843	A	10015	157	875	DDPVRGRGEESAMPSSGRRNRSVSSSWV GSMAGITTIEAVKRKIQVLQHQADDAEE *AEHLQ*EAEGKRWAWEQAEAEVASVNG RIQLVEEELDCAQECLATALQKLEEAGK AADESERDTKVIEIWALKD/E/EKMELO EIQLKEAKHIADEADGKYEEVACKLVII

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EGDMGCTEERAELAESRC*EMDEQIRLM DQNLKCLSAEEKYSQKEA*CEKERKIL TDNLNKSPMR
9943	23844	A	10016	579	30	CGISTKKNKWMIKQNSSELSTCVHNQIT LHKIAMATQWG\KNSFFNK*C/W/BN*V ST/CKKIKLSPSVTCTI*KQYLKWKYL NIKI*QTS*IS\NGGKYDIGLGTNFFLQ KTKNLMSFS*L*NQMHKEQIEKWDYIK LQNFCTSKKEFGVMSPKKW/DEIFEN HIFDRS*FSQYINNV*NTKSE
9944	23845	A	10017	44	228	EFVCRVRGLWW\CVVLASQLLWEAEAGG SLEPKSLRLQ*AMIM\DTTPPW
9945	23846	A	10018	471	40	PGEGRFQQTFRPPFLPPWPGKGGPFKK PKKKKRKEMIKLS*KPRQANQ*LGLLCQ /TSQVVNAKEKFLKEIKNATPVNTQVR KLNSLIADIETVLVVGTEDTSHNIPFG QSPIQINILAVFHSMAEQSKEATEEKF EARS
9946	23847	A	10019	217	486	KKIS*PVYLSLYLSIYLSVCLSVYYLSI YLSIYLSIYLCIYLSIIYYLSIYLPV YLSINLLSI/CLSPIYLLTYHLSSYLLS YLPTYLP
9947	23848	A	10020	327	1245	TENQQGV LALAALSKIRMMPTRLKWFNL IDYTKFCEAFHVFKKRRKKKINKNIKQL KMPLTKRIYLAFTYSTQ*QONTH\FFL SADETHGKIE/HVLGPKTRHNKFKR
9948	23849	A	10021	329	490	GESPTDNHCRSPKSQVEKVIYTFETES RSVTPAGV*WCNLSLQPPPP/GTSD
9949	23850	A	10022	3	394	YRVLEVLGYMLNIRFVVLGCSSCGQAAQ FREGSRCTACRHPAHTLHAAKMSRRKV SSAKCR*RETPKKRSARWSAKPAP/QSE TKPKKAAGKDKSSTSS\FSSSSSLKAEK GGKEKQAEVADQETKDLSE
9950	23851	A	10023	448	477	SQVFETSLAS*MSKNIL/WAGTGAHTCN PSTLRGQGGQIT*SQVFETSLAS
9951	23852	A	10024	198	455	SLKTNRRREIPEDFHGQPCGKLVHSEKPR VRMGQTESKYASYLSFKVILRRGGVRA S/TRNLIMLFQTIEQFCLWFPE*GTLDL KDW
9952	23853	A	10025	469	26	PPRAVQPPFLPSSSLHTCVPLCRTVFSA TSRPDSLLPALQVSAKMSPV*SSLLLP SLGQGFPMASIAAPRL/PHRSLRSCVVA AHSRAELDRHEAFLQCSLGQWPRNDFLF SFFRDRVLLCHPGWSTAA*S*LTASNS GAQVMEFQ
9953	23854	A	10026	222	489	KKKKKKKKFCFIARVKSNGAISAPCNLC LSGSNYFPASTSLVSGNTGACPLARVNF FY*NL\FLVKMGFHHIGQESI
9954	23855	A	10027	313	2	QDWEISKLYSYCHS*VRRL/IFLKIRLS LYYILQHSNLNCNIIG*LQFESCYIKLAG DKIAFRFLTKTNHQLGLVAHAYNSSTL GGRDGWIT*QGEFKPSLANM
9955	23856	A	10028	49	388	TPKIRGVFPFKGWFLGVGAFPPQKDI FYFPRTPMGTSLVSPGKKKKEV*RVLY GLKKAKKIFVLKVKFSHKRGFFGEIQFK KLFWK/HLKRNPPPKKKR
9956	23857	A	10029	394	231	GRQIASAQEFKTSWGNMAKLCIFI*RDR VSPCCPSWS*IPELKQSACLSLPKY*DY

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						RC/RNTTPGL*HLLFRCLLIILPSYLFCKSFKLLYMDI
9957	23858	A	10030	265	2	HDNMRGSDYFPASNGLAVPFKRQVFTIASNFLEKSPRLAFT*LVQD*ERKWAG\PVAHTCNPSTLGGQGGWITRGQEFKTSLANMPKP
9958	23859	A	10031	235	413	KAGKLFFFTETITFKKGKAGGGGSFLKPHLFGPRPGGNHRVRIL*KRGFYKMGRRVVLKSLPCDSPPLASQKGGVSRKSPPPRPFCPF*RLFP*KKAFRLFIPKKV**ALV/SLFFIGEGKTLFFFF*DRALLCRPGWNAVAPSGCLKLSSCLSLLS*DYKHVPPCLAMF*KFF/CRN
9959	23860	A	10032	167	424	GREFDLRMGHMVKPPLSFFFFPSETMSLSVTQAGVQW*DITALSASWTPVISDSPVSASRVAG\IGTTGVRHHTQLIFL
9960	23861	A	10033	252	3	VEGCLSSGVQDQPEQHSSETPSLQKKIFF*IAGHGSMCL*SQLGRLRWEDHSSPG*SCSEP*SCHCSPAWE*DPISKKK
9961	23862	A	10034	175	492	CPTCPFVWIPLCSEQPVQLYMVVHTHTHTHTHTHTHTHA/HLLFSLSFSFLRQGLSLSPTLWRSGLM/CGSTQSQSPRLKQFCSPRYSRG*GWRMA*/DPGGRGCSE
9962	23863	A	10035	200	448	LYLHLVQLSPLDFPTPLFRVPCVLSLCLSF*FP*VCFVFLVSLGLF*GRVLLCRPGWSAVVQSQLTAD/SDFPVLKHSSCL
9963	23864	A	10036	229	463	MILGISKISFSLAITLANFPPTLNLFIPLDTGSCSVAQADVQWHNQSL*/SELLGSSDPPTSAS
9964	23865	A	10037	164	422	GLSSQLTDGHLALLRVGSEVGSREESEREEAGREREGERRDSRG*RRERREESGAREEREKKEKRER/ERDREEK
9965	23866	A	10038	1	490	PNQIQNAVLIMISFSICFVSVIFFKSEIYNGQPKFKSFFFF*DESCSVAQAGVQ/WCG/LQSQQPRPPG\SSNP\PTSASGVAGST
9966	23867	A	10039	255	446	FFLRQSCYVAQARVQ/YAIHRCSTLQLPALASSNPSALLAPRVAGTAGMQHHNQL*YFFRIHS
9967	23868	A	10040	157	390	DHTCPPPSTADYRLS*FLYFLLLLFRRLALPPMLECSGAISAHCTLCVQETRETDAAHFKAARTIRAPHPAQLTIAFQVQTHVYQDGH/DGSWWCDLRTHPPRS
9968	23869	A	10041	290	30	TLKKRKEFSSVLCPRGYIVLLLLVHQFLFFQTGSCSVTQAGMQ/W/CDQSSLP*TPG\SNNPVSVASQVAGPTGMHGFHLHTEYESRGPP
9969	23870	A	10042	190	929	NHRYISYLTRLVKIKNFANKSWLESLSPTLKH*/W*CK*V*SLWKTVWHYLVNL\KDDLTFDPAIFFLMIYLIEMCAQVHPEIYARMFIAVLFEIFKHQ\NNPNKLWYIHTRESYKTIKIKE
9970	23871	A	10043	457	724	HFGRPRQVDCSSGVQDQPGQHGEVQSVLKL\KKLAGHGGAHL*SQLLWRLRHENHLNLGGRGCSEPRWCHFTPAWTTQDSV*NNNNNN
9971	23872	A	10044	111	429	KPDEDTTGRENYRPVFFTTNDANLSKIKCMYPCISVH/HVNMYGKIPEMMFT*Y**

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						*LFLSFFFYEMESGSPRLCSCGVISAHCNLSLPASSNPPPGFPR
9972	23873	A	10045	30	220	LGVLYKKNSVFNKCYN*ISTWKR\GLDPYLTPHTKINFKWIKDLNIITKTLC CSWMKTKA
9973	23874	A	10046	203	361	TYKLLVIFIVIDHF/LFSFLSFFFRDRV SFLPRLECSGAISTHRNL*LPGSSD
9974	23875	A	10047	198	358	IQRKCF*TTTTFFEV*SCFVAQAEVQYCG SPG\SSNLPSASEVSKTIGVVILPS
9975	23876	A	10048	270	272	RKNQRFFKIARKRLNKMTRISPLISII LNVSGLNPLKRYRLAEWTKKKK\DP II CCL/QKTHFAG/RDIYRLKIKGWKKIFH TNGSQ*QRSEFF
9976	23877	A	10050	256	1	GVTTNLYFWKNFLNPPFLVKKCENCPI NKVFP*KPDLKKTLFFSKKKFCGV/HPT EKFFFFFFESLALSPRLQCNGTILAHCN LR
9977	23878	A	10051	112	359	SKVSEPTENEVEHNLKV*SFILPLKQY SM**QKKNIH\ISFYKK*ELTWPGMV AHACNPGRLGTEAGRSPEGQEFETSLA
9978	23879	A	10052	346	2	RVSSYTLITLNLNRLNVALKRYRRLNGF FFLKKP*PN\ICCIQKTNLIYKSTYSLK VKGWNH\HANGKKQAEVAI\LFISD KKDFKSKIVKRDKEGHVMTKGSIQQ*D RTIL
9979	23880	A	10053	376	6	TRPSQHPDFILLNKCLLEATPFLVICY SGHRKLRPVAPP IIRGSKSQIIPMPPAVL PRWHLSCLSFRIPSSFF*LRLPRLCKSR /SAWGPVSPHLPQFLFFQAISFFFL*D GILLCHPGWSAVA
9980	23881	A	10054	102	347	FLSFFVDGKLCLEAKIWLAPAVFIVTR VLLLLSTL/RQVELRNILCSNVHIFH LYFCIYLSAYILQTMSLY*HL*YHSNV
9981	23882	A	10055	251	51	ISLVNWLFILENMKLDPLYSPYTKINIR /WQ*DLNVKNGTTKVLEEN*GTIYVMVG WKRPIACQQPKS
9982	23883	A	10056	169	342	SQKQYSTQNVFCFVLFLETRSHLV\TT LECSGAIMAYCRLDLPGRHPPTSAS*V DG
9983	23884	A	10057	1	586	AAARPAQKGKARPGLLLRRGRVVELRAGF LTAKGAFRWWLSQKHVKMSYPPQSRGCG GGMGAAGPPSLTVHQELCGAYSPDGTTE ALPLASWPRARPSAKAPAYDTAKLPAL ICGSRRPPGVNPGASSLKPGACVSEGA GPTGTLESAGSRPPTPLPPV/CPCGPP ARADH*FCHVTPQCR*/PPRPS
9984	23885	A	10058	393	43	HARPGAECERPAEGEAARADAFSGRHAC PHSLYCRL*RGFFVHKLHLNKA/RLIKR RKADNIKCWQRCGAPGTMHC*WDYETM GLLEQTVFSFEIRSHCAAQAGVQRNNHG SLQEF
9985	23886	A	10059	228	466	GLLHGPPPIYDLPEPVSTPSLYHPPIVP *ASPLGPSAILTLPHSPPPA\PLFSPP HSVLGSSGPRSLPT/SPHLPTLTPH
9986	23887	A	10060	293	9	DILQFYTFSPIQ\CPVYILHL*YISLQR L*FHQKYLIGIYFIETWSCSVARLECSG RITPRCNLNFPGPTYPTTSASGVAGTTG VCDFLGLPWSR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9987	23888	A	10061	199	428	TAYCRTLP LKKS NPTTISGS FFFFL ETGP RSVPG* RAGG\DLMAHCSFDLPGSRDSP ASPRQVVGATGCPCHHPWLIFE
9988	23889	A	10062	191	2281	LQTRGKLFKYKEKGICTFLHRSEITIGK QWKEAVCPPTGQAQSQGGLDPKSREALR GGHGFVPGGGVCGHQEL*LHSDGLKAVH PAGSEPSDPGGVQAAACQDAATGGTPLQ PMPETARGC/TATASSREAGPGMDP/RE A/GPEAWQLGKARSSWGSSTSGGPAWV FIRDTPSWWGIPGTVSPAGPRCPPTTR PQWEQLGSGRPG*MQTTABETNAAPRAG QERTPSRGPADPGVSQHVLSHRSCPK CERRSVPPNG\AGPTLWTELHPSDASVS ALTPL*GDVEVGPGY\CEGYIKPGRRT QHNWLDLDRPAASRTCRKMLELPRV*F LLRLPELAETYSSTPPACAQRPRGTGGG /PPQRCVLMMSGSHQGGAS*KGRDAPSLG SGLERPREGGPGWLS/RQPSPHAVQPC HMLCLGPAF*RGRGARGVPVVRASHFP FHGAAWWPGDHMSQP*WQMLSRPARGHR PSWQVRRQCTVLGALKPGLPDLKCPGPT AFLPG*GVS/BEENGQIPNVSTQLYLQNL PLPREQN*RRFPRDLSSGGAGPGTG*CG GGGGHALSPTPSRRLRAHSDNSWAQPL CCWMPAASGC\PGICNGVPPVAAS*QA AA*TPPWSEGLPAG*QPSAHCVRTRV PGGRI PHLLAQAVPPDDRAFPNCQASGQ LLGVHSRPSLSAAGCRQPLAVSGIGCNG VPPVAAS
9989	23890	A	10063	65	453	ISREFLFLETKSLYIMLKGSIQQEDIIIF VNIYTLNTGAPRY/IK*ILLELKRQIES DTVIPEDDNTPLSALNRPSRQK/VDLIC TIEQMDLIDYRTFHTASEYLFSSAHG SFSKKYYMLGHKICLETFLN
9990	23891	A	10064	100	466	LGILPLQSRPSGPGGQCTPTLPFWVSLP LPVRGCFHLHCWCLPYSGALGSPCHTGL VCWHIPCF*CCGVSP*R\SCLEVHLYTH THTHTHTHTRFVLM*MRTPLRKGRQ VMRLCGGGGRA
9991	23892	A	10065	226	377	GLAGSPCISGSVSFCSGCIY\RGHGIMF ICNDCKVFRFCKSK*NCFKEHNP
9992	23893	A	10066	292	458	KVSSICLKMSFLFLFFRTGSHCH*KVS SICLKMSFLFLFFRTGSH/SSPRLECS GMIIAHCSLKLLDSSDLTASAS*VAG
9993	23894	A	10067	252	36	TGFNPLHFYYYYYYY\FESKCSHAQ AGVQCCDHGSLKPQP\PSSSHPPTSAP* VAGSRNAHQANSTAWPMVS
9994	23895	A	10068	56	481	GILKNCHNLMIKLERMRSCVLMGEQRK/ WIY*DESTPGEDTVNTVEITINDLEYFI NLVEKTVA/GVETVDSNFERGPTVGKM\ IVCYREIFHEKKSPSMQQL\YF*KFPQP LQPSAATTLVS*QPS\SKQDPLSARRLQ FTAGSD
9995	23896	A	10069	263	435	HFSFLSFFF*KTESHSVT/RVEGRGGIS VDCKLCRPGSRDSFASASRVPGTKGISQ GRG
9996	23897	A	10070	116	474	RGAGAWGVSGRSSPPLSALPIQPPPHLS TPPPLETP/PPVLH*PLKDLGGWGALLA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						Q*RLPG*HSPKKKKKKKAPRPPYK*GP PKTPVDPPDGPFLLDPPLFGWPPPP\VFLL PGERPPPL
9997	23898	A	10071	159	377	KSHMPLTLNQKLEMIKLSEE/GLMSTAE IGQKL/GLLLPNSQVVAKEKFLKEMKS TSPGNT*TIWKPGAVADA
9998	23899	A	10072	180	473	AIETQLLSRPLCLWPSGRFPDAQVANIR VRVAV*GNPLR*VGPAEPGEQRSPWGF PSIS/WDISPTWSSASPPGLSADCKFT CHYRCRALVCLDCCG
9999	23900	A	10073	98	440	GQLNKLSGPYPENVGTYLPLVLIPLAQP VIYSTIFAGTLITALSSH*FFT*VGLEI NMLAFIPVLTCK\INPRSTEAALKYFLT QATASIILLIAILFNNILSGQKKKKKGR PF
10000	23901	A	10074	358	404	PCLYTYHLHNSNST*SLRLVSIIMEIVT SNLHRTVPHSYTPPTQLSINLVMAIHL AGAWIISYPSMIKNALVHFLPQGSPTPL IPILVVIETISLLIQ\PRPLAVRLTGN TAGHLLMHLIGSATLAISTINLASTLI FTILILLT
10001	23902	A	10076	3	419	KWRKKMWCLQKMEYYSS*KGKKLLSHVT IWMDEEVMLS/EIS/SVTEGQILFNST YV
10002	23903	A	10077	335	414	DKSPF/D*RFPLPPNSNGFLVKMPSPVK RLPFFFFIFPFSFFFFFETESRSVT\RL EC SGTGLAHCNLRPLGSRDS
10003	23904	A	10078	279	1	KDTQLPFTQFFETGSCSVPEAGVQWCD HSSLQPPPP\GSSGSSPLSL*VAGTIGM LIFKIFSRNPLNFFFFLRLWLSLSPDWS AVARSWFT
10004	23905	A	10079	397	3	KSSSLFQNLHWANSSTYSHLIPTLGYIL NHGNQFDPTL/RDKM*NFECTIVCPHY ELPSLEQW/VSLGSLNYDTILPLDLFCK RQGWSEIPYAQDFMTLYQNLTICQT/P QNPPPPPKESSKVELDIIDDPH
10005	23906	A	10080	281	1	IFLGEWGPFPFPQKKSFPKIPQWVEFT PPYRKKIFFFLPR*NWA/HPKIFFKRPP PFFFFFFFFFFFFGKENCIFLLPKEHI TQAPAWGFAG
10006	23907	A	10081	207	35	QENRRC*RGRGES/GTLHGWRECQTQV PLWKTWQQLKRLNTEFFYDLAIIILLGE FH
10007	23908	A	10082	2	408	IAPLHSSLGDRARLRLLLLKKKKKGIKIRPL LALFFKNQNPSPFKNSHSFYGALMEF/P PPHIPPPFFWKVQPPLPFFRGTLFFPGP IGTCKLQTLGSPG*WDPPCPLPHQSPGR GGLIPGRKGEDPPSFRGLPPPHF
10008	23909	A	10083	195	2	ECKQRPQLEMVSFRRRSHEPFFFTGPR SVAQAGMQWH/DLSSLKPPAPG\SGDLP TSAS*VAGTI
10009	23910	A	10084	219	1	RLKIKLLKIIITTTIDSGICFSKSKL* H/LKIQNMWLDKLAHAYNPSTSGGRGRQ IT*GQEFKTSLGNMVKP
10010	23911	A	10085	364	413	KKKGGEKGPLLKKER*KTNGQLVHTNF /RLPGLKYFF/CPPPPSKWGLRAPPPKP GDFFFFFFFFLVFLVETGFHHVQAGLE LLTS*PIPLGFPKCWDYRRE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10011	23912	A	10086	200	3	INFILLFFIFVLLIFETGPCSIAQATVQ WRDHGTLQPOPLGLKQAILP/ASAP*VP RITDVHHHARLN
10012	23913	A	10087	154	329	FSLSDFKTYKAAGHRGSC*YQHFGKP \RRTDPLRPVQDQPDQRGETPSLLKKK KKK
10013	23914	A	10088	157	390	NSSSFFPPSCGAQ/KSEVKKSSGPHSSS SSG*RGE/CLPLLVSOGSWHFLAYGSLT PVSACVFT*PFSMSLCVYIQISVS
10014	23915	A	10089	305	1	KKKRAQSLPGQKGRGFSQPVTAGDRSF RPKIRKEALGLGLGLTDLCRTFPPTAT G*TFSSAPFPG\YPPV*PTKKKNTNLN *FTRIKIISRIFSGHEK
10015	23916	A	10090	329	2	RGFFQPLGFWDGPIISNLGGPPKNLLK AEIMGYNFCVPPFPFPGGLPTTHFFPPR NPPF/CFPFTPSLGFSPNPPGFFFFF FFLSRVSLCHLGSVA*SWLSAAS
10016	23917	A	10091	84	408	EKKGENKLFWGFLLGLTIFIGGYRFKII FCLVGYFIFYLFGEME/FSLLLPLG*C NGTCSVHHNLPLPGASGSPASTSGEGGI TGMRRHPRLY*IYLGRWSFALVARAVMQ WHVLGSPQSPAWCKRFSCNLRRGWYY RHAPAPPSLLNIQKIIILGFWLAPVY
10017	23918	A	10092	184	359	FQINSSVTRRSFVLAAGVQWRDLGSP LLPPP\GSSDSPASAS*VAGITGLHVGL SHK
10018	23919	A	10093	298	386	KLCEK**ITPIRMAII*KKREGENS\KC W*GCGEIGTLVYCL*EYKMOVPLWKIVW QFLKILGIEL
10019	23920	A	10094	310	1	ICMNEMLYKQDFGRITTIIRKIVIFYWI FN*FGH*IRIY*NLRYKTCML*RG**I NLPQRSFKNLRLKI**W/WPGTVAHAYN PNTSGGRGRIT*DREFETS
10020	23921	A	10095	40	407	EHTHTTACEPGGI*IRPVD*MVLISWL* HGTITCKMVTLGETGQKPGISLIIF FFG\TQSLFVPRNGVHCRGPISAR*KLC LPGPPLSPT*AS*VAETTACYCCTWFEN NFFLRRLPLHCY
10021	23922	A	10096	189	2	PPFFFFSNLFKKSFYEQGLALSPLKCR GIIIA/HCS/L*TPG/YK*SSCLSPL\S SWDDRCAPPRV
10022	23923	A	10097	260	401	DHLRSGVQD*LGQHGETSLLKVQKLDG RGGLQLIP\RRLMHENHLN
10023	23924	A	10098	187	464	WYMTRCGSLGPSSAAHESHPPQQLMN P\PSPSSAAHESHPPQQLMNPITPL SS*IPSPSSAAHESPGRVGRPEFTGGAH GYLHLSPP
10024	23925	A	10099	397	1	FFGGAPCPPPRRKGKTPPPRKLFPFFF PKKPPLPKNC*NKNPLLGPKKKNRPP PGRFFKKGFF*NPPKAPLTNFWKKKKK \SPFFKGVFPPGEPKPPPPFFFFF FFFFPTRPPRVRPRVRPRV
10025	23926	A	10100	253	3	NAINRNKMQ*TKTSEWKVYADHNATIKQ KQKRKCQVL/WRGCGETETLVACWWECQ MEQPAPVEN/W*HLENIKIQLPYDPAI HE
10026	23927	A	10101	121	404	VLASVVSIFFFFFFWKGLIFSPRLEGG G/LILG*LKPPLSLGPGFSCSLTLPGEWE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LKPPPPDPGFFFFF*GKTGFPRGGQEGLNFLTWEPPPLAL
10027	23928	A	10102	468	1829	IRDTYTQNPDKAKGYFSCIFFEIEETTM SRKQKQKDSGFI FDLQSNVTIAQGGAF ENMKEKINAVRAIVPNKSNNEIILVLQH FDNCVDKTVQAFMEGSASEVLKEWTVTG KKKNKKKKKPKPAEPPSNGIPDSSKSV SIQEEQSAPSSSEKGGMNGYHVNGAINDT ESVDSLSEGLETLSDARELEDPEASML DMLDRTGSMQNGVSDFTKSLTMHSIH NSQQPRNAKSLSRPTTETQFSNMGMED V/RPRHQ*KS*VPIFEKSVKDLQRCVTS LARYRVVKEEMDASIKMKQAFAELET LINGSRKWALLAEMDKVKAEMEFLSR QKKAELLKMTHTVAVQMSQQQLVELRAD IKHFVSEKDYDEDLGRVARFTCDVETLK KSIDSFQVSHPKNSYSTRSRCSVTSV SLSRPSDASAASSSTCASPPSHTSANKK NFAPGVY
10028	23929	A	10103	254	2	KKKDFPLTPLGFGGLKIQLEFFFLQKKKN FYFPP*IFPKIFFFFFFWFGTQSCPVTL RLECSDRIPAHYNLHLQSSSHSRASVSH E
10029	23930	A	10104	256	419	KVIELHTGR/CAVGQHVGRPRRVDCLSS GIGDQPEQHGEPHLY*KNAQSSQAWW
10030	23931	A	10105	153	439	TTVTSLCIYYTIYYFRLLSTHAYTHIY THIYV*KLTIKQPQAGPSEGF*KKEF** RRW/WVGTVAHTCNPSTLRCQGGWMT*G QEFETSLANMVKL
10031	23932	A	10106	424	157	SSHLGRPRWVDHLSPGVPDPWQHGETP SL/LKLAGGACL*SQLIGRM/RLSSGGR GCSEP*SHHCIPVWETEQDPI SKNKQTI FRMFKN
10032	23933	A	10107	213	3	NYKCPPTPNLNTLKALYFKKLILSPKA* AIKEKID*/IIKIKHIFYASNIINRMKRO LTEWKKIFANHVSDKG
10033	23934	A	10108	300	1	TPKQRGKKGSPREKPPFNLPGLTFL/Y EV*FMNPLK*QKKKNQGFFFFLICGT VYHQFTSK*ERGVPGTVAHTCNPSTLGG RGGWIT*DQEFETSLG
10034	23935	A	10109	120	421	KKIKKKKNHMIISIDAE*AFDKIQHR FMIKTLNKLGPBGKHI/KIMKAIYGRGG QDQGLHTAKK/EPLPLRENKISGKP
10035	23936	A	10110	102	418	TLVCVCVCVCVCVSVLSVFLSLCLSL QAGVQWCDHSSLQPRPSG\SGDSPTIAS VVGGITGVHCHIWPFTFYFLFLIRLKSML L**TSSEMALTKMGVHSHGLEFN
10036	23937	A	10111	382	2	VNNATMPSPKCSSTEKSHMSLTNSQKLEMI KLSEKGMKAKIGLKLGLLC/QVSQVNV AKKKF*REI*NPTPVNIR/DMQKVLV/V KTEDQTSNIPNLNQLIQNKSLTLFNSI KAERSEEA*EKCEDSRG
10037	23938	A	10112	61	427	ENTYVQVQCSIKEEYLQRRTLKYASLFQ KHICGSLAFLHLL*PKLYHSRSNAESDW IIQLFSVQPNVKEISKHKIGW*RGHACN /RQHFERPRKDHRLGVRDHPQHQGET PSLLSLKIH
10038	23939	A	10113	71	399	NVLGKEARSVGWEAVRGQISRVS IQMKW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KGLIKGEKLMKESQACICIFYFFFFETE TNFIAQAGGQGHDLGFMEPPSPG/*SDS PA*APHEQNGL/TGMHNNPRVIFV
10039	23940	A	10114	362	1	SKKKSWSGSHSGSKCHTSFLSYPTKEQKS YLSLFYKCNLQSLTFKELLDHFRPVCLP TIY*NKNWP/RDLPLKPSFKTLM* NQT L/WPGVVAHACNPSILGGQGGWITRGQE LKTIKANTVK
10040	23941	A	10115	314	3	WRERRCGAHLMRCSANMAHDKPSRMLNL *KPKMAT/RNTDHDNFW*GHGETEILNH YWDYKIM*PLWKTII*QPKMFNIKLPY VSYIQLLGIYPRNLKINIHTKT
10041	23942	A	10116	44	394	PGFORVSQDGLDLTS*SAHLGLPKCWD YRHEPLRPAGIYSYPAVFLVSTYRASN IT*MLMTPKPTSG\YSPLLSFRFSSFSY LRDISAYMSLSCLKLNVFASKPIIFLSP LWLLV
10042	23943	A	10117	398	3	MESCCFMGIEFVLKEEVLEIGCRTM* IY LHY*SLHLRMVKMVTSLLCVFFHN* TIF KKSSVFLYAGNKQL*I*ILKNYIY VMIP FTITSRNMKRNNLTGDKDMST ETYKTQ LKEITD*NKWRDITTFM QON
10043	23944	A	10118	104	386	KVPVWATCGVKMHRLAGHGGWRLWTRL P WRLRRDNRLSSGSRGA\AAEILPLCH CT PTWVTEHDSITYKY*KKGAPCWR ASS*C TLSGHALFFFA
10044	23945	A	10119	258	401	YNYPFLTVMKEKIGAGMAAHACNPST P GGRGG*\TRGQHLETSPTNMV
10045	23946	A	10120	310	384	GVFPFLTFLYGGIKGGPPPPRFFLF* FA FLFFFF/ETGSHSVAQANCSSVS AHRSHFLPGPGDPPTSAS*VTGTTG ICHHS
10046	23947	A	10121	245	479	TSSLYRKIQKRFYMLALEVLKICNTYF MNTERFPLKLFQFS/FRIISI*FFPFL FPKIYHYFLRDRV*LCHPGWSAV
10047	23948	A	10122	268	469	NSVFWLGVVAHA/W*VNPSTLGGRGWI TRGQLEETTPANILPP
10048	23949	A	10123	221	423	GOAGAVAHACNPALGRPRRDSLRPGV GDQPGQHKSPTSL/LKSDNF* KMGWLG P WAWWLTPII PALW
10049	23950	A	10124	73	183	AGGGWALTNTVINPT\PPSTPFTPCLSY SCTISTASAFRFP*\STSTAVLTHVRIL KSTPDAPHPPLKIPRARRNIQRDHTLSS NLFYYNHQLNVTEELTYDIT*INPTAT IHAIHTMPLLLFLHNLNCISI
10050	23951	A	10125	342	2	PNLGPCPPPRGTGKGGPFFPSFHP SI\IG PPNFFSF*RP*FF*MLKSLGVP/ SPITGP IPKFPFFPGFKNYFSPPL\PK GP LKPP RALFFFFFFNRHRVLL\CPG WSPTAGLRSSC
10051	23952	A	10126	85	442	KKVINIKCW*RVWRTGSLIHCSWG* KMM PHWRAVWQSFR/SLSMYLSYEPAL PLPG SYPRALRTTCVCTHSRCFSLLELP QA/W NH
10052	23953	A	10127	180	484	KSFFFFSQAQPIKVIPAP*NFHFFGVK RSSCLSFLRKWGPWWPPPPPPPPPP FFFL IFVEMRSHYAAQAGLKLASS\VP PPSG IPRTLD*SYPD
10053	23954	A	10128	376	1	WSPGAQLLFISCLYYNLWSLHTGRTPAK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PP*GWTLQKTTPLSCPAP*LPPPLPSPL QQIDLKEKLVFTAPACSL/PHSPNSSPW PQRRWPSVS/P/PVAHPAAPRLPPPPVC ARPLWLPEAPLLGIPPH
10054	23955	A	10129	140	454	CLIRSSINSVHNNIYIHTSPDRHLGCFQ FLVVTKNAAVSRLAYVF*I*IPTYDHI HTHTPAGYIPRHGIAGSQLTNIFNFSS* LSSNSF\QVGCTSYFLFPSHI
10055	23956	A	10130	340	473	AGARHSVLRRPPLAGSSCPSS/CGGHC VALGVSCPGGGCRAACVPGCCCLLGLP SDVCVC/SVCWGGSMGSRLLGGWAAPGF* GNSREGPGNCSSGRKAGLACGLPAWA EQAPDILCCGPGPHWLGAPAQVPLAPPL SPPPCLYGCLYSDRGDL
10056	23957	A	10131	280	2	DSLALLPRLEYNGVNVACHKLKSSWIRR SSHLSLPKHLDIRSMH\LPGLEIF*YS YCK*CLLTSPYFEFLMNSLEDISSCFIP IRVMPKCRMK
10057	23958	A	10132	244	3	IISTDLISHSWTLYLISSLVYVFLKQHS LAVLPRLDSCGMIIAHC/KLQTPGLKR/ FL/CLSLPST*DYRHTPENRANFYYYF
10058	23959	A	10133	272	3	VGKPRVFPYRIAFNFRVTSILGPHIKK YHFQCRGKHCFF*KAPPPFF\FNETG FCSVPRLECSGTIIALCSINLQGCNSP TSVSQV
10059	23960	A	10134	217	3	FFRFRPLVSPALTELGQF/HFLTRGL*K KKPFPFLFFFFSETESCSIA\RLWGS GMSAHCNCLCPGSSRTRG
10060	23961	A	10135	229	3	KNDYLKCWQCGRTETQMLGCWDIK/LI QP/LWKI IWQFLLKLNHLLCNPTLPLL GIYP*EMNVYVHTQTCICTDAW
10061	23962	A	10136	84	352	RREFKTGLATWQNLVSTKKYKTTVRYHL TSTRMDI IKGKR*QVCW/RKC/GDKGTL LDC/WMRMLVQPIWKIV*VWKFCRK*KL NLFFPPPPQ
10062	23963	A	10137	280	2	KCVVVPEERILREKSQHLGKIKQEGRLN AVVLIQPGQHGETLSLQKI/QLAGHGA PLRSQLHRRMRREDHLSPGVRSRSEP** LSLHWVTEQ
10063	23964	A	10138	2	386	HIOEQQLPNKDSTLNPYFLLISILKRKD EKIQMPSKHMKRCSTSLVIREMQIKIRS HPPH*VGKILKSANIKRW*MCRKR*\TL ITCW*TYK*TYKLVKTF*RIILQHPLLK THQSYYPAPHLKETA
10064	23965	A	10139	229	1	TRSYHESLTILHTNHLNCSFPQAITP *SRFPYSNRA\WLGSAHTYNPSTLGG RGRNA*GQEFKTSILGNLFPK
10065	23966	A	10140	261	429	LSHLFHVALI*LGLVW/SFVVFVFFETGS LPRLECSGVITAHCSLDLLGLSLGPTSA F
10066	23967	A	10141	377	34	WVFGSSGPPPPGFKFFSPPPPKKNPR GPPPPPIFFFFCKKGVSPLFLPPGGGP /HPFLSPPPPGVKPNFFDPGGGGFP*T KIFSRPPPPGGKQNFFFLKKKKKKKEHQ IKR
10067	23968	A	10142	208	424	FFSLFMQTFHIHIFYFFLAGGGGAGVD RVS/LLSPRLECRDTISVHCYIHLPGSK QFSCLSLLSN*NRYHAP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10068	23969	A	10143	1	297	PTRSPQVSNLHNKSFISFYLFIDLLSVC LSVSVYFETSLTLLPRLECSGAIITLHLS LLSS*GHRHAPPCQV\FFVETRFHNVSQ SGIELLSSSHLPTPA
10069	23970	A	10144	185	488	SGFPRGTELGAVCVVCVCACVCVCIK LGYI*NHKRIYI*LLYIYSTYIFNLSL *LSVY\SYVNRNSM*DRSQSI*IFILPK LKTCLNTHTLKNTHEGG
10070	23971	A	10145	283	3	LGWPGRKADGSGKLTIDYGRLDKLVSP\ I*SAISDMASTTKAVLQQRDQYSVLDL AHAFSSIR\NQSQFSFIRDSPQYATLP SEHLNSLDGQ
10071	23972	A	10146	146	380	CFLWDNFFFFIFTEKTGSCSIAQAGAGT Q/WVGIIISYCSLKLMSGRDPPTSLSCVA GTTGMPHHAQVIYFFIFL*RQGL
10072	23973	A	10147	275	3	IKGMLKAKTG*KLGLLCQ/TSQVENAKE EFLKEIKSATPVNT/RMIRKRNCLIAEM EKV*VTLLDQTGHNIPLSQSLPQSKCLT LFNSKKAER
10073	23974	A	10148	281	2	KIFLPQPPQEMVFGGFAPPGG*IFLVF* *KQPFPPPLGRFVFK/LPGGIPFFFFFFF FFFFFFETESHAIT\RLECSGTISAHCHL RLSGSSDPTRP
10074	23975	A	10149	413	139	SLRVWPIFGLLOANKKKFFWILFLS/IR PLFFFSRERGGTLPFPFFLRNPGKKS PPG*PPPPLKIQFPGKYFFTSRPAPFFP LFCQPPGKNLNYWGLGPGFPKIFPPPL FFFF*DRVSLCRSGWSKVARSLTWGK AFTWVS
10075	23976	A	10150	100	431	GPRLTDHLRSGVPNHPGQHGETSFLLI/ HNYSGG*GRKIANRLNPKGGGCEPKSC HCTPSWGKKRNFSVSKKKKKRE
10076	23977	A	10151	134	417	GLAAPLVG/WGKRNPFP*PFG*GEXTGW GPHPGKIFLKKLLFFFFFF*KGGLSFPP GGRERAHFWLKKTPSRKKEILPPPPR RGGGGPPPPPL
10077	23978	A	10152	403	2	LAFFPILQEVPCFCNLLHSLRMYSTGS KLFPLASPQPHSLLYHLTLARAPNILEE LQSPNTALLKYL*EAALKKKS*HITS SL*KVDLSFFLETKPRISA\RLKCSGTI SAHCSLRLGSPNSCATASQVAG
10078	23979	A	10153	382	297	GLN*ESWSGEKGT/LHCWWECKFVQPL WKMV*RL
10079	23980	A	10154	209	15	SSPKF*FFFLSPKKIPLPFF*PIFFFTK TP/HFFF/SFFFFVCVSGSHSVPRLECS GAITAHCSSTS
10080	23981	A	10155	153	422	RTSGKNGNRGQIILVTMTNWLFSFFFF PLKTGPHFVIQAGGQGRAHGSQA*IFG \SGDLLALVSLQAGTAGFHHHAQLSFFF KKTGLF
10081	23982	A	10156	257	3	RRLQNSKDCCLFFPLEAPRGATARCQPE LSCMRCLSA\LLGGVSQSGYMGVRDPHK EAV*PLAELKR*AGRSSAPFKAQRQGL S
10082	23983	A	10157	37	386	DATFRINSGTAEGGLDRIEPLNDLQ*Y INLVGTAVRRPDRIESNFESSTVGKKLS NNIVCYRSFFCERESQLTQQTSMLYYFK KLPQLPQPSAITTLH/SRQDPPSARRLO

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						LGQ
10083	23984	A	10158	407	272	HKGGKREKRKKKKEKKEGGREKGOERRKERE/RERKKGRKREMKKNRYSKCTQ**LLSN
10084	23985	A	10159	248	478	VKVVRHRLLLDPSVEDPWKSLKGPLQP*/RL*IFFF*NSGLLCHPSWRAVAQSRFTGVSTSQAILPSFSLPSSWDR
10085	23986	A	10160	458	129	GFSVLNRLEDEDLRQENLLMPAV*DQPGQHSKTPISTKNNMNPAGHGGVYP*SQLLRTVRPEDHLY/SNKPCSYLCAPAWATETLSLKNAFSCCSNHYGLSFQTSFHRILMF
10086	23987	A	10161	82	291	YSKTKSLFFAGHGGTCIYSQLFRQVQVRQEDHANPGV*GCS/DTMIMPMNSHCTPAWAA**DPVSKKKKK
10087	23988	A	10162	6	409	LRINILPEPISLSPLTAPAVFMPWNTNYS CDTFSLASMTLLPLHFLSTSLALPWSLFLAPSLFQISKHQLYLSFVLLTLSSCYFLNPCFRNHILMNLGRPRQANYLRSGV*DQPGQRGETPSL/LKNTKITWPPW
10088	23989	A	10163	249	415	APPECSLPLLVLVLLLLLLLLLFLRWEDHLGPGG*GCSEPKSYHCTSAWVTR\GDPVS
10089	23990	A	10164	1	405	RSEWRLRQPERQSETVKKKKKGFFFSRGGGGGKIFGLMEPSPSGLGQFFLFTPLENGGYRPPPLGGPFFFFFKGGFPLCGPGGFEFPALGTPPLLFPKGLNFRGGPTPPARFFFFWGPVFSVFS PKN*NPPVFRGKNGKNRPPKKKKPGRG\WGPPRKFNPFGNKRGVPRAGNSKPPGPQRGNPPFLKKKKGPPKGGGR*PPFSRGVNKNCPKPEGEGSINPKIFPPPPPREKKKKPFFFFLTVSLCRSGWRNLHSL
10090	23991	A	10165	175	404	AIKMWVIQAVPSQCLHGVGFYLP RSVCVKTP*NKRHRQGVVAHGCNPSTLGGRGWIT\RGQEFETSLTNMVKP
10091	23992	A	10166	317	2	PFKNSPLLLNEMTNHFEPTCNVNVNSPFLK*HKFLFF*EMESCSVT\RLCSVTIIAHCCCLKLLGTSNPPTSASWAPGMIIGMRHCPAPKVCSHASAHASAHAS
10092	23993	A	10167	325	2	KMGEKQGHFIKEETIRKANKHIERCSRLLAIEEM*IKATVTI/RKHQTKC*QG*RESGSLVHG**KHKIVHPLWKILSVSYKTKHSIIIIIGYSSVLLGTVLVHSGSDAW
10093	23994	A	10168	245	3	GEPFLFCFPIKKPKVFFCPYFNQAVFFLETHRGFFEFFFLF*KKKKK/LGMVAHTYNPSTLGSRRGGQIA*AQEFKTI LGNMS
10094	23995	A	10169	164	1	MNKMSQYTFPYKN*QWGG\SVAHYPNPS TLGGQAMQIT*AKEFETSLSNMAKPC
10095	23996	A	10170	214	419	LS*PPPPFPFGKKFNRLRFYGKSKPGP/FMFVALFQKGGPFYQNI PPPVKLEPPFP TILRV SFFFL*DGVLWCHPGWNAVA*S QLTASSTSRVH
10096	23997	A	10171	168	1	WTWWLFPFGFSITNNYCSHFSSSLHLAIW/LGTVAHACNPSTLGG*GARGQEFETSLT
10097	23998	A	10172	139	3	PAH/CES*PPGLKRSSVSLPSG*DYR/HTPPH\QLIFV FVVMGFHQPA/SA/FPKC*DYRS\DHKKWPT*HLK/SFHF I KK*N*LKRYLACSRWLWYLFCLIRCMV**NLDDL SILYLHLNKFQFLFIYLF FEMES

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10098	23999	A	10173	253	2	FPLKICNTLPPQIFSTQRGLLSLPFTTF LLSLILLRPFFFFF*TESHSVPECSGMI SAHCSLRPLPGSSDSCASAS\QVAGKTCA R
10099	24000	A	10174	300	3	GRAFFFKGLVKWVFLTPNPFPFLKLNFL KRVFLLAPSEKFVFFKFNWPP*LSFLIFG EKNFFFFFFFFFSEMESCVA\RLECNMG ISAHCNICLPGSSDSP
10100	24001	A	10175	117	381	EILRYIVSIRIRRTNLKFOEELRVNIK NNLSSSLGNMVRPRL/ECSGVITAPTAVS APGFK*SSHPSLPSSWDHRRAPLHLGDF FLIETRSHHVAQAGQVIFNVYSKFLLLK FKISPSDPYRNNISQDFLAIGPTNMVPL QPYIVLCACRTKNNKIIDLSEQSSRT
10101	24002	A	10176	194	412	TLKNLLLSLHCLSFVPTDLYQPERLSKP PRPAKKYKFLIL/WLGVVAHACNPSTLG GRGGWIT*AHEFDINLT
10102	24003	A	10177	100	339	VPVKSLLLCVCVCLLL*RI SDHLP TLY ANLG*CFFSYLVISYS\NSTYCILQRHL LAIQKQP/CSFLRQ/HLVGWLHKKKHTH THTHTHTHTKSNTHTHTHKSKDLTGTQ NTEFLLK
10103	24004	A	10178	229	2	KEKYIKSKLHFEARHNGSHL*SQHFGRP RLMDCL\VQDQPGKCGENPYLQKNTKIS QAWWLVPVVPVYSHRASKTLS
10104	24005	A	10179	368	2	SGSSPSTSPQGRPDPLGLFSAKIVLGQL ATIPPLCFLKIFHPLTLPPLLLGGE FNLSPQQQDSISLPWFLCYRGPTYKAF FYV*ASVPEKI\FFFFFF*DTVSLCHPG WTVAQSRLTA
10105	24006	A	10180	398	1	QNIMLYTINTYNFICQLKKKTIQWGENF FENKWC*ENWIFTCKRKNLHPYLIPYTK TNSKWISELNL\KSLKVNRCGNLHDFQF GNGFLGDTKSKTK/AKISKLEFIKIKNF CVLNDIIKKVKRQLIEWKKYLQ
10106	24007	A	10181	252	419	GARFKGSNFTSAGGQGITFFMGPPKLIS RPVF*HRGEGKTPGVTQLNRLEEHPLFA
10107	24008	A	10182	101	380	FCWIYNSWLIGYLFPPFRTNLNLAACGG SCL*SQYFGRQRQADHLSPGVRDQPGQY GETPS/LTKISAWWHVPVVPATQEA EV GGSLEPREVK
10108	24009	A	10183	2	377	PGQVDCFS SGVQDQPDQYGEILFLLKLQ KLGGHGG/IR*EDHLSLGGQGCKEPRLY HCTPAWVTEQYLV SQKKKKKKK
10109	24010	A	10184	140	3	DGVLLSLPRLECNCAISAHRN\SPSCDS PASASQAGCCGTC*SQL
10110	24011	A	10185	364	3	SVCPPRLGGVSQSGDMGVRDPFEEAV*P LAELERCAGRSTAFFRAIR*AHL SLLK\ FTRNHPFPHVPCPRVMSR*FGLLPFFQR CPAQRGEIWRRLAVALRSCGRLQVR TCWQLCLHR
10111	24012	A	10186	2	249	SVRLNKNKENTQIRNKRKGTINLTETKR IIKEYSEQLFANKLH/SLDEMKNFLER* NPLRPGAEAQRLVS*RFWRATAIDMRP
10112	24013	A	10187	270	2	PWAQRGCVFKTNQKIFFGFFEIPHLDP*P CVFQRPPS\F*VRLIFIGGGFKPFFFFF FEMKSCSVARLECSTISAHCNLRPLPGSS DSPASA

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10113	24014	A	10188	428	28	PIFDKG/E*GN*WGKKSI*FNKWCWEKCI C/KKL RDSSLT SY/TRNLKWKIDLNVR TK/STKLLEENIDIV/IYDLGLGIGFLD MTLKARATK/AKIEKLDKIKIGNFYASK DPKKMKR*FIEFIEQGGKIFTNHVSDDTS I
10114	24015	A	10189	85	243	DRVS/LLSPRLECSGMISAHCSFDLPG* SDPFTSVPKSSWNYRCPARKLSFT
10115	24016	A	10190	96	440	LQSNHINTLNVNRLSSSMKRFRLSDEIF \KKHGPALCCL*EMYYKDKGTCTLKIKG WKNIYHANANNKKT/GMVLLSGKIRLES N/TVIRVKEG*LVI/INGRLI/QEDLIL LFILNVYAP
10116	24017	A	10191	137	423	AKDLDRQFSKEDIHMTNRYMKTC/SGRQ LIRETQIKTMRYPPLTPDLRKSDDKS ***YEQKGTPAHC**ECKLVQPLQKII* TFPKLLKINL
10117	24018	A	10192	221	72	AKVK*VVVFFCFLFFF*DGVS/HVVVAQ ECSGAISAHCNLCPLGSSDSVRVG
10118	24019	A	10193	460	121	SDKTKYW*RCRAIKTLTHF*LKSKLVPL L*KTI*CYLAKLKIHIVFDSAIP*DTY FR/E*FCICAPKTYSNMVEALFVPAHQ TSKKKNWK*LSCPQIVDNFLNIHLMKYH LE
10119	24020	A	10194	393	2	ATMPYQRLLLTAVHELESPE*MDQFLD TYNLPFRFNQEEIENLNSPIMSNEIQSVI KCLPFGPNPGPNFGFIEFYHTYKEE/LP ILL*LFQKIEG\ILPNSFHEVSITLIRK TDKDAT*ETHKPISLMNTDA
10120	24021	A	10195	3	353	EAAPMPVKFFQLLEPSGPPGLSMSCLD CNGYACFSVSLHQSANQSIDQ/SIYQSA IHLIIY/VSIIY*SI\YLL*SLI*PMY VPIYPLSCLSIYLSFMPLSCLSFNNLSI TRHGSML
10121	24022	A	10196	118	395	DEFNAGLLPSYQVLSLYFCF*NGV\CHCT P/RLGDRPRLR/PPKKKKKTPPPPLGG SPPGGEPYTERPGVGP PPPPFHPREN PGCFHPPPKAWP
10122	24023	A	10197	437	160	FGYPRVFPLPALLRGPGILFWGPNKKN YSSPARGSKICFFKRGPPFFFFFYFFF* QTESCFVAPVGVQWCDHGS LQPQPG\S SGPPPSTS
10123	24024	A	10198	259	3	RQGNHVTHVYSSRLQLILSPASLAVFI QKIYVNLCTYIHIVNLYA*MCICVCICY TCIL\ICIYGLVAVAHYNTTTLGAKLG GS
10124	24025	A	10199	1	416	IISAHCNLHFPSSWDYSRTPPYPANFCI FSRDRVSPCWSGV*HLEQHSKMLSKK* NKIDMHGGMCL*S*LLK/RAE*DVLROE NCLNPGGRGCGEPGSRHCTPAWATRAKT LSKASYASSSSSPKKKKKSPS
10125	24026	A	10200	369	3	TAPPPFFFCRDGLRTSLIIFPSRATFYS LVTSGSFLPAGAGGRGLSLEIRVLDLVQ DGCPCSQAWAALGGPGWWAPFLCFFET ASCSVAQEGMQ*CNLGS LQPPSPG\SSD SPASVVLWTSK
10126	24027	A	10201	314	2	LHHRPEV*FTPSKLGVTGYMVSNISYP WRCRAHK*SQVLVSLRHKLFLPEMESG

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						SEVQL\DTNRCISANCNFCPLPGSSNSPT SAS*EAGTTDSRQPDADAW
10127	24028	A	10202	68	413	KIGILLKTH*PSIC/VSITNF*YNDTGE LKVKG*KNIYYANINQK/KAGMVMFVLD ETDFRAKK/DYQGH*IMEVSVHKE/E/ LVLLNLVYASNKRVTKYMK*KDTDIKGEI DKSTTIVGDL
10128	24029	A	10203	351	1	PKFPPLNPAGWTTTIKIFFKKKNHNWFS PRKEKALQKIHKKG/RLLAKEISFLGGF *TDYKTNPDQSQSIRTLGEKKKKIRPGTV AYAYNPSTFGG*GRWIT*GQELKTSLAN MVGRV
10129	24030	A	10204	2	392	FLEGVLLLLPRLECNGAIPAHNNLHLP PRFKRLSCLSLPSSWDHRHAPTRPANFV FLVETGFHHVGDGLDGLTL*SPCLGLP KCWDYRH\DHHAQPSF
10130	24031	A	10205	264	2	PLSLSNLFPILNSILKIFFILK*L*IH GKLHKMYRKV/LV*TSPPSPQC*HLR*V *HNIQKKLMGLGAVAHASNPSTLGGRG GWIT
10131	24032	A	10206	281	2	ISPPLFFLFSPPKKIFFSQKHIFLGPPL FYPPPLFFSPPP\PHFLWGFRPVNEMP KIDPQTWAKNKDKGNFPPPPFFILPPK KNIFFTKTYFFGPPPLPPPPFFFSPPK KK/SYPFLKKNSPNPPPS*K*AAISLP PPFFYFFFFFSSFFLENTWKMAW
10132	24033	A	10207	340	1	STKKLVQKLGEHTQCWQGCATGTLHC RWECKLVQPLWK/SAWQILRQL*NFMHL PYNPTIQLQGSYSRE\QHTCPYKDLYVA ALFTIAKNC*QAKFLSTGE*INKLWCIH ITE
10133	24034	A	10208	136	3	KNRGPPPRSGKFFPFLPLFFFFFF*DRV \YPSHPGWSAMVPSQLT
10134	24035	A	10209	327	2	INKKYYEQLYA*KFDNLDEIYQFPGRYN LPKLTQEKANNLNRPVSLRETKSTINNL PKRKVPDPDGFTGELYQTKEEITP\F TEAKGILPNSFCEVTIIVRLFLLRQ
10135	24036	A	10210	89	485	EIVPLLRFPVIFIASPTTFYTYGFVSG EKSQYKKREKCLKDTLEQSRSLGMHST CGIALHPKREGQMCTLCACFY*FFLKES HSAARAGVQWHNLSSQLPP\PSSSNS
10136	24037	A	10211	361	462	IQQIGSNTGNIPAMELALKRNSKNINRL AGWNGP*VFAC/PKNVLFYLHP*LFG*I *IYQLKITF*NYEGMVE/FVFRFLFETR SLLSPRLCSGTITTHCSLELVGSINSS ISARAEFLQORGANL
10137	24038	A	10212	62	469	SLLWKLRSRGASTSLRCLSA\LLGDVVSQ SGYTGVDRDPLEEAVCLLSELERGAGRTT ALFRAVRQGRSLLEKL\LLPFVQICPAP GGGIYR/GQ*ALLSCGGLCPV*AS*/M CLPC/EA*TRLLKPPPGS
10138	24039	A	10213	197	1	VVTQPNNEWCVTNKDASFQQRCTKKIKT/ WPGMVAYTCNPSTLGGRDGWIT*GQQFK TSLANMVKPH
10139	24040	A	10214	31	213	HASLDEGFHHVGDGLNLLTS*STCLGL PKCWDYRHEP/PAPNWWKKFLSSKAFKR *LGCY
10140	24041	A	10215	442	29	PTINPTMACKCLSKRKSHTSFTLNQKLE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TIKLSEEGMLKAEAG*KLDHVH/QVSQI VNAKEKFLKEIKSATSLNI*MIRKQKRF IVNME/KKVLFWTTEDQTSNIPLSQSL IRKRP*LFNSLKAERSEEAPKLEASSG G
10141	24042	A	10216	195	533	LVWFVLRVTYGVAAKMSSGTTIIGRLSW GWRHLHF\KMAHL*GYWWEASVPLHMKLS SCHGTG\SLRVKDPRELRQKLQCFYDL VLEVITYWHFYCILFIRSKSLSPAHIQSK RI
10142	24043	A	10217	274	494	CVLKGLPFALPWFFFF*DKVSPSPRLE CSVAI/SAHCSLNLGSSDPPASASQLA GPPGLRR
10143	24044	A	10218	142	480	VTIKIYLHPHDTTTPLRQGSRLKEILV SY*QKQVETRPESHVIFTVISTQPKKT TTRSGAVAHTCNPSTLGGREGQI/T/RG QEFETSMTNPVK
10144	24045	A	10219	163	464	AVYFSFWRVCEHDLASLYFENSGKRDNK FVFLVLQAQGPAPWRQGEVHKHLLPCVYH FAFVVLTPQPQSFF*DG/QSHSLAR/LE CGGVISAHCNLYLPGSSNS
10145	24046	A	10220	379	469	V*KVQM/WPGMVAHTCHPSTLGG*GGWI T*DQEFETSLADVAKPC
10146	24047	A	10221	211	473	VTWLLLFSTIFRASSLSTDSVSYVIAFQ FYFYLFYFYLFIFETESCSVA*AGAQW CDLCSPPPPRGS\SEEPSTLQMTSGSS NL
10147	24048	A	10222	142	394	GVCQSLGSLCQLGGTGVRDQLEEAVCP LAELEPCAWRTLRLRCCSLQSQAGIF /RFC*SYIHICFPFQVLLSSEMGLSIR P
10148	24049	A	10224	77	396	KRKTKKSFWTPSGFGLRPPIPKKKKFFN SRGKQGGFGRGSGSRGGGSGTSGRGGY MGKVFQMGQ*NFTGDQGLAKGGFVFL GRTTIGIKGALKRLFA/NEHDLR
10149	24050	A	10225	155	443	GQAREGLKSGFPFPPSPGWPLILPGGV FSPKFFFFFFETRV/CAVAQAGVQNCNI DSSNSCASS*IARITGAHHH\TELIFV F*ISPPSQ
10150	24051	A	10226	290	485	KRGEQPVQKKKFFFFFFETESCTVAQAG VQWHNLSSL*PPPPG\SSDSPAEFPR
10151	24052	A	10227	228	424	KLYQNLHDTLFGFELSHYEEVH*KMLKG SSWEFVMHSS/VSNKCILICSAXKKKKK KKKKKKKKKKKK
10152	24053	A	10228	269	454	DLFAASQGHQALLLELMATTLSTHTHT HTHTHTTPWSLF*SR/SALSVC
10153	24054	A	10229	255	1	FYIFSKFLYVWLVNVDLSDHICFCIQSV IISCFGVFYFYYY\FF*HQSCSVHTGV QWCDRSSMQPQLQGQNDPPTSASQVAGS A
10154	24055	A	10230	18	472	GPEEFGTRRERDRERERETRDRSERVER VRERER*/RQRERERERERERER
10155	24056	A	10231	52	361	WRKNYYFQIKITVYLENTKDFIQKLHTK CW*G*KEIGRAIHCWWECKM/VIQPVWK R/VWQFLRKLNMILLPHNPAVELLDIYPN ELKTHVCTKALYEAGRGGSRL
10156	24057	A	10232	3	402	APRLPLGGWISFSSPMGAMGLNRATGIM GSFFFFFFLKRKSPLGPQGEGRGQNLG*G

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NPGPRG*THFP*TP*KAGNNGEGPPPR GNFGFLKKKGVPQKGQGSKP/RDPRGT PRLGPPKGLE*RGGPPPPAPQK
10157	24058	A	10233	48	470	PGRRFTTAGLGKQEPAAAGPRAPRPAQT PLKREAAARPSLRHLPEGA*APRSSARSP LLI PAASLRSPRRRTCRRRLRHFGI ITR PFQPGVRLPDSPGGLA/RWACAAPPAAS RALPALRRPL*RRPGHGAPSSKSHGHSR SP
10158	24059	A	10234	169	446	CPPGPAPSHLLEDRDDPQAGRQSSFYAG WDRWREKTLFLFLRQSLTSLPTTFFFF \FEAESHVTHSGMPGVISAH*NLRLPG SNNPPTSAS
10159	24060	A	10235	264	2	KLKPIFKMVFLKIMFMSYIMEVFFFIET GSRSVTQAGVRWHDLDLSQP*PP\GSSD PPTSVSQVGKWHKTWEAELAVSRDHATP RAKL
10160	24061	A	10236	306	3	SQDMVKSPKKKFP*LV*GLTEI*KIRAL VFNKKFFFFFPETGSGSCSVA\RLE CSGTIIAHCNLQLLGSSNPPASASRVIN SIKKLFANFIVSANPRPT
10161	24062	A	10237	20	469	QCGAIPRRGDHLRSGV*DQPGQHGETPS LLKIQLSRHDGH/CRRLSHKNGLNPPG RGCSELRSCHCTPAWATR\GNSVSKKKK S
10162	24063	A	10238	313	3	TRPRPTQGPPHSGGRACL CIFSPHGPPQ TRLSTPVSPSVRPLGFQVLLSARHGFLI CQHGMF\PSLFTMSNITLWPGAVAHTCN PNTLGGRGGWIT*GQEFQTS
10163	24064	A	10239	274	49	KGNPFFVFETGSHSIAQDGVQWCNHS SLQP*PP\G\SSDPPTSASRVAGTTGVCPC EDKLSHILRRCYAQVFMLAG
10164	24065	A	10240	144	454	VCKIKIYILVLLLEDYIN*FVKSSL*LK S*K/LIQMWAIISLPECLNSVCLGKV G*KRCSQQGTVAHTCNPSTLGGRGMIP R
10165	24066	A	10241	289	178	FNYSIKNNTDGWVWVWCLLPVLPALWEV EAIESF/CSRDEIPLSCPGWSPVPKLKR FYCLNLP*CWDYRQEAPHPAISIIFDA TVIELFS
10166	24067	A	10242	352	294	PBRTTKMVV*DQPGQHVAVTLQKMQL VERGGKHPQSLC/REDH*SMGGGCSE PRP*PCTPAWVTERDHVSKIK*NKIK
10167	24068	A	10243	293	1	VSLCRESSNSFIWQCPVSHILALCFQR EKKRLDLP/S*MVGK*EIPFLVPLFLP HWPLLLMK/YM*IFFGNRVSLCHPGWS AVAQSQLTAASVPRR
10168	24069	A	10244	218	3	LERHIPVRPIICDYKWVRF/HFLRPL HN*FLFSFFSFFFFFFTGSYSVT\RLE CSGTISAHCNLCVHLLL
10169	24070	A	10245	185	1	KKQPQQTKNPLNNVKKEKGQHFFFFLE T*SRSVAQAGVQWCDLGLQPPPG\SS DPPPS
10170	24071	A	10246	2	265	AHKKKPAKHIA PSTFLYGETEARRSMPK AAQLKCGRAGIILFVFKTESCSVAQDAV LWCNHGSLQP*PPG\SSDPADSACRVAR TTSI
10171	24072	A	10247	2	430	EAGGREALDGCGLTGRESGVQRRRDSMG

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						CQGTAGRGTRAGKEGPWRPEHLSRRPPA SSVLLSWATHLAWVEGS*TGSLCDLEAP GPTLSPWCWSPELLQLHV/HHHTHTHT HTHS/HPNTHDTQSLCHQPSFSVS PRA RTVL
10172	24073	A	10248	201	16	TPPGGVFFLGFFFLFFFETESCCVAQA GVQWCDLGSPPHPPASRRPGRNSSI/AAA *GYHFK
10173	24074	A	10249	167	2	GFDPFEGMLSYLEKEET/WPGTRAHTCN PSSLEG*GGWIT*GREFKTSLTNMEKP
10174	24075	A	10250	92	389	FQPGQHGEILSLYEIKKI*/ELAGCIDM CLWSY/LLRRLKQEDCSST*VQGCSEP* CLSCIPSWVTEQDPDSGRQI*KKKKISL GRRGGIFLFLKIWHVFFL
10175	24076	A	10251	221	415	KKKKRGGRFKGSNFTSPGWRGNIFFMGP PKLNSRAGV*QRRD/WEKPGGPQFNCFG SNPPFPFPGGK
10176	24077	A	10252	94	383	GKLNRCGIWLLGRCQSPAVSNALWLHR VAPEEEAGEAWAGTSLQLSCKSKITPN KIVY*KKNKI/WLGTVAHVCNPSTLGGR GGWII*GREFETSL
10177	24078	A	10253	249	2	YPTMIFKCSKRKSPTSLTNQKLEMMK LSEEGMSKAELS*KLGLLH/QVSQVVNA KEKFLKEIKSATPANTGMIRKRNGLIA
10178	24079	A	10254	132	414	NNTYFQGKIFILNSQVKGMLICCWBECK *VEPLWKAVWRFLK/DLEQNSKEYKL*T WNQPRYPVVDWIKMWWIYFMEYHA/A IKKNEIMFFAA
10179	24080	A	10255	359	3	YSLRHNIEMRPVSNPTRASCKSHERRSV ISLTNLNGKREIIQEASKEGTLKANKPKA KLFVPVRQVNAKEKFLKEAKSAAPLN\ RMIRKQNSLTADTEQV*VIWIEY*TS HS IPLSQSL
10180	24081	A	10256	283	2	SLQPWKLYVHVFLPKYATYPFGTLPKT HFFHKILPSKAGSDLNSIYAMTYSRHI TIFFETESHVTRLECSGAI/SAH*NLH LPGSSNSPATK
10181	24082	A	10257	216	386	PSKNPPPLINPFFFFETDSCSFA*AGVQ WRNLSSLQTPPP/GSNNSCASAS/RIAG I
10182	24083	A	10258	263	1	FSQWLILPSPLSYSFLFLRQGFALLPRL ECSGEITA/PSSAS*VAEITGACHAEF LNFFVEMEFHHVVQAALKPLGSSEPPTP ATK
10183	24084	A	10259	248	47	IPKSRVKRENRLNPGGKGCN*PRSPPCS PEWVAKQNSLSKK/NKVKIYQNLHTETQ TVHGDIRQEK
10184	24085	A	10260	159	2	KRDMSSLKLEY*KKE/RIWPGAVAHTYS LSTLGGREWIT*GQEFISLTNMVK
10185	24086	A	10261	190	405	ASLHMFMYFFFFFFFPKQIFFFVQAEHQ WGNLGKRNPPLPGLRDF/PASPPKEAGF RGGPH*PGLFLVF*GE
10186	24087	A	10262	39	293	PSSSTSRYPEDTPLITQKYICKILFIV ALFIFPKHWKLCCKPHIG/E*IKLQCTIY TWRYVAVQKNEENLYQLMYNDYQEILV SD
10187	24088	A	10263	282	3	AFYNRFFLKIFFKRGPRGKEKKGGKKEK KKWGKKKKKKFFFFSPGQIFFLGGVFFF

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						FLFFFEAESRSVT*AGVQWCDQ\SSSQP RPPRLKPPFQ
10188	24089	A	10264	196	376	KKGGGHIINFPPHKGKYPGPEKKKFFFF FFEMESCSVA\RL*CSGMI/SQAHCNLC LPGSSN
10189	24090	A	10265	514	157	GLTSLFRLEYSGMMSL*P*LPG/FR*FS RLSLPSSWVFLPMYVYHYAQQSFCIFFV ETGFHRVVQAGLKVLGLRQSAHLGLPBC W\DYRCEPL*LTCLICFTYGLR*RSKPP FFVDGIQLF
10190	24091	A	10266	57	378	RSRIW*DSVILCS*LVSV/VDQSYFY*V TEILEQIKLLGSKIMCFCILQLHFLCFL CGSFVGGT\IFIFSRNIWLGTVAHACNP STLGGRGRWIT*DQEFETCLASMK
10191	24092	A	10267	1	212	LIQKDTNIYYIKEAL*IPNKHI/KKISS IVSHYKMQIKIMR/YHTRMAIIKRTDKC LYECRETRTLMHCW*GC
10192	24093	A	10268	3	399	MANKHIKIFSASLIRMEI*IRATMRE/H *FIPIKWLVLKSKRESNKCWQCGRTGI VIHFQRECKIVLLL*KTV*QFLKKLNIR LGAVAHSCNPSTLGCLRPRVQDQPGQHG KTLSSLLEIQKLAWHGLHLSPS
10193	24094	A	10269	190	386	FSPFLPLVTILECDKACRRGKSFDFFL LGPSFYFFKLLL/FIFYF*ERVLLCGPG WSTVAQSWLTA
10194	24095	A	10270	166	327	KTNSKTAEVCPLSVITLNINGLNSPIKR QR*TDF*NPI\ICCLQETHFRFKGTN
10195	24096	A	10271	180	1	IFFLFEVETCSVA*AGVQWNDLGSQQPP PP\GSSDFQLIFAFLVETGY*IMVPSSS CRT
10196	24097	A	10272	273	3	FLGLFSGNPLKANKPVCHLTLPILQRIF FFFESEFHS\VAQAGVQWCDLGLSKPPP PG\SSDFPGRRR*Q*AMITPLHSSRGDR VRLRLKKK
10197	24098	A	10273	399	27	YHFVPTRMAIIRKNN*CW*TCGEIGNL VYCWECK/LV*LLRKIWQFLK/DVKQ NYHPVILLLSIYRI*FDCLFLCKSHVEM *LISGVRVGAWWEVIGSREWFLMSGFTI SSCHQDCEFSQDLIV
10198	24099	A	10274	275	462	KINLVQLDFFFEVEMESHVSTQAGVQWC HLSSPQPPPP/GSSGDSRASDS*VAGIT SVHQHAGL
10199	24100	A	10275	2	379	RGPGRGLGSGTGFHPGRGGEPIVYQHL F*FFGP\PENYILILPGFIISH/IVTY YSGKKEPFGYIGMA*AMISIGFLGFIV* AHHIFTVGIDVDTRAYFTPPYHTFEPEG YIISRRRKTKGFLF
10200	24101	A	10276	2	407	FPSPSPSPFASVLSLSFHLPLPEHTW FIDGSPTKPNRHSQAKAGYAIVPSISII EATA/PAPFTTC*QAEILALTRALTIK GLCINIYTD/SHILHHHAVMG*K/GFLT TQGSSIIDVSLIETLLKAFLLPKEAGA
10201	24102	A	10277	203	545	FLWRGQSLALLRLLECSGSILL/AHCNL GPHRFKRFSLPQPPE*LSNW\DYRRLPP CPANFCTFSRDGFTTLGQAGLQLLTSSD LPTLASPKCW\DYRHEPLVHGLTFNRSF NFFF
10202	24103	A	10278	250	3	AKWFLEMKSTPGEDAANIEM/TKDLDY

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						DINLVDEAVAGFGRIDSNFERSCTVVKM VNSITCYRELFHERKSRIMCQM*LSYF
10203	24104	A	10279	333	3	SLILLFQSMNHTHVRTFIDQFCVCSN YSTDWLFPPLSPISLRTPYSLRYNIKIR PINHPTMAMASKCSSERESRISLTNLQK \LETIKL/SEEGMSKAQIG*KLGLLCH
10204	24105	A	10280	251	3	ITSKVIDSNPTTSITITNLNGLNTSF*R QRLL/DWASSPK*DSIICYLQEMNFYK IFKKIGRRIYYANISQKKVGVAVLTPDK V
10205	24106	A	10281	22	226	TKINSKGNKELNVRAKTIKLEENIDRN LCDLGLGNCFLD*YCIL*TKINSKGNKE LNVRAKTIKLEENIDRNLCDLGLGNCFL LDMTNPNAQTTKGR\IDKLDFIKI*NFWL DT
10206	24107	A	10282	238	383	DAKRKVSSTEGDSEGVHERRSAHLSAK PCPAEVE/AKPQKAAEK*SSSE
10207	24108	A	10283	127	377	RIPGGSALGKEIRQCFVKGQAEIGKIE MSQPTQEREVVEGIGSQKAAQVDHLRS VQDQPGQYGETPTLLKIH*LAGHG/GRC L
10208	24109	A	10284	328	370	VGPGPFG*SSGRVSSCCPGWS\PSELK* SAHISLPKCWDYRCQPLRPATFFFKTAS HYVAQAKVQWCNYSSLQPGTLRLKCCIF KKIQVVQVV
10209	24110	A	10285	341	1	KVVCVLTAPLSGRFSVCLPFLGPPYFLQ HSDIEIKPINYPTVASKCSNERRSHTSL TLN*KLETIKLIEEGMSKAETGRKLSL L/QSVSQVNAKEKFLKEIRSITPVNT* MI
10210	24111	A	10286	199	329	LEFFSFLNCLSPHRIEESY*KEIKSAPPI TPGIPRK*TSIAGKKNVFMWDKQTNH NIP/LSQSKTITLFSNMRAETVEAEK L/ERGCFFMRFKERTHLHNIMKGPVVA HTCNPNTLGGQGRQIT
10211	24112	A	10287	358	387	YTNALLLYV*DQPGHLMGKDSL FNKWC* KNEYSHAKKQNH\P*FSLYTKTNSKWS KDLNVRAPIKILEKK
10212	24113	A	10288	111	373	SAQCQPDQHGKTPTLLRIQKLAGPDGAC L*SQLLR*GCGEPRSRHCTPAWAT/EG KTPSQKKKKK
10213	24114	A	10289	197	375	IRIGLCKFII*FLETKLHTVAKVECSA ISAYGTLSLVDSGDSPASAS/RVVGTTG
10214	24115	A	10290	118	371	QCLLMMSPLGKT*MTGRRLQENRLNPGG GGCGEPRSCNCTPAWATK\GNSASKNQ T\KNKQQQQN
10215	24116	A	10291	214	368	CGYHQKNKKTNPKNKSCWQGCIGITLM HYWKDHKV/Q/PL*TIVQQFLKTRI
10216	24117	A	10292	2	376	PFPLMAQRPTHLPVLSASSGTSLLMPST LLWLPWLYKAHAVPTVPLSKLFDHTKPY AVSKNNLGALSI*SY*VIPVPPRSRF/S FIRDKPTS
10217	24118	A	10293	1	379	NILHNLDFFKNTTLEPQSSRLQRAVIAP LHFSLGNIVRRCFKKSGWAQWLTVPVIS ALWEADVAGSLEFKSETTLGNMMPCLN FKKKKKKAFLFGAPGFFFFMGGKILFGI AAPF*SSGRVSSCCPGWS\PFEK*SGH ISLPKC*DYRCQPLRPATFFFKTASHYV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AQAKVQWCNYSSLQPGTLRLKCCIFKKI QVVQDI
10218	24119	A	10294	201	384	GEERLSVQCSAFK*LR*HINISLQTFFF LRRESHVA\RLCSGVISAHCNLCPLG SSDSPA
10219	24120	A	10295	161	400	VCVIESVKANHLVDEHALKSLSFHLSLL FGV*GVCVCVCVCVYMCFCVCIIYVC
10220	24121	A	10296	1	433	GEGGGGCSGWSGVETAGSRPAPGAEQDL LPAPALGRWQGLNSVCYPAPWPQPNRRQP LALLCAAGLPGPQRLECSGMIHAHSLD LPGSGDPPMSAG\SIAGTTGTCHHAW\E FHHVAQGGLELLGPSDWPTVLGLQM*A TTPGH
10221	24122	A	10297	209	1	LTPELLYHHYTLTYFF*ESGSCSVAQARM QWCDLGLLQPKALG\SGDEPPASAS*DA* STGVDDYYSWHTCI
10222	24123	A	10298	225	1	RPGMPLSALPCTGHAPARQPHSAACSGP KCPWCQSPQPAVGWTV*VCPLPLSPCLC /FCVPQPPWHGGLPLPCPPV
10223	24124	A	10299	212	367	VTAGSGHMCYTWEERLEQSL*KTVWRF LK*LKVELRFDPAVPLL/SIYPED
10224	24125	A	10300	97	406	LHRCPTAWVTERGCKLTNNQNGQHNE GEACSSRPFTTIC/EEKIHLVCAITRED *RLAAETTANTTDIPIGSAYRILIKKLK PSKLSTC/YVAKQLSPGQLQTK
10225	24126	A	10301	3	422	YRSSSKTFLIIRRGFIPSSFTLLAHLST TLSTLSHFQKGWVKLFFFFFFFKKGFPFW PGGGGGRAKP*F/HGNPPPPG*KNFPAI PRQGGGKKG\GPPPPGQFWFFKKKGVSF WGGGAKTPELGNPPPGPPKGGGITGPP PP
10226	24127	A	10302	330	1421	RTKGRPLLLALPVLVLLFLHLAFAFSAPP GPSSLSSTEDLKWTLSPAQSRKLPQPS LHRAGVRDLQWQGRAGBELTAAC/WPAP PRPETAVLLQGLPC/QEGRLLLESNGF ALVVSAGETIFYASATIVDYLGFHQTDV MHQNIYDYIHVDDRQDFCRQLHWMDPP QVVFQPPPLETGDDAILGRLLRAQEWG TGTPTESAFLTRCFICVRCLLDSTSG FLTMQFQGLKFLFGQKKKAPSGAMLPP RLSLFCIAAPVLLPSAAEMKMSALLRA KPRADTAATAD/SKMRS*LTLSERLPN *FEIWDAAAPGTLPSPFFGAFDGHIF CIHTRALRGSTRTRQICAAALEGASFRN HVEL
10227	24128	A	10303	172	383	KIENKVVQGYBEIETLVYCWWECKMVQL LWKTTWVVLKILKLGPP*\DSIIPLLGI NQGTETIRFKRYSNT
10228	24129	A	10304	205	2	NEYPA*KTDFFLVGSLFIYFE*ASHPIIT \RLCSGTIVTHCSLDLLGSCNPPASAS HVSGTAGAHHICI
10229	24130	A	10305	423	30	LLEGKLTNRKDIRTKTPSVRRHLHQSPKV DRTAKMGKKQSRKSGNSKNQSAYPKPE HSSSPAMEQSWMENDELREEGFRQSS/M SKLKEEVRVNGK*VKTREKRLAKSLTRI TNAEKYLKDLMEKTSVLRPL
10230	24131	A	10306	211	387	IFFFF*IKACSVAGAGGQGRHLGSLQPP PPGKQDSC/SPSRGVGTGTGMTYHAQFI

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						FFGF
10231	24132	A	10307	229	382	ERAVVQPG*HGET/PSLKKL*KLSRCGG MCLYSKLLRRLR*EDHLNPRSWG
10232	24133	A	10308	168	417	GSYCFVRRNLLIVKVMRSVHLLFIMLL YRGD*WYVTTQYNFCILQKQEKLIYRIA /HVRNPSSLRGGG*IT*GREFKTSLAN
10233	24134	A	10309	253	402	KGGGGGVKTPARGNPPPGPPKGGKRG PPPPTQKGFF/CFFFKGTRPPGGKTGE RAKPNEIPAPGKKEFLPKPPEKGEIKG /PRPPGQINF*FLKKTGFKGGGGGSKP RPGGTPPPGPGQGGKNGGGPPPPKGF FGGKKKKKNPPR
10234	24135	A	10310	182	400	LHVTMIIFWLYLIKNNLLNFTYF/CYIF SVATSTFKIVCV/WLGAVAHICCPHTLG G*DGWIT*GQEFKTRLANM
10235	24136	A	10311	371	400	FIWGN*ASNKHKKT\STSLAFRKIQV K\TTMRYLSPPTPIRMT/I/I*KSYSSK CW*GCEEIRSLIHCKMIQPI*KT/WQFP KIINIQLLYNPAIALGNRTG
10236	24137	A	10312	113	404	QRCGKIGTFFHCWWEYKMQPLWKTOWN LLQRLNIELPCDLAIPLLNLYPREMKTS IYICT*MFIAALFII/AKWRQP/KCSSA DE/IGKMWIHCIMK
10237	24138	A	10313	146	1	FLTQKFFFFFFETESRS*AVVQWLDLGS LQPPSP\GSSDSPASAF*VAG
10238	24139	A	10314	157	434	FFFSEIFFFGPGVFSPPFFFIGPGIFF FCPLKKKILPPPRGKFFFKKGP/HPF FFFFFF*EGVSLLLPRLECNGAILAYCK IHLPGSSDLP
10239	24140	A	10315	277	2	FFFTAFFLGVPGVFPFPRFFKPGPGFFF LGP*KKNFPPPRGK/IKFFFLKGPSPF FFFFFF*EGVSLLLPRLECNGAILAYCN LHLPGSSF
10240	24141	A	10316	1	388	KTITHEVITECIWLKVLVLLYFPNCMIY VRMHICVCVHISI*MDHIVSYKCIHI \LCIY
10241	24142	A	10317	134	399	LGLPGDTRGGGTIENPPFERALNSONG GK\NPLLGPKTRPLGWGLCSTPKFWEKP RVRVVDLN*TPCLEKRAPWLKAKKTPA FEIRI
10242	24143	A	10318	233	3	EFLFSLICAICL*CALQFSSCFCLAL IELLGSMLLFH/SSELTQPPFLQIFF /SFFPLFFGANYTYNKPFEYSLI
10243	24144	A	10319	221	8	CDQPKSPPLSGVQMGDILVVLVFFLFLF AF*R*GSHCVAQAGLELPGSSDP/PQAT SQVAGTTGMHCTWLVF*F
10244	24145	A	10320	1	407	RSTPDVPVYLGTSGGCKTEKRAGCFFLW KLHTKGAPARCQPELSGMRC\R*PLGG V/SQSRMAVKDSLEEAGCPLSELKRCA GRYTGLFKGGRDLHLNLLRLCPQTTLC P GALSQEDGSFIYKPLTGAAAFLSYM
10245	24146	A	10321	115	398	ADEELLMNKQIKYLEMESTPGKDDVN TVEMTKESEYSI/NLKAVAGFERIDSNF ERLSAVGKML*NSITCYKEIFH/RKSQL MSQTSLSYFKLP
10246	24147	A	10322	137	454	FFSLYFQGGFFFFFFLGEKFFFSPPGKGI CPKPPFPPPPPGKGFSPPPPGKAKKK GPPPPPP\GFLFF*KKPGGFLGGFFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LGGKIFFSPAGGKGGPQKPPFP
10247	24148	A	10323	246	372	ISTKSYQLW\LGGVAYACNSSTLGGRGK WIT*GQKFKTSMANM
10248	24149	A	10324	415	1	IWGAPRVFPPPPF*NPPPEKNFWGPKKK KKFPPPPG*KIFFFKGPPPLFFFFFFF SETESC SVT\RLGCSGGISAHCNLR LPA SSNSPPPSLRMPSTPVL RPHGDL LSPQ LSAWVLSWPFPLPSLLLPDLDFIVQ
10249	24150	A	10325	3	559	GDGITGLSPTISKFLFFVFESISLSPRL GSSGAIMAHCSLTSRREPPCRSINFFVS VITLNVNLTNGKIGRMDFF*MM*YTIQ ICNLQNT HCRP/KDTNCFKMKRRKEIIH ANSNQKRAGVAILIPDKIDFKPKNVTER HRMLVRES/ISQEDVTIINTY
10250	24151	A	10326	24	387	NQGLGARNQKSQRVFLAGFFFFESSCS VAQAGVHW*DHSSV/PGSSAPPASATVV VGTGTVHNHPWLIF/VFVETGSH
10251	24152	A	10327	145	396	CDYFGEMFSLLLNIYLCDPDAIPLLPY VPYENENTDSLKDMTDAHSSFIHNSPKL ETKCPGTDEWI*MTKKS DYCKHW*GYRV TGTLLYEGECKIV*LLWGNV*LF\LLN TYLCDDPAIPLLPYVPYE\MKTRIHSKT *PMP IAA LFIAPNWK/PKCPGTDEWIN TL*HTHAVQYHVAVER
10252	24153	A	10328	94	639	ASISSSIKWDNISFLVGLGELNEIRNI CKAVNMKQALNKWKLILFVIENN NVSA SSNNFKIFYAYYIAKAVLLIITEHITLS IVLILKKQNNTRAVTKCW\RGGREK ETL IWLVG*ECKLVQPLWRRVWRFLIKV KIE LPYDPT/ILGIYSKERKSVYRK\NICT PMF\VAALFTTAKTWKH
10253	24154	A	10329	143	3	SAWFFFQDRVLL*/SPRLECTVSISNHC NLRVPGSSKNYCLSLISIWDR
10254	24155	A	10330	153	389	RQGLTLFPGLVSNFWLPVLSHLLGLPKC WGYQCYHAWPS*CF*NRSI/WSGTVTHA YDPSTLGGQGPIT*GQEFETSLA
10255	24156	A	10331	382	422	RYKLDL*KLNTLPYDPTVPLLGNYPKY *T*AF\SKTCT*MFIAAYSQPPKGRSKC SSPE*INKMWPYIMR/YYS AIK
10256	24157	A	10332	194	1	CKRQCNKEDRNI/CSK**NPTILF*TTK RKG/WLVAVAHACNLSTLGG*GGRAS*A QEFKTSRANM
10257	24158	A	10333	348	1	NSGQSWIMYPLLKKGVGRVSPDPDIDVN SISMVWCGRLFSNERFASLLTIKKKLA GHGGTCLQSLPLGLRLRREDRLSQGGQG/ C*GYSE*LCCRCIPAWAAEGDLWSWSPN SVAY
10258	24159	A	10334	388	2	IPGSPKRGPGEKKKTFFHYFLFLRAAPP LPRFIFFPKPNPLKGGGGFFFPKPL KTPRLRKKKKKENFCPWKKFFKKQTPQ RGRFFFFFFL RQSF AVAQAGVQWCDLGS LQPSPP\G*SYHPARTRG
10259	24160	A	10335	3	396	LLRPPCSLRHNDIEIMPHDNPMIASKCS SKKSCISLTLSQLDVIKLSGKGM LKA KTGQNL/GLGHLYRTVRHAVNVKEKCLK EIKNAALLNTQMTRK*NSLIADTEKM*V V*IQE*AS/HSMPLRQNLIQNK
10260	24161	A	10336	165	442	GQMELLILARNFGILHLHFNLSIYRRLF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FSIPRYLFIFTYLFIFTYFESVAHSD AQVECSGTIMALT*KKNASLP/ASAPRA AGATG
10261	24162	A	10337	33	430	TGSTHASANFCVSLVWVTQLISRSSGQGL ARLQLRCLPCCILFFSFFSLVIYRLHSY LRLPWRRICLQVPSGC*QNSFPCNFRIQ GSLLL*/MQQW
10262	24163	A	10338	284	3	SQHFGRRPRWVDHLRSGVDRDQPGQHGETL SRETP\SLKIQKLSGHGSACL*SQLEFG RLRQENCLNPRGGGCSEWRQHQCPTV*V TEQDSVPKKK
10263	24164	A	10339	414	2	ERAGPFSRKIFFSPPLAKKVYFPFPPTP RARAHKRPIFSRYVKKERGNPDLEWFP FFPSLW*KQ*GPSLGRLFYFPV/SWGIFP SKP*GFPGPRPKVFCFLG/LPPGPFGGP FFFFFFGDRVSLCHSRWSAVAQSOLTAR
10264	24165	A	10340	211	422	ASLGNGGRPSPSLAAALQPD*LRAGIT FALFKAARQGDLSL*RLLLSF\VCLCPA PRGGAYRGRQAFLSWGGLHPDRASRLFC LEKQAWAMAGAPPPALLLPCSLISYCRA SNQODSGGIGPSEPSAGYKLLVPGFLLP AEK\RTIYGGVTRFFRGP
10265	24166	A	10341	116	432	SRQRMPSYHVQSGDRTKTEKPCANGN KCGSSILRSLHRKRFSF*SLKALVWC GGACLEAQLRLRLRQEAHLSQGVPGCNE L*PGYCTPAWATEP\DSVSKKK
10266	24167	A	10342	103	458	SLNVCVLTTLPSSCSPISLPLRGPPYSL RHRNIEIRPINNPTMASKSSKRKS*MS LTLNQKLE\MINLHEECMLKAKTG*NLG LLHQIVDQVNAKKKFLKKIKSAIPVNT QMRKQN
10267	24168	A	10343	53	408	SFQFFCSVFSPSLWFYLLLVFDDGDVQM GFWCGYPFCLLVFLTDKTLSCRSVGVP CRVRCQA\LLGGASQLG\SRGSGVRDP LEEAVCLLSDQLRAGRRTTLF*AVRQG HLSLQRL
10268	24169	A	10344	265	421	NNFPPSPRRGGNPGPPPPRFFFFFLK NPGLPPF*VIYLL/YFTLTSPFCLWCYT ISVYGC GFVFFFSFFFFFEKKIFFFP RVEPKNRIPVYPKILFPG*NNFPPSPPR GGGNPGPPPPRFFFFFLKNPGL/HPF* KKGAKFPDLINPPWP
10269	24170	A	10345	207	420	WQKGCPTFMELGVVGLYPCFLHLWIQ PTSHRKYIHL/WLGMVVHTCNPNTLGGQ GGWIN*GQETSLTD
10270	24171	A	10346	115	3	APRGAVKKR/RPWMGAATHVCKPSTLGG RGG*IT*GQEY
10271	24172	A	10347	41	421	FTFVSVCVHFKGIFLSFLSFFFETEVPG SPLGPKRGGGGNSGPNPPPPGLRGSP PPPPQRTGKGGPYPPPPGNFFFKFFRK RGV/PPL*HPGGPQSVT*GTPPPGPPKF WGAQSGGPVWGKNPLF
10272	24173	A	10348	228	1	SKQVKEKYDSFLHKIQKQAT*NRTFFRV TKKHVEITKK/WAGHWAHAYNASTLGGQ GGWITLQGEFETSLANMVKP
10273	24174	A	10349	405	1	GGFLKRGPPFFFFLRLQGLSLPRLECSG MTVAHCSNILDSSNLSLRSDWDYSHQA QLIFLVSF*VLGSHSVAQAGVELLAS/P

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						KCWDYRHEPL/WPSQSQNLNSFFLDGFS LLLSRLECNAAISAHCNLRLLGSS
10274	24175	A	10350	301	546	RHIFMNLPPHNLVKIIFHCRGKTLFLDI SNPYLKKQVSSSKPNCK/HLKEI*LPLE AKDYWLGVVPHAYNPSTLGGQGRSITG
10275	24176	A	10351	873	1258	FCYQCYFHLLHLLHHHRSPRLPEPPPG AALPPVPEGRIIPLPCPSSGPRQTGPG KGRRHPPAPHRTPAASAASLPARRTLPA PW*PLSFQNTTPGSA\PGGGNQPASGAG GNSRT
10276	24177	A	10352	184	576	GLSPLSHLKMAASSSEISEMKGVEESPK VPGEGPGHSEAETGPPQVLAVGPDQPEA PQPGPNTTAAAPVDSGPKAGLAPETTETP AG\PQKQPRPQTS*AQEGNQRPATAAPK THAQETVSKPEVSKEATAD
10277	24178	A	10353	110	384	VPGSPRKTRSPQOMERVLAPKTAKKGCP RPGDHRSLQNCRDTRARIKWADSVERP PWAG\PVAHACNPNTLGGRGGWIT*GQK FKTSLVNM
10278	24179	A	10354	123	422	RKQIANDKSKLFIINKYLVNVELNSPIK /RERLAGWIRKEKHDPSCIHL*KTHLT\ KDTNSLKMEG*KKIYHANNY/QKKAGVA ILISDKIDFKFKKKVREK
10279	24180	A	10355	36	426	PPEPQYSARVCVCVFYTECRGLAPKPE CRGAIIAHCLLNLVLSQ*SSNLRVWSS* DYTQLIFKLFVQTGSHCIAQAGFELL/S SKDPPTLA/FPKHWDYRH\DHHSW
10280	24181	A	10356	193	3	FQTRIFKISFFFFKEFLKFKKFFFIILI* ESRSIAQAGVQWRDLGSLQPPPP\GSSS PPASASLY
10281	24182	A	10357	205	377	SPVVFQPYRLTIPYQKC*LATVCI*VY *FFKLILYPAILLNSIIWINFTSDPL* FSSHITG*LSLIKNVWVGPGMLAHA*\N PSTLGG/RGGWIT*QGEFETSLANMVKP
10282	24183	A	10358	51	376	LCRPFQLCHGDRDMDWCPPEELQDRCS CRSTSMRVAKGTTPCFLKVLQNIYTV* MFCRTFRKHGVVPLATRLV\IYKNSGPV TLQGRGTTYLSCHHGKAGRVCRAHQHAA GVVVTKQRACI
10283	24184	A	10359	295	376	ASELTSQSPGSLFENQKKGRCTAFLPC* KCNSEILVHCWWGCKM\WKIVW*FLKTL \RLELVYDPASPLLAIPRCI
10284	24185	A	10360	451	1	CQDIKTILRNEQEVLVIPSVTKYQVGVK SFVSRRLWSGCVLCYAFVTEASKTWHH FPYRSPGFWRSGRQFDS*PKSQADFR APQGPPTPPEPEGAERREPEIAPPPTADP SPKPT/HSPPRSGAPPSAPFPLGRAER GVG\PGQGRPRP
10285	24186	A	10361	2	776	FFFRLWSLALSPRLECSGAISAHCKLRL AGSRHSPASASRVAGTTGARYHARLI/L /YLFVETGFHHVSQDGLNLLTS*SACL GLPK\C\WIYRREPPRPAYFIFFLRRSL ALSPRLECVQWCDLRSIQAVPPG\LHHS PASASLVAGTTGAHHHTRLVLIL\FYY FLRWSVTLSCRLE\AGVQWHNLGSLQAP PPGFTPFSCLSLPSWDYRCPPCLANF LYF**RRGFTMLARMVIS*PRDPPPSA SQSAHDLFIVGQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10286	24187	A	10362	188	365	CPQLHTQSNLINMDASQRYQFELKIQAL/WAGTVAHACNPSTLGRSGWIT*GLEYATSL
10287	24188	A	10363	146	1036	GWAVYQTLQAAWLGPRTESGVSFHGRFS LPHHPPQPTLHAWPAPPLQPEPCVPLRE DFMPESW*LPPSIPAEGVSF*ECDFSR RMMGKGSVPVTVAPPLGPAPEPFCVTAG CAPMHTPTHTQ\PPHCSIFLPKISFKSK HFY*LLFCKCLSSSVFSLPESILLFFIV ESVCQPGERCLALNMGWDGKSGRRWAT KSQGVMDIAATQTPA/VFSPV/PATSCP AGVSGGK
10288	24189	A	10364	229	1	PLENAKSIYWGKGRLLKNNARLFTVA*S WNQPQFSLMVDWIKKK\MWRMYTTESCA AI*R/DEIVSCAGTWMELEAMY
10289	24190	A	10365	186	449	RFFFFFFPKFFWVFLKSPFFFFFFG/RLGI *EKDGGFFFFFFFFPEMASGSA\RLC SGAVSAHCNLQFPGSGSLPASAPRVA
10290	24191	A	10366	445	3	RVDNGVRGRYRGKRGRR*TRWGWGHP QRWDQDRSRERPRETGRERAAGRRRETE AAETGRRRRERGRSDNRN/RGRPRERM IEAGRDAGRERR*ARQESWTEKKTARQE EGDRD/RQGHQETRAHKGWGN*D*GRQ AERSENRRMY
10291	24192	A	10367	1	491	NTAPFPTSLESFAFVVAVQDRVS/LLSP GPECRGAI\LTHCC/LRTPG/FKPISHL S/LPS/SWDYRHVPPPLDNLILCRDNVS QSGKLKLLASSNPLTSAPFST/YDYRRET PGPRASP*TQMPCFMP/RS*SQP*TQI A/R*QSNWGSQ*VLNNRELAFGTMFFGQ RPKAFF
10292	24193	A	10368	572	40	LHSFRQHFSNTYPQCTPGTP*VTQSLAA RPAGLPEPTSASGGAGAVTPPPRTD\PP SVRWSGKKGLDPVLRGGAPRPSPANPAP APQGPAPRKGTECVPTASKTPRPGGRWE PAAPPHAHPGKDLQPPSTLVKECPEARC PRALTGDLPSNGENRNLGSAFQQRPA QKSGENCEN
10293	24194	A	10370	36	517	PFLFSDIDFLFSFYFLSFFFF*KRGLIL PP/GPEGQGNGK*WPLHPRG*REPPNL TPQTRGNKGNRQTGPVIFGILRKNGFPP FGQGGFKPPGLREPPGLALQRGNGNQ PYP/P/PKGFF*RTKRGEKSPQPPYNKP NKKFNPAPMEEFSSFKEGRGPSLN
10294	24195	A	10371	60	403	DVEQPKLRSYPTLKCKPRSAITLTCPPWA LQYRSHGLIFGFSWGFSLSFETESCSVSQ AGMQWCDHGSQT/PTDSTSQAQAIDPP ASAP\QAAGTTGACHHTCLIFVFL*RWG LAKP
10295	24196	A	10372	358	33	DSLGVPGAPLLSPGVTPHKQWFFRPTQ IKKLGFPPQIFFGFKV*KAPFFWGFNG LKKKGKGGFFFFFSEMASGSA\RLCS GAISAHCNLQFPGSSSLPTSAPRVA
10296	24197	A	10373	264	3	RQTSVSGSNDGKSWPPADIDTI\KYVIG NRLITTQQ*LIKLTSKQMITIHNTKGRT *SLILVSLIIFIATNLLGLLPHSFTPT THCI
10297	24198	A	10374	298	384	TLVI*KDGVHTTPHHQQHAYPGPKEYML

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						HKAPLLHSVSRDPSPFQAQSSNCYNRSIK QEPVDPLTQAEPVPRDAGKMGKTPLESEV SQNGGPS/HK*GQYSGDV
10298	24199	A	10375	84	518	IMKLRQKSRSSSLKIMRSKLQHTRAS/GT QLR/PMLGGNFIALN/AHIKKLGRQTQIN NLTSQLELEKQD/RNPKARGRQET/K I*AELKETET*KKEIQKIYEFVR/WFLE NINKP\PASRLIQRMIERNTIRNDKGNV TSAPPDV
10299	24200	A	10376	70	363	FHQKNLVPGLWVQLLGRRTLQSQHPPAP PPSSEPEVNPSEVQAD*LCCIFYDVK VRKCSTPQKTRKRKKGCLF/CAPGQTR /CLC*KRGEKNLVGKT
10300	24201	A	10377	299	2	YPVAGRGNR*GCGAHLGVGGAAMPLGA TISSVSLTISSLCAPRRGGLEPLPAP HTPPPPE/P*ASSPSRGEWHLVPPCMQ PGLPPLPPRLSPLV
10301	24202	A	10378	302	3	WPTVATTCSCKERSHSTLT*NQKLEGTQ LSEEGMSKAEIGQKPGLCQHT/VQVNA KKKLLKEIKNATPVNTQITRK\QNSLIA DT\EKV*VIQIEDQTSHV
10302	24203	A	10379	125	375	NEYVFLEKSLKLAGRVGSCLLGRPRQVD HLSSGAQD*PGQRKTPSLQNIQXLSRH GGMCP/RRLRWEDHLS/SRGG*GCSETR ST
10303	24204	A	10380	458	3	ITISTISCKATSFERAPRASRPFPDEWV SQAGPAPLRGWEN*GTRRRDDWPEASLK DPRRSGEPEAPL/PLRLML*SRLPPPLR WRRRPPPPDSHTPSPGNGKSPRVPTGS KDKRPEALPP*FAAGEPLEANVPVQHG GGSVRSRGSYLTAT
10304	24205	A	10381	327	2	LSAPKKFFFOKSLFLGANFRSPFPGRP FTNRFSDLVNPLTKKIYFSHKSSNPPT FFFFFFFETGSNSVT*SGVEWRNHNLSLRP ESPG\SGDRP*V*HTTGAPYHTWL
10305	24206	A	10382	754	1	NTALETDTTFSGGGGGHQLCVRSRVSGG G*LIMPDHNNHPLQQTSGRNQRLQGEVT DPSPGMSGGAQTGPKAPPRPPSALRHSG SLQGGP*FAHLYCGTIPYPCYTAPLPR APPPTPTGH*CPGEA\PDDELPCVGCSP WPRPPGQAQAGRKH*FSGQRSSRDITA CSPCSQSKQSPSRPPCVNDS/PGQGP GP KAPAGPPPALPEASLGSVHCSP*VGVMPT PRPGHFLVPGKVTLEQAPGGGASGGPV P
10306	24207	A	10383	39	433	SHDQTYTEELLFMDEQRKWFLLMESTP GEDAVNVVEITTKNLEYCINLVDSTVA/ GVSNFERRSTVGQMLSNSIVCYGKIF/R *KR/SQSMWQTSLLF\NKLSQPP*PSTP TILISQQPSMWRQDPPSEERL
10307	24208	A	10384	283	1	NVFSCKPTSSCLISPDSTPDRRFKAD TYRNFMFPLRRHMHHTHTYMHTHVHVC TQLCLHLRPH/ITHGLSL/TCAPPVL*R PSFKPLHPTPV
10308	24209	A	10385	12	471	SPPWWTHGFRYWEPTPPRFSPVPHDALGQ FHTALFRLTRRFQLLSSCINISHTCLP PCLGLCVGGPLEPAVCWAR/CP*RGMV SGWKASPLG/CPPTLLPFC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10309	24210	A	10386	287	1	SFCVRSRPAPTSGRTFPFPAAPPFPAAPP FPAATTPSTAEDGVPG*/G/PAPAANCSP HSSQRGSAAMGIPLPQAS/PPAPTAPP SP*SLPFPFAPMY
10310	24211	A	10387	336	3	LIEGKLTNRKDIRSKTASVRHHQSPKV DKPTKMGRNQRKAENS\KIKSASSPPK ECSSSPATEESWMENDELREEGFR*LVI TNFSELKEKTGKLNPAALVCGRSEDQTT
10311	24212	A	10388	15	470	APSPDAMGR\FTEEDKATITSLRCKVNL EDAGGETLVRLQVVYPW\QRYFDSFGNL SSASAIMGNPKVKVHGKKELTSLVDAIK HLDDLKGTFAQLSELHCDKLHVDPENFK LLVNVLVTVLAIHFGKEFTPEVQAYLHK MVTVVANSLRYK
10312	24213	A	10389	3	438	QTQREPTMVLSPADKTNVKAAGKVGGAH AGEYGAEALERMFLAFPTTKTYFPHFDL SHGSAQVKGHGKKVADALNNAVAHVDDM PNTLSDLNDLHAHKLLVDPVNFKLLNHC LLETLDGHLSAEFTP\AVNASLEQFTAF EITWLT
10313	24214	A	10390	2	444	TMSFNTLAICLDCLCSTLQPTRSIPGY SSPLPGNPTPPMTPSSSVPMSPNQEVK SPFLPDLKPNLSLHSSPSGSGPCDELR LTFPVRDGVV/SGALPPAAQPGC
10314	24215	A	10391	405	3	KMILTCLALPAQHCPFSACPQTMAQPPL PLSIKGAASMSDKLPYKVADIGLATWGH KALDIVEN/EMPGLMGMELYSASRLK GACIADCLQITVETAILIETLFSLVQVE QWSSCSI FSTQEHAVAVFAEAGMP
10315	24216	A	10392	248	5	RLNKVGGHGGNYEHLYVNKLETLQEMYK FLDIYNLPNLSLEEIE\NLNRPITSNKF ESVIKHFPPTKISGLDGFTEAFLTN
10316	24217	A	10393	262	3	LPRDRQAGRSQGPVVPQAVGRARKMPF ISYQVYSKNFFEIEESCVTQAGVQWRNI SSMHPPPP\GSSDSPASASQAPGIPGAH HHA
10317	24218	A	10394	287	410	ALKGSSRILIMLGAWLTFVIPA/LWEAK AGRSSEVRS
10318	24219	A	10395	175	1	GGREVDDEIPLVRESTIFHIFFFEFETE SHSVAQAGGQWRDLGSLPSS\PPG\SCH SPA
10319	24220	A	10396	661	963	STLIAFIVISTLFLPLDMTEIYFSLDDE IVDTLGEAGFGKVVECIDHKAGGRHVAV KIVKNVDRYCEARSEIQVLEHLNLTDP NSTFRVCVQ\MLEWFEHH
10320	24221	A	10397	1	268	PQTHREATMGLSTADWTVKAGWGKGA HAGEDGAEALERMFLSFPTTKTYFPHFD LSHGSAQDKGHGKKVADALTN\AVAHVD DMRNAL
10321	24222	A	10398	33	302	SRGATLIYVDNENGEPTGRVVAKDGLKL ESGPSIKALDGRSQVSTPRFGQTFDAPP ALPKATRKASGTVNRATEESV\KTRGHL VQEHP
10322	24223	A	10399	16	233	PTDYEFNTTTYRECGRRPEFSTSLDLL SQPCRAVYM\VGKENDIPFELRIVDLIT GKSILGFGEPSQEGDR
10323	24224	A	10400	177	1	KLLDLGQPQSPALAACLEYSGAIAAM\C NLCLLGSSNPPTSASRIARITGVHHAEP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						YA
10324	24225	A	10401	185	419	HVNKDTLESHLVWKLKLSALLGRKSESVT GPSCHPEPSDKTVEL/WQGAHAHACHLS TLGGQGGWITLAQEFETSLDNIV
10325	24226	A	10402	104	3	GIILIPKPGRDTTKKEN/RPLIPIDAK ILNKILAN
10326	24227	A	10403	3	344	SQVMAVAGPAPGAGARPRDLQFLQRF QILKVLFPSSWSSQNALMFLTLLC/LTLL EQFGNYQVGLIPNQYYGLGNKDLEGFK TLTFLAVMLIVLNSTVRSFPLSVSLVLS SPV
10327	24228	A	10404	3	404	ARAQRRGDLSATGRNWSPLPPAGLPATV VLRHSGSLMAATCEISNIFSNYFSAMYR S\EDYTLASVPPAATFGADDLVLTLSNP QTSLEGTEKANWMC\EQSQFWPKTQGLD WISFQAEKNKYEASAIGFPRWDK
10328	24229	A	10405	254	443	NQLSSIMVMFKKIRSFEEDFNDPEKVYG SGDKVAG\RLIVEVCEDTRVKAVRILAC GVAKELRM
10329	24230	A	10406	26	461	GEVARRSCCGAMAGTALKRLMAEYKQLT LNPPEGIVAGPMNEENFFWEALIMGPE DTCFEFGVFPAILSFPLDYPLSPPKMRF TCEMFHPNIYPDGRVCISILHAPGD/DP HGLREQ\PERWSPVQSVEKILLSVVSML AEPNDES
10330	24231	A	10407	1	463	QQAAKMAENSGRAGKSSG/T/PARGRGR C/PAEQVIAGFNRLRQEQRLASKAEAL EMELNEHSLVIDTLKEVDETRKCYRMVG GVLVERTVKEVLPALENNKEQIQKIET LTQQLQAKGKELNEFREKHNIRLMGEDE KPAAKENSEGAGAKASSP
10331	24232	A	10408	180	446	KKAAASVSAASGSHLSNSFAEPSRSNGS MVRHSSSPVRYPSDKPFLNSDLRRSPS KPTLGYPESNSRAIFSAL/KNLQD/KIR RLNL
10332	24233	A	10409	1	417	EAGLVTMEEIGILGEKAQDEIPALSVSR POTGLSFLGPEPEDLEDLYSRF/KKLQQ ELEFLEVQEEYIKDEQKNLKKEFLHAQE EVKRIQSIPLVIGQFLEAVDQNTAIVGS TTGSNYYVRILSTIDRELLKPNASVALY
10333	24234	A	10410	305	53	LEAQPHAPPLLGHHLPWCWRIPSHLGT CRPRAMRVQGESEEGVA/GQAPPLPWVHR GSLPLVRRRPAGKPTGGNAREEKGVKVEG
10334	24235	A	10411	419	2	NNSRKFGNGTLKLVEVEITYPLISEIPD KSELLLPQDKKHAPLPSAVPNPSA/CP DLRPHTTPASPV\PAKTVETRPAPQG PLPGPVRRPRGRFSVRAASPQTSGRPGA PRPPGPALREATDAPRAATPPIAALAGH S
10335	24236	A	10412	74	322	MDEMA"TTQISKDELDELIEFAKVDLSS NGFICDYELHELFMENMPLPGYKARET IQKLMLDGRNTDGKIS\YDEFAYVSM
10336	24237	A	10415	1	415	PQTHREPTMVVASADKTNVMAAWGKVG A HAGEYGAEALERMFLTFPTTKTYFPHLD LSHGSAQVKGHGKMVADALTNAVAHVDD MPNALLYALSDLNAHKLWLDP/VNFMLLS HCLLVTLVAHLDPDEFTPAVHACLKLL
10337	24238	A	10416	19	454	APSPNAMGHCTEEDKATITSLWGMVNVB

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						DAGRETLGRLLVVYPWTQRFFDSFGN\LSSDSAIMGPNPKVKAHGKKVLTSLGYAIMHLDDLKGTFAQLSELLCDKLHVDPENFKLLGNVLVTVLAIHFGIEFTPEVQASWPKKMANVA
10338	24239	A	10417	2	395	ALSSSQPSAPMHPFYTRAATMIGEIAAAVSFISKFLRTKGLTSEKQLQTFQSLLAEHYKHHWFPEKPKCKSGYSMIGVNP\KMISLILQACIEGGI
10339	24240	A	10418	2	374	LSTPHAFGTGKWTGISLFLFSSAYSRGVFRDDAHKSEAHRILKDLGEEDFTALVVIATAQLHQWPFEDH\VLANDVTEFAITCAADESENCDQSLHTLFGDLLCSRA TLDESHCVQDGRP
10340	24241	A	10419	48	347	DPKAQLPEPLRVLWQLTYAMAAGSR/TSL/L/LAFALLCLPCFKAGPPNRPLRLFDHAMLQAHRRITAITDYQEFENLYPKD/QQYS/FLMTPTSSALDSIPTPS
10341	24242	A	10420	166	1	NFLKKPGPFQKFFQRLPLILITFFFFF\FETKPHSVSL\LECGGTVSAHCNCLLPV
10342	24243	A	10421	2	251	LGCTQHRSQELVAAATSHQTCIQASEDVKEI/FARARNGKYRPLKISIEHQMLIGSY/SSQPSDSDNDYDSFVLPLEDKQLCY
10343	24244	A	10422	251	1271	KEDLSRAPMSGTQSTITDRFPLKKPIRHGSILNRESPTDKKQKVERIASHDFTDSSSKKTKSSSEESRSEIYGLV\QRCVI IQKDDNGFGLTVSGDNP\VFVQSVKEDGAAMRA\GVQTGDRIIKVNGTLVTHSNHLEVVKLIKSGSYVALTVQGRPPGSPQIPLADSEVEPSVIGHMSPIMTSPHSPGASGNMERITSPVLMGEENNVDHNVKVEILRKMLQKEQERLQLLQEDYNRTPAQRLLKEIQEAKKHIPQLQEQLSKATGSAQDGAUVTPSRPLGDTLTVSEAEITDPGDVLRITDCSSGDASRPSSDNADSPKSGPKERIYLEENPEEQKKG
10344	24245	A	10423	198	569	QRNMVGQRLVEPRRLKPGFINVKSYNQDNEWHQGFLLVCFLLRWSLALSRLSCSGAISTHCNLCPLPGFKQFSCSLSPSSWDYRHAHCTQLIFVFLVEMG\FHHVGQAGQGFFSLEKSLTII
10345	24246	A	10424	2	343	PQTQREPTMVLSPADGTNVYAAWGVGAHAGEYGAEALERMFLSFPTTKTYFPHFDLSHGSAQVKGHGKVS\DALTNVAHVDMPNALSALSDLHAHKLVDVFNFKLLSHC
10346	24247	A	10425	31	342	RAAVMPREDRATWKSNYFLKIIQLLDDY PKCFIVGADNEGSKQMQRMSLRGKAVVLMGKNTMMRKAI\RGHLENNPALEKLLPHIRGNVGFETIKEDLTEIR
10347	24248	A	10426	196	2	KNLIISQTKKVICPNTFLVFPKRVFFF FFFETESRS/VSPRLCSA\SISAHYNLCPLGLSDSS
10348	24249	A	10427	1	405	RLECWLPEPPHAGLQGLGWVWVSCSVSTGPTMQALV\LLLCIGALLGHMSCQNPASPEEGYPDPDSTRALEDDEDPITFDPENKLPEAGSNFGYDLYRLRAIMSPTSNVLLP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PLMVATDLWDLSEAAQQLTESII
10349	24250	A	10428	223	361	EGPTEENMAAKVPES/IGKFGLALAVAG/GPVNSALYNVDVGHRAVIFE
10350	24251	A	10430	3	359	LTQREPTMALSPGDMTNVKAANGKVCACHAGDYGAELERMFLYFPTT\KTYFFHFDLSHGFAQVKGHGKKVVDALTNAVAHVDDMPNALAALSDDLHAHKLRVDPVNFKLLSHCLLVTLA
10351	24252	A	10431	273	1	NHKDGGKKQSGKTEKSKNQASPPPKERSSSPATEQSWTENDFDEFREEGFI\RQSNYSELKEEIRTHGKEVKNLKLLDDRITRITNAQK
10352	24253	A	10432	211	3	SFLWKFCRLRGIPSHVSCQSA/LLGGASQLGYSGVRDPLEEAVCLFSDLKLHAGRTTTLFNAVRQGHLSLQ
10353	24254	A	10433	281	2	TNQEKKKGDENKIRSGKDDTTTNDVTIIRDYTG/HTYTNKLKN/LEEVDKFLDTY YLPRFNQREIENMNQPIITSNEIESVIKSLQTKKSPGPMAS
10354	24255	A	10434	219	1	SFLWKLRLRGAPGCMRCQSA/LLGGVSHLGYSGVRDPLEEAVCPYSDNLNCAERTTTLFKAVREGCLSLQKF
10355	24256	A	10435	133	2	FPKPPGNFFFFETESHPVT\RLECSGAISAHCNLHLPSSSDSPA
10356	24257	A	10436	248	376	KGGVFFFFFFFETESCSITQTGAQWHT\YGSLLQPRPP
10357	24258	A	10437	250	1	KGTRKELTFIEQLLSAKYWAAGCMHYFRGSGKYSNGYPVFVFVIFSETESCS\VAQAGQWCDLVSLQPPPP\GSSDSPGASF
10358	24259	A	10438	354	2	KRGLKKNPFFNPRNMGEFLKLWGPNNPKKIFKNCKIFKMGLKKKVLGFYKNSKNLKRKGLNPFVIFFFFFFFFLETGSYSIA\RLKCSNSGTNTAHCSPELPGSRDLFDS TTQVAG
10359	24260	A	10439	126	1	GMVDCVCLFCFAIKEGREEREKEREKERRERQREKER/ERERDKERKREERK
10360	24261	A	10440	29	347	IQKPTADTKKFFKKKLKYTTRENHLHNKEDRKEGKKEEKTTKQHSSSKSLINKTLNINGLKSPIKTHRAE/WNKNKDPMLYCIQETPFTYKDTHRL/RIQGWKKIFH
10361	24262	A	10442	405	1	IFFPHPPFFKKSFRLSPOVEIQGIFLGPWKLFPPGFNNFS/CPNLNNLGFKGLPPRPSYFFRIFCKKKGF/H/RVYPEGFPPFALGFFPLFPFKSWGFGDPPSWGPFPPFFFFVLVAEGLTSEGCRILIRGRWKNLVP
10362	24263	A	10443	122	372	LYNDPISITYQVTLYRRVFFWVLYSANWSLRWKANFLFFSFFKMASDPVAQAGVQWCDLDSLQPP\GL\SDTPTLASQVSETTG
10363	24264	A	10444	171	3	RHPTMAGSSEMFLGSGFGCRLTVFVLFE TESCSVT/RECSGAISAHCYLSLPGSSNLP
10364	24265	A	10445	173	3	CMNVVCSIFIFLKNIFILETESHSVSQAGVQW\LITVHCSSLKMGSSDPSSASQV
10365	24266	A	10446	187	329	SFLWKFCRLRGVPGHVRCQSA/LLGVASQLGYSRVNPLEEAVCPFSDL
10366	24267	A	10447	27	226	YSYPVYLLHLIFLCWKCSLYFIYFVFEM

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						ESCSFAQAGMKWCDLQPLPPG\SSDSLAPASQVAGVDAA
10367	24268	A	10448	119	296	SPIHYILVITICFIHVILLIIIFSEVGS HSVAPAGV\SGAIIAHCHNLKLGSSSP VSVS
10368	24269	A	10449	111	363	SLKKLVFFFSIYTHNFFPFDPTLKNST RHSLYLSLSLSLFLSHSV\SRLECGGTI IAHCSLNLPGSSDPHTMSQV\AGPTGS C
10369	24270	A	10450	218	1	QRFWGPDPNKVFKNLGSAFFLGRGKLF LEIWGGFFFFFLVFFLRQSHSIAQAGVQ WCD\LNSLQPLPPRFK
10370	24271	A	10451	179	3	GPFKLTFFFMGKFALGREKCHFFFE SCTVAPAGLQWRDLGSLQPPPP\GSSDS PAS
10371	24272	A	10452	71	232	SSPLSDLLFNIVLEVLAKDIMQVE/IK LILIGKDEVKWSLIVDKIILYVKNKSH
10372	24273	A	10453	153	3	ARGELYFLEIGGGFFFFFLVFFLRQSHS IAQAGVQWCD\LNSLQPLPPRFK
10373	24274	A	10454	338	221	MGFLHVGQASLKLTSICP\LGLPKCWD YRHEPPRPVIPS
10374	24275	A	10455	214	366	YNYKYLIIHYSYLFFIFIFP/NIHYIF FILFFYLTSPIFLSYFFFFITLF
10375	24276	A	10456	155	2	DRVSLLLPRLECNAILAHCNLCLLGSR HS/PRVAGITVAHHHARLIFCIF
10376	24277	A	10457	870	1249	EGPRWADHLRPGVQDHLQOHGETPSL QKIQKLARRGGTC/LCQSLLGRLSQEN CLNLGDGGCSEPRLHHCIPTWGDE\GDS PKKKKE
10377	24278	A	10458	222	404	KQRPGRQWLTPVIPKLWEAELGR\MLE ARTLRPAWAT
10378	24279	A	10459	122	362	LSEDQLNCYPQRLHHFIFLPVITRVQMS HYLCQQSCLFHFF/SFFFLYFEMESSV T\RLCTGMISAHSNLYLPGSSQSSG
10379	24280	A	10460	3	102	AASTLALSRLCNSAILAHCKLH/LPA FTPFSC
10380	24281	A	10461	133	339	KLKFKQSGSKPEIKANSDLALFYHNYI TRQCFTSYSNFFGDRVSLSPRLCNGV ILAHCNL/RTPGFK
10381	24282	A	10462	3	193	ASNMMTELKSQIPILTLNVNGLNAPLKR HRVAGWINDPTICYLQETYFT/CKNNHR LTAK
10382	24283	A	10463	126	314	RLGGSTIKVQDLSSDRSKPGRFLYTSN SSYVRKGKRNKACFTERV/PVNDII
10383	24284	A	10464	1	332	KKNLFLSKDCLSSLFREKSPAILGPP RGWTPKTRFIGPKAFFFKGSLGRKY HFGLKPVP/CPPFLSKTRFLPGVPPFFF FFFETESHVA\RLCSG/AISAHCKLR L
10384	24285	A	10465	173	365	RFVCSTIKVLRDLSSDRSNPGRFLSLQI PP\LRKDKRNKAYFTK/RSPVNDIIST
10385	24286	A	10466	335	3	PFKKFYFKISTRALLEPVFFGKKIRVPP QRLSPIWAPLFKRGPPNSFQVNGVPLFF FFFFVRHGLALSSGVECSGTRLECSGAI /STAHCHLCHLDASHPTASWVARPTG T
10386	24287	A	10467	818	1008	VHTDVLADILKSINNAEKQRT/RRCFLS \WLQGHCPFLTVMQHGCLGVELGGLPG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PGDFCKRPR
10387	24288	A	10468	111	1	MVSFGRPRQADHKV\GVRDQPGQHGETP SLLKNIRI
10388	24289	A	10469	204	1	LWGPILKIFCQILKTICEGNFRGPTFFI FFFEMESQSVTQARMQWCDLSSQLPLPP GS\SNSRASAS
10389	24290	A	10470	190	330	ERIKKQDLSTICCLQVTHFTFKDSQRLKV KGWKK\IFHTNKNQKRIWT
10390	24291	A	10471	162	2	IKGPKRAPPAKNGRAFFFFFFFFETESC SCLQAAVQWHDLSPPQPTP\GSSDS
10391	24292	A	10472	120	3	SWGFFFFFFEVSYSVAQVGVQWCDLG SLQAPHVMILVK
10392	24293	A	10473	298	1	RRALPCPANFLYFYFLSLLFFETEFHS \VAQAGVRWHELGLSLQTPPPG\SSDSPA SGEYSANYTGEYSANYTGEYSANYTGEY SVNYTGEYSVNYTGEY
10393	24294	A	10474	1	380	AVTGRAGSMVAPR\PLRLVLFYQGLR SMAGNFWQSSHYLQRIIDKHDLLNERQK DLKVLSEEEYWKLRFFTKVIALCEHL KLRQPGIATATAYFKRFYARHSLKSIDP VLMAPTVCCLASTAN
10394	24295	A	10475	289	2	TQGFPPINNSFYALYPKQKIPFFSDKLF RVKGFGKGPVFHYGVKDFKNKDGVFVFF FEMASGSVAQAGVQWRNLGSLQPP\PG SSSLTTSAPRVAS
10395	24296	A	10476	138	402	ITGRAPPKPFPLKRGYLSGGLTNIGFSF SFSFFETESRSVTQAGVQWRNLGSRSWL EST/SPDSSNS/PAPASRVAIT
10396	24297	A	10477	2	336	ARETNDTTQTRLPANNTMRSDPYISI LTLNVNGLNTPIKR\KRVASWINKGLM GCCLQETHLSSHETHNDTHKLKIKTWRK IYQANGKQKKARVV/ILISDKTDFKP
10397	24298	A	10478	51	250	RKVSFLFKKWCNTLTFICK\LSLDTYRF AKINFEWITDLNVREKT/IKLLKGNIKE NICDLGLGKDF
10398	24299	A	10479	216	2	GFTRKALSGFKTGWFVFPNFSKLFFK KNFSERFFFFFFFEMESHVS\RLCSG PISAHCNLHLPSSLV
10399	24300	A	10480	191	3	FSTDGNVNCLVKYSIYIYIYFFFLIFF FEMKSCS/VSPRLECNGLSAHCKLCLP GSCHSPARA
10400	24301	A	10481	135	768	LGGQVLSCASQPVSLFPLFFFLISFLGC LLAFLSACFASTFSCVLGSPETSFSPL HPPPKVLSSH\PPCSR/CPQPPKG/P PLPKHACPP
10401	24302	A	10482	126	333	MVVGQRYCVMCFVI\VLCLFLV/VVW FLW/CSVYIVWYGYAVLFIFFFFFFFS LLCFVCLFVWLLDRF
10402	24303	A	10483	240	2	ATEKNMGLGTSVRGLSGSNPSYGRVRER IGGGVCLWSQILLRG\LRWEDHLGLGG GGCSEPRSSHCTPTWVTEQDPVLV
10403	24304	A	10484	136	2	NRPSYIFSFETESHSAQAGVLWHD SSLQPLPP\GSSDSPARA
10404	24305	A	10485	161	328	EKNFKPYGSCRHFLFIYFETESRSVA\ RLECSGTISAHCNLRPLGSSN/SPAS
10405	24306	A	10486	193	347	ILFSFLLFIYFFETESCSVAQAGVQWHD HGSLRSRAP\SYNAPALDSQTE
10406	24307	A	10487	114	2	GAVVQSEVQWRDSGSLQAPPPG\SRHSP

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						ASASQVAGLV
10407	24308	A	10488	314	49	IRRSTERSEPRYSMVCRQRQGGPCL\RSQLLGRRLRQEDHLSPTAGDCSEPRHL\ LACTPAWATEQEPLVKKMSPTLFCFLW PLPCQ
10408	24309	A	10489	291	1	KSPPPPPNRRGLTLRSRGQIGNGVSFYYE APVTDFI FFFQSLVLS TQAGLQWCNLSS LQLPPPG\SSDSPASASRVAPVSQGHAT APQPGRQTLSSC
10409	24310	A	10490	226	3	GSRCTMPRRRLAHAFPAARMPPKRKVSST EWATEEPPKRRSARLSAEPAPAKVETK/ PEKAAGKDKSSDKKVQTKLV
10410	24311	A	10491	2	153	ARGLVFFVYL VEMTLCHVAQA AVKPLTS SEPP\LG LPKCWDYRREPPRPT
10411	24312	A	10492	123	342	THYLCLLRFFFLDRGFLLLPRLDC/NAP ISPNLNLRLP ASSDSPASASRV TGTITVV NHYARLTLLFIFQNETLF
10412	24313	A	10493	194	2	IPGWPFKNFSLFPLFFFFFEMESCVAH AGV/GSSDFPASASQVAGTTSMRINAWL IFVFFSRN
10413	24314	A	10494	373	1156	KVQLKVYLF FFLRLSLALLPRLECSGTI LAHCNLP PPSRFEQFSCLSLPSSWNYRRP PPHHARLIFVL/SVETGFHHVQGAGLEL LTSGDPPASA/FPKCWDYRHE
10414	24315	A	10495	181	3	SFLWKFSLRGVPGVRVRCQSA\LLGGASQ LGYSGLRDPLQEAVCPFSDLKLCAGRTT TLFK
10415	24316	A	10496	156	2	AASTTRLGDRDQPGQHSETPSLLKIQKL G\SGGGHLRLRQENCLNP\GGRGC
10416	24317	A	10497	157	300	IQSWFNILKSIHVTHHSNRLK/EVNHIV STDAEKADKIQHPFLIKKQ
10417	24318	A	10498	3	289	LVKKMLTGSTLGKSYRHPFSINQGHNA LRKAAG\PLPRKAGY\LQGFSPRYGL\ WDGKDLTIHQPDTRGSLVSRISKRGRP L/CSCPLGTECLSI
10418	24319	A	10499	138	1	WYGLIYLLLEMESCYVAQAGVQWHDLP S LQPPPP\NSSNSPASSC
10419	24320	A	10500	138	1	WEGLIYLLLEMESCSVAQAGVQWHDLGS LQPPPP\NSSNSPASSC
10420	24321	A	10501	200	343	LEAHSFLSFFIFIIIFDTSKHSVT\RL ECSAAISAHCSLLLPSSNS
10421	24322	A	10502	84	339	PRDGKRRDKQKQETGGEHYKSQLRGRIR QEDHVSPPGGRGCSEPRSRHCTPAWAT\E SNSVSKKS
10422	24323	A	10503	141	362	EWNCCVCC/CCCCCRCF
10423	24324	A	10504	198	320	TIKKQKNTGGLIFNSYILPPLFLEPGDL \RFLDVDNRVKLPV
10424	24325	A	10505	30	356	GYPNCNPIYYMSTVGFTTSLLD FDIPL EHPILKVCPTHTRALRDLSSDRSNPGRIL STSNSSLY/EKDP RNKAYFTK/RPSPVN DIIST
10425	24326	A	10506	16	375	KKFFKKKKKKIFFPPFP LKNFFFPKRVN FFGRGWPKSPPKKVFFKKFPGGFKKP PLKKKKIFFSPPVKMGPPKGFKKGPPP FFFFFFFFFFFFFFFFFF/LCLIPR
10426	24327	A	10507	156	2	AASTTRLGDRDQPGQHSETPSLLKIQKL G\SGGGPLRLRQENRNP\GGRGC
10427	24328	A	10508	313	2	QSKWLLLEESTLGEDAVNIVEMTKDLE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						YYRNLVDKAAAGFERIDSNFESSSTVAK ILSN CIVC/Y/REILHEGKSRPMWQTSL SYFKELPQTTQHS AIIITLSPRA
10428	24329	A	10509	325	1	EC AKEMNAETKRNIADATETQRIIRD C YEHYNK MENLEAMDKFLDTHNLPRLN HE E IENLNEPIMSNETETV/I/NSLPSK KN SGSEGF TAEFYQRYKTP LILKLFKK
10429	24330	A	10510	126	14	DSSGQVQWLKPIIPV/LWEPEAGRSPEV RSSRPACPTW
10430	24331	A	10511	435	769	PFKFPPLSHACDGGSLFCRLRLC SGVIT/AHCKPQLPG/SQSDFFASTSQ BELGP/TGACHYTRLICCREEVL/HVAQ AGLELLCPKDPPTASQHARDYRH/GHP AQL
10431	24332	A	10512	147	412	RFVCSTIKVLRDLSSDRSNPGRFL STSN SSLY/EKDKRNKAYFTK/RPSPV NE
10432	24333	A	10513	251	466	QTCPTGSPASLLELFNSIATQWEL VRS L IAGNALKDEND\SAVKMLASLIM SYKAA A AEDYKADCPPRNPGP
10433	24334	A	10514	286	1	SFLRKFCLEGVPSRVKQCSA\LLGG ASQ LGYSGVRYPLEEA VCPFSHLHLH AGRTT TLFKAVRQEHL SLQRILLPLV GRVGRPN DSRCDRVIGH
10434	24335	A	10515	28	428	RFVCSTIKVLRDLSSDRSNPGRFL STSN SSLY/EKDKRNKAYFTK/RPSPV NDIIS T
10435	24336	A	10516	263	2	IKKPADSESAGALILD FPASQTVR NSFL LLTSHSV CYFCYSSPNGLRQ QLKIIFF FFLRQSCSV\SRLECSGMIL AHCNLC L P GSNN
10436	24337	A	10517	62	292	PATLFSGVILPPTNSINAFSGSDSK SAH K/CEMLGTENFNFFTCHTHIAE HSNST HTHHTHTQTHTHTHTPLLFYE
10437	24338	A	10518	172	2	RGKKIFFPLEKGKNLVWWTALFF FFFE TDSHSV\TRLKCSGTILYHCSL CLPGSS DF
10438	24339	A	10519	42	194	ILVETF\CLRFVSL ENLVKMRFLK LKKK KKKKKKKKKKKKKKKKKKKK K
10439	24340	A	10520	120	1	IFAKRWPIKFFPFFFFFTETV FHS \VAQ AGVQWCDLGSP
10440	24341	A	10521	202	375	SFLWKLHLSGVPGHVRCQSALTGG \ASQ LSYSGVTD TLEEAVCPFSDLK LRAGRTT TL
10441	24342	A	10522	272	402	PKIFYVT KKA WNYYPYTITEYTC SF/IR KFFIHIETKYEDNKGSN
10442	24343	A	10523	147	439	LILYVNYISRKSTVYDSRHPCTYY LIPE KNCYKYHCNFLT/SSSIPFPT STPSR ASPKKKKKKKKKKKKKKKK K KARGG
10443	24344	A	10524	7	415	RFVCSTIKVLRDLSSDRSNPGRFL STSN SSLY/EKDKRNKAYFTK/RPSPV NDIIS T
10444	24345	A	10525	321	442	TSFSFLFF/LETEFHSA\RL ECRGT I LVHCNLC L PGSSNS
10445	24346	A	10526	477	3	IEGKL PNRKDIHTKNPSVCRHHQ RPKVD KTTKMGGKQSRKTGNSKNQ SASPPPKER SSSPAMEQSWTEKDFK LREEGFRGSIY SKL/REEIRTINGKE VKNFEKELDEWITR ITNAKKS LKDL MELKAE AQELRDECTSR AASANC VAVPQAFDRSHGVQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10446	24347	A	10527	265	411	RFVCSTIKVLRDLSSDRSNPGRCLSTNS/SPVRKDKRNKAYFTK/RPSPRN
10447	24348	A	10528	81	390	RFVCSTIKVLRDLSSDRSNPGRVLTSTNSSLY/EKDKRNKAYFTK/RPSPVNDII
10448	24349	A	10529	253	23	RIFLFYFHSFLRQGLARAEGQPHNHSSLQPPPPG\SGDPPASASRAARTTSAYHHIPLFFFRSYCVAQAKIINMLSL
10449	24350	A	10530	10	398	RFVCSTIKVLRDLSSNRNPGRFLSTNSSLY/EKDKRNKAYFTK/RPSP
10450	24351	A	10531	289	423	RFVCSTSKVLRDLSSDRSPGRFLSTNSSL/QRKDKRNKAYFTER
10451	24352	A	10532	152	401	PHCSIHSQVRIQANVHKHGRQRTYGSVIPHILPLHLVKKTFSLRDFHFSVSLKKNLVLTLHLFL/GVRTPRNDPFVSMMLLFT
10452	24353	A	10533	2	515	LDRISLLLPRLKCSGPVSAHRNLYLP/GFKRFCSLGLPSSWDYRRASPRVAKFVFLVDTGFHHVQGAGLKLLTSSDPPSLTY/PQCWDYRREPHLAAF
10453	24354	A	10534	469	566	PTKNTKISRWWCVPV/IWEAEARESLEPGKQRL
10454	24355	A	10535	354	47	KPKNLPGGGGPPFYSSFSKGGKKIPLPWKAKVPINQILPLPPHPGGGKKTFFPKKKKKKERKKKKMATVQKGM/PHKYYHGKTGSYNVIQHAVGNAVNTNRTRGS
10455	24356	A	10536	1	409	TPKKRFFPKPKPGFFFFPPPKKKKKKIFSPPEKFWPPQKNFKKAPPPFFFFFFFFFFF FFFFLKSNPPFFFF/SKNPILKPPLPPLFRVFPKKKKKKKDP
10456	24357	A	10537	204	435	TSGSLYKLLGMGDLGLGKTTIFKQGGHQNSS\GWHPEATTG/VNWAFFKGLHWDPKA LAHLQLWNIAL/QER/FGKMTKACY
10457	24358	A	10538	208	382	RFVCSTIKVLRDLSSDRSNPGRFLSTNSSLFR/DQRNKAFPPK/RPSPVNDIIST
10458	24359	A	10539	63	409	GWRLTNFPVGKTPSTSGTGLLFIFLLNLNLMGRLKPSSISMKREFRKQNRGQKC/EFMKKKKKKKKKKKKKKKKKKKKKIGGAF LKIFRGGPNFPGGGKIFFFLGGGIKSRGGGFG
10459	24360	A	10540	3	1322	RGYAWPNGALPASTVPCGFAACPGEFCLSVNGRQAPAGSSGFLPPVPSLCPHTVCRATFQCKEDSTCISLRFPWGSETHLLCPAPIPSVPGVPCGTFTFQCEDRSCVKTLSASPLPLLLCPPHLLPPSPDCGLQGPPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIAADRWVITAACHCFQEDSMASVLTWTVFLGKVWQNSRWPGEVSKVSRLLLLHPYHEEDSHDYDVALQLDHPVVRSAAVRPVCLPAR/SENREQGLQ/CSWITGWGALREGGPISNALQKVDVQLIPQDLCEAYRYQVTPRMLCAGYRKGGKDAC/QGESPG
10460	24361	A	10541	154	3	GVGNFFFFFLRWSLTLAQAGVQWRSLGSLQP/LTSGSLFRQFSCLSLPSTRP
10461	24362	A	10542	3	406	LMVLWTAHLPALAPGSRSTSLLLAF\ALLCLPWLQE\AGAVQTVPLSRLFDHAMLQAHHAHQLAIDTYQEFETYIPKDQKYSFLHDSHTSFCFSDSIPTPSNMEETQKCNLELLRISLLLIKSRLEPVQVLTSMF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10462	24363	A	10543	3	414	HSSAHAYGTYESGKRKYLRPSRTAEL KKALKEKKNRLLQQRSKSVTSSSSSR DSSARDSSSEREETSTSSSEDSDTDES SSSSSSSAYSTNSSFSDSDSDSS\SR GRSTSTDSSADD/STNEESELE
10463	24364	A	10544	240	509	TFTSFIIGTPNLGEFCCKNNFGI/GKFR MKVACQIETLGILSFFETESRSVTRLK CGGAILAHCKL
10464	24365	A	10545	275	2	GCSRPFDTAIPLMGPYPPEKKLLFEKNK /DTCTCMFIAAHFPVAKMWIQPKCSIN EWIKNPVTHIYIHTHTYMCIIYIYTHICV CVIHIYI
10465	24366	A	10546	233	2	WSWMAIQSVLPQTAFTELKNKYSQIQT PILFYFLKQSLPLSPLECSGVIIAHCN /LQ/RPGSTTFPASASKVERTTGA
10466	24367	A	10547	2	420	KKKIPNRGGCLKRDTKAFLKTPPMLQRR TPPAFPKPGGFLPDNPLPPSKGNPPI YSWERFFPRFFKNIWAPVPKANLLSFFF FSIFWRTGSRYIAQAGLELLGSSYPFAS CLPESWDSRR\DHRRPTI
10467	24368	A	10548	190	1	AASTFFACVCFRLFFVFVFETESPSVAQ AGLQWHSSSLQPPPNLG\SGNPALAS PVAGNC
10468	24369	A	10549	155	1	ARGEKYFLEIGGGFFFLVFFLRQSHS IAQAGVQWCD\LNSMQPLPPRVK
10469	24370	A	10550	223	392	RFVCSTIKVLRDLSSDRNPCRFLSTLN /SLAVRKDERYKAYFTK/RPDPVYDIIS T
10470	24371	A	10551	183	3	WQKLLFLFGTESCSVARVGVQRHLSSP KPPPP\GSSNS/PASASRVA\TGALHHA RLIFVFL
10471	24372	A	10552	297	10	TDEELLCMEKRKWWF\DMASIPGEDTV NTDEMTKT/DLEYINLVDKVSAGFERT DTNF\ERSSTVSKMLSNSITCYRKI/F/ RERKSQMQWQTSFLSF
10472	24373	A	10553	509	3	LLTDRTLSCRSVGVPCSVRCQCA\LLEG ASQLG\SRGSGVRDPLEEAVCPFDLQL RTGRTTALFKAVRQGHLSLQRLLSF\V CLCPAPRGAYRGTOASLSCGGLHPVRA SRLCLPKQAWAMVGTPPP\TSLPPCSL ISDCCASSQRDS/VGVGPSKPGAGYNLV VRRF
10473	24374	A	10554	262	453	GWGILTANLLVFGGGSLSISERIFFSPL ATGFCSSVAQAGVQW\LIIAHCSLEFLGS SD
10474	24375	A	10555	112	372	KKKGGGPPFFFFFIFFLIRQRKAKLVVL AFNRRGLRKP/IFYAGVGKIVKKKYS GFFIELVTTCGKNYLMCALAVIDPRDSN IIRS
10475	24376	A	10556	50	358	RFVCSTIKVLRDLSSDRSNPGRFLSTSN SSLY/EKDKRNKAYFTK/RPSPVNDIIS T
10476	24377	A	10557	203	350	QLHADKVS RFATHAECRGVIMAYFNLNL PH/FKRSSCLSLWSSWDYRHAP
10477	24378	A	10558	98	387	IQDLDLRGVYRYRDKKRAREKDSPPER EGEREIEKQKKER/ERKKERKKEST HQKE
10478	24379	A	10559	237	3	EVFFKNIFEIESCSVTQARAQQQDHGSL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QPFTPG\SSSPPTLASQSAVITGVNHHT QSGLTFFQSPKQKALGKMCISSGG
10479	24380	A	10560	37	359	RLKCGGPVIA YCKLEILGSSNTPSTSW VAGTT/TCHHAQ
10480	24381	A	10561	170	3	RPFLLPWGKKFQGV SFFFFFLVFFEI GSHSVP\RLKCSGTITAHCSLDLLGSSN
10481	24382	A	10562	1	388	LPEPLMVLRTANLVAMAPGSRRTLL\LA FALLCLPWLQADAVQTEPLSMLYDHAM LQAHRAHQLDIDTYHELEETYPEDQKH SLHDSQTSFCLSDSIATPNSMEETHQK SNLEMVRI SLLLLIETWLE
10482	24383	A	10563	224	392	CVDPIKWFPLRTATROGCPLS\LFNIV LEVLTATIRQEKEIKDP/QIGKKEVK
10483	24384	A	10564	185	2	RYFGGPDSPQNGKTVFNLF FFFETRV\ HSCCPNESNGTISTHCNLC L PGSSNSPA SASQVA
10484	24385	A	10565	175	324	APGYGTKYRVILCKILLRLRHLNHLN PGGRGCSEPRSHHC/ITPAWVTE
10485	24386	A	10566	3	367	HELLWSTIKVLPYLRSDRSNPGGVISTS NSSL C/EKDKKNKAYFTK/RPSPVNDMI ST
10486	24387	A	10567	128	391	GETCEGVYGPQGGKQTKV FHSKRD EG PCSKTWDVGLGSSPQFIFLKKVR FFFFF FETESH SVTRLECSGTPGT/HCNLCYPG TS
10487	24388	A	10568	251	485	SFLWRFPLKGVPGHVRCSA\LLGGASQ LGYS GVRDPLEDAVCLLSD LKLCAGRTT ALFKAVRQGHLSLQRFLLPLFSY
10488	24389	A	10569	176	3	FVPPILKKMGPFLLKKKEGK PFFFFSEM ESRSVT\RLCSGA/TISAHCNLC L PGSS SNS
10489	24390	A	10570	212	386	RFVCSTIKVLRDLSSDRSNPGRFLFTSN SSLY/EKDKRNKAFFTK/RPSPVNDIIS T
10490	24391	A	10571	134	489	SLFFLPSPRDRWSLTQSTEMPPSWKFP REIRSPLLAMLHSLLOPTAFLCPSS TL LLSLKPD SLRTGSLFSLFFSFLYFEACS VA\RLKPSGTISAHCNLC L PSSSDSPAS AYIVSG
10491	24392	A	10572	1	470	GQSRGIP LLLTLDLEKPVSLLSVTNLY SKNSAQFSTILQTLSPATFTPPSPSIPL SSAYFFFFS DRVS/LLSPRQEC SGLNLG AHC RPQP PRFKRFCLSPSS\SWGLTRR HTTTPGLIFC I F/SVEAGFHHVAQTGLE LLSLSNPPASA/FPKCWDHRR
10492	24393	A	10573	242	410	VMLRMQIYFSLHNPI FFFFTGSHFIA\ RLECSGMIPAHCNLC L PFGSSNAPASQ V
10493	24394	A	10574	236	1	ARTFFIHLKASCGDNAITGV LWH RATW CPSVLLDRDSLSEVCEILCIHAC/VMR IHEHTHTYIYAH THTHTHTHT
10494	24395	A	10575	241	35	RSSYLFI FNFVETRVAQPG LKCCSA WAGTPG\SSDPPTSSSQSAGIIGMSLNL FLOWLIIDQAGNTN
10495	24396	A	10576	294	72	FKNFKSLPFLS LFFFLILGTRFCYVAQAG LK\SWPQGDPSALASRVAGTRGVHRHTQ LQVSFNYYKVLAMHSGSQL
10496	24397	A	10577	1200	1625	PDGWSYSSGHSWLPPEASNGRKA WSSCW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VFPQLSPPPQAPPSPATHLGPTPPLA/SP PQAPPPPPATHLGPA PPPPLSSAP\PPPD TLLGPAAPPPPPSSGPD PFRYSP/EVPPQ LSPPQAPP
10497	24398	A	10578	226	325	ERHTHTPHSHTRSHTRLTHTHA/YTHTH AHTHA/YTHTHAHTHFPFS
10498	24399	A	10579	108	320	TINVLKVNVMKLSYLRFNTRNCSFFFL AGVQCEDHGSLQLQPPG/SSCDPPSSAS RVAGTTGAYQHTQLIF
10499	24400	A	10580	1	288	ARGRERERERERERERERERERERERE REREREREREREGLSFFFFSRSGGKWLW CVC/RPSARPRERERHAVFSAPPSLQKK KKVFGGREGTHSLFYPPCGNSLRR
10500	24401	A	10581	1	476	KEWGLALSPRLCSVVIHAHCSLGSGL KRFSCRLRLPSWKDYRCAPP CPSLNLFFV ET\GPHYVAPGWSLLLGSSD/PPPLASP KCRDYRHE
10501	24402	A	10582	210	346	PHCSIHSQVRIQANVHKHGRQRTYGSVI PHILPLHVLKKT/FSLRDF
10502	24403	A	10583	316	461	LPNLIGVVLFFVSETGFCSVTHAGVQWC DEHGSLSQSQTG\SSDLPTSD
10503	24404	A	10584	172	383	NLDLYLTSYIKINSKWIIDLNVIAKTIK LLE\KNVAGENIPDLGLGKEFLD/KTQK ALS\TNKKIDKLNFTTR
10504	24405	A	10585	273	374	GPGTGAHTRNPSTLGGRGGAIT/R/GQE FKTSLAKM
10505	24406	A	10586	150	344	KLKCKIITIKLGIKISFAVIVVVEIGPHF CYLGWVQW\PIRTHPGSSDPPASASQSA GITSMSHHT
10506	24407	A	10587	199	3	SFSYIRVHLGHIKTRHKASCEVYANCK AKGIITGIKKK/RFWPGTVAHACNPNTL GGRGWITRLV
10507	24408	A	10588	216	1	PRGAPT CMRCQSAL/LGGVLQLGYTG\V RDPLEEAVCPISSELKRCAGRTTALFRAV RQGRLSLQKFLLPFLV
10508	24409	A	10589	190	3	ISAGPWAAFEKRFIFIYRAPA/LKFMIF FSPFKGVPPFFTTTTFFFEMESRSVARLE CSGVISAH
10509	24410	A	10590	369	40	KTERNSININKNDVHTKTPSKGRQHQR KADKSRMRKNQHKKAENKNQNPSSPP RDHNSSPARKQNMENEFDELTEVG/FR KVGNSSELKEHILTPCKETKNRTRGW
10510	24411	A	10591	114	398	RFVCSTIKVLRDLSSNRNPNGRFLSTSN SSLC/EKDKRNKAYFTK/RPSPVNDIIS T
10511	24412	A	10592	132	1	ILYLWCVCVCVCVCVCVYLLILV/CKVL SCLGEPALSVGAFQMS
10512	24413	A	10593	3	287	IGFITLNVGLYLILLCYIYVYFFQVNYI VFILVLAVFLKNRLLRYNTALYNEEVT REKISHYFI/NSYIHTVGKINKND
10513	24414	A	10594	2	363	RAEVGVMAPLYLLLLLSGALGLTDTWAG SHSLRYFSTAVSRPGRGEPRIAYEYVD DTHFLRFDSDTAIPRMEPRKPWVEQEGP QNWE\WTTGYAKANAQTDRAVLRNLLRR YNQSEAGE
10514	24415	A	10595	156	3	NGLELSDDDGIALLLFFYFETFECS\VA QAGVQWCDLGLSKPQPLGFKPTRP
10515	24416	A	10596	80	306	MDSELLFRDEQRKWFLEMESTGEVAVNI

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						V/EMPIKDLG/YRNLVDKAVPGCERVD FNFEISSTGWVWLTPAIPVL
10516	24417	A	10597	232	389	ILCWVFCFFFFFFFETEFVLVIQAGVHWC DLDSLQ/SPPPGSSDSPASAS
10517	24418	A	10598	463	154	MGQGKPRFFLFHHPFYIFFFLKQGFSL PRVQGRAKKVPGTLASWGQKILLPQPPR /RVRQENCLNPGGGGFSEPKIPSPPAW GEKGGSLKLNKKKKTKHIC
10518	24419	A	10599	208	38	LGPFGFFFTAPPPFFFTETESRSLAQV GVQWDLGSLQLPPPG\SSDSPGLSKKFL LL
10519	24420	A	10600	200	3	CQPELSCMRC\QSLGLGLSPSGGMEVR DEVEEAVCPALAEKRCAGRALLVRICCS LQSQAGTFK
10520	24421	A	10601	73	427	RVCSTIKVLRDLSSDRSNPGRFLSTSN SSLY/EKDKRNKAYFTK/RPSPGNDIIS T
10521	24422	A	10602	193	401	GEVSLSPRLECNGVISAHCNFR/LPGF KRFSFFFL
10522	24423	A	10603	181	395	RFVCSSTIKVLRDLSSDRSNPGRFLSTSN SSLY/EKDKRNKAYFTK/RPSPVNDIIS T
10523	24424	A	10604	384	10	PRRPGGECVHCLGDSLVTDRLRYSGLRSS DQTLSGDPMBAVPWSNSLSCSHYRLKPA SGITWGCKQAGFFSFFLFFKMESHV\T RLECSGAISVPCNLCLPGPSNSPAPGGS LGPRSSRPPTT
10524	24425	A	10605	215	379	RFVCSSTIKVLRDLSSDRSNPGRFLSTSN SSLC/EKDKRNKADFTK/RPSPVNDII
10525	24426	A	10606	1	163	QTHREPAMVLSPADKTNVKAD\WGNVDA HAGEYGAEALERMFLSFPTTKTYFPR
10526	24427	A	10608	283	2	TQKHGLIIRCPQETPFKNNDVGMQKVKG RGEKSIHQIL/YFFFFLNS/HLSPRLE/ CSGAISAYCNRLRLSHSSDSPA/VDGTIG ACHHTQLIFLFLVE
10527	24428	A	10609	144	327	CSWSWFCGCVRVSTLIKKKNFFFEFR S\VAQAGVQGRDFGILKPPPPG\SSDSP ASASRV
10528	24429	A	10610	137	1	HKCPSTDEWDERV/WCMYTKKEYCSALTK EEIMSFSGKTWMELENIMI
10529	24430	A	10611	201	334	SFFWRFCRLRGVPSRVKQCA\LLGGASQ LGYSGVRDPLEEAVCPF
10530	24431	A	10612	146	2	KTPLKKGLKRVPPFFFFFETESCSVTQAG VQWHNIGSLQVPPP\GSRHSP
10531	24432	A	10613	205	259	TTMPGLSFCTRTKSNKNSFLTLDGSAR VDLFLYLLLFRTIFQNF/CGRDKVLLCC PGWSQTPELKQLICLDLPKYWDHRYEPL CLAYPFALGQNLTKI
10532	24433	A	10614	153	2	GVLMSDGLVLSMLANLFFSFLFF/LFET QSHSI\SRMECSGVISAHCNLCLP
10533	24434	A	10615	213	8	KPPFFFFFLLFFFLRWGSHCVVSGY/C KGTIIVHCGLELLGSSCSPPAFQVSGIT GLCYCASIFIFEE
10534	24435	A	10616	146	1	ILTIRDYVWKITLFFFEFPKFHS/VLPR LECSGAISAHCNLCLPASSDS
10535	24436	A	10617	208	2	NNFWFSSSGKYQYFSSETESRSVTWGH DLYSLQPPPP\GSSDSPASASQVAGITG SCHHAQLILVFIVE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10536	24437	A	10618	120	2	SFFFFFFETEFERSVAQAGVQWHDLSLQPPPG\SSDSPSL
10537	24438	A	10619	162	1	SFHWKLRLRGAPGCMRCHSA\LLGGVSQ LGYSGFWHPLEEA VCPFSDLTLCAG
10538	24439	A	10620	193	419	TFFFFFFETESRSVAQAGVQWRDLGSLH/S QPGQQSETP
10539	24440	A	10621	313	460	KPGLWRGTRSQKQVLFEPESHVA\KLECGGTISAHCNFC LPRSSDFSA
10540	24441	A	10622	243	505	PTGCPKQEQVQAMLRPVVFFVFETQFN S/VPRVECSGTISAHCNLRFPGRSDSPA LASRVAGICRR/CATTAQLIFVFLVETG FCHLVG
10541	24442	A	10623	67	430	LARRTWKNOHSSTHGCDFFFFFFFF LIIKKGVFFFPPEGHGHRRFFFINIKFLN YKRRFFCLFEDVLMISVGPPLAFFFFF WRGGFSYLLRCV/LTFLALGAPLFAPM FFLFLFGCEL
10542	24443	A	10624	3	207	PGGQLGSECSGVRMDEDVL\TLKSLIIG ESGVGKSSLLRFTHTDFDELAATIDP SSVVNPARNATP
10543	24444	A	10626	151	380	KMLFGQVQWLTPITIPALWEAEAGGSLE\ LRSSRPALKRSETSSPSP LCPQKKKKKK KFPFRAGGQMLEVPFPGRVGAG
10544	24445	A	10627	210	3	NFCQVKGFWKQKSSQIKGFGKNKKKGG SFFFFFFFETESHVST\RLCSGTIIIVHC SLDFPGSSDPPTSA
10545	24446	A	10628	237	2	LCFLSGASCSPYIDVYTEVNGVNPTFII LTNKTNTFGPLFLIIFFGETESLSIA\ RLDCSGAISTHCKLC LEPGRHSP
10546	24447	A	10629	1	352	RGPLSIQDYISKALFFLLFGFLLLLLF FEVRSCSLTQAGVQWCNHSISSLQSPT PG\RSPSPDPASAS
10547	24448	A	10630	48	200	AIKPKNLFFFSETKSSSVTQAGVQWRDL SSPQPPPP\SSSDSPAPAN
10548	24449	A	10631	209	376	SFLWKFC LKGVP GCVRQSA\LLWGASR LGYLGVRDPLYEAVCPFSDLKLCAGRTT
10549	24450	A	10632	141	1	AGFFFFFFLFFLETESRFVA\RL\QCSG AITAHCNLC LWGSSNYHAS
10550	24451	A	10633	18	522	PLYSLTRHTPREA/KDNLKSTQLLSVI DAISEGPIEGPVDGLKSVLLNSTPVLDT EGNINISGVTVVFRAGEQEQTPEGFES SGSETVLGTEVKYDTPITRTITSANIDR LRFTFGVQALVETTSKGD RNPSEVRLLV QIQRNGGWTEKDITIKGKTSQYLASV V
10551	24452	A	10634	127	2	NLSPLFFFFETGSRSVTQAGVQWSDLGS LQTPPP\GSRHSPTK
10552	24453	A	10635	336	452	RIFFFLFETEALSVAPAVAQWFDLGS LQ SPPP\GSSESPA
10553	24454	A	10636	259	3	GTRIFFFPNSSPLSFPPVQKKSVSPFFF SF/LFFFETESRSVT\RLCSGAISPH CKLHLPGRHSLASATRNVLRLPLWRIHA SCA
10554	24455	A	10637	96	413	GDNTSQHSAILINYFIFFFTFLEFF/ETG SHSVAQAVRLEYSSVITAHCNFLRGSS NPPKKKKKGGAVLKD PWGGQSLPGLATY YFFPYRGANKNLLGDFWEGPLFV
10555	24456	A	10638	180	473	CYMGRKAWLVLSNLLTLKKKKKKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKKKKKKKKK/EMPVKQKNRGRALYKK KKGRRPFFLFWPFFFFFLGGGKKHPGG FRRKKFFFGGKKKK
10556	24457	A	10639	312	480	ETVDSTSGEDDVNIAEMATKDS EYINL V\GKAVAEFERTDSNFE\RGKMMSKSI
10557	24458	A	10640	2	516	MKPLENLSQTASLARGATLLRPVLRRLC GLPGLQRPAEMPLRARS DGAGPLYSHH LPTSPLQKALLAAGSAAMALYNPYRH/E ERPRISTSTLDLGKLSLPEGSLGREYL RFLDVNRVSPDTRAPTRFVDDEELAYVI QRYREVDHMLHTLLGMPNTILGEIVVKW FEAVQ
10558	24459	A	10641	56	455	PLCSYIQFIYHSHKFNNSQISLVHTIPLS KLFQYFSQLYSIYSYLQHFHLLSIFI TVFCIVFYWVFWHLISVPMYICVCLCTN VCVCV/CCLW
10559	24460	A	10642	272	33	GRWFLFLGPAKYFLTGGRFPSDFGGLPK INPPFFFFFDDTESHSVAQAGVHWHNL GYLQ/SPPPG\SSDSPAPAEFHHTV
10560	24461	A	10643	285	1	MGNFLKRFKNEKKFFPILRAHPFNFF PGKSPFKTPRRALPLGVPPKHPPFFFFF FSETESRSVARLECSGMISAHCNL\NLH LPGSGYSPAL
10561	24462	A	10644	100	466	FLLKFRLEVPSSRVRCQSA\LLGPTSQ GYSGVRDTLEEAVCPFSDLKLCARRTNT LFKTVRQGHLSLQRFLLPFVQLCPVPRG GVYRGRQASLSCSGVHPVRASPPCLPK VPPPS
10562	24463	A	10645	260	460	LKPHAERETIDKGRLPYYSFFFFETESC FVAQAGVQWHDYSLPPPP\PGSEGSRA
10563	24464	A	10646	360	504	QIGHICAYVEKTELRLIFFFLFFFRQS CSVT\RLCSGTILAHCNLCL
10564	24465	A	10647	241	45	WEVEVPRVAPCHILKRDYFIIILFLFLF FEMESYSFT\ELECSAISTHCNLCPPG SRDSPGIPPH
10565	24466	A	10648	76	462	FLWEYQEKAHILWSLFSKLILSRSRFTV KEKVRQKPGILFIYLFIFEMESCSVAQA GVQWRDLGSLSPQKKKDS/DQSKAITFV EGINSKRGGWTGPHF/HCSLKMIFLI
10566	24467	A	10649	3	359	QTQREPTMELTPADKTNVKAAGKVGAAH AGEYGAEALERMFLSFPTTKTYFPHFDL SHGSAQVKGHGKKVADSLTNAEAHEDYM LNALTALNDLHAHKLWVDQVNFKL\LSH CLLVTLA
10567	24468	A	10650	266	3	TPEKKKKIGGLGAPFGYPKKIWPNNFF FFKKTKEFFFQRVGWAPPKSSFFFFF EVESCSVAQAGVQWRDLDSLQSPSP\GS RGSP
10568	24469	A	10651	278	461	KKIICGFFFDTGSCFVAQAGQQWRDLRS LQSPPPG\SSDSLTSASRVVGMSRHMRA VF
10569	24470	A	10652	161	456	VFFFFGENIAFVENKTLSYHFMFTRMT AAKMKENYKGCWGWETIGSFMPCWLESK RVQSLW\KVWQFFKWLNVKLLYGLAIPL TGICPKLKKYVQGY
10570	24471	A	10653	91	486	PCFNHGHHTTWYMYFFSLSLILFFVFSK PVILAYKTFSPITIRVLLQRRHRQKFV LDGFNGVDQNNILGSI CVSLIKIFFLTE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SCFVAEAGMQWCNIGSLQAPRP\GSCHS PGISPPVLG
10571	24472	A	10654	267	470	NLHMRCEKEQNFNKLSFKDLFGLGWLWF FIFCFWRRILTLSPRLEC/RG/MIFAH NLCLPGSGHSPASA
10572	24473	A	10655	775	1401	TFPSQIRYGLRKRPNSLTLSPRLECSGA ISAHMQRPPPGFTPFSCLSLPSSWHYRR PPRPAICVCVCVCVCVCLVETGFHRVN QDGLDLLTS/S/IPPASA/FPKCWDYRR E
10573	24474	A	10656	287	454	LPLIYFLYFYETECHPLAQAGVQWRDLS SLQSPPP\GSNDSSASASPTVPTSAM
10574	24475	A	10657	212	64	LFLSKFYFFEMESCSVAQALQWCDLGS VQPLP\PGSEDS PASAWGYLD
10575	24476	A	10658	368	473	GFIDHTRRRERPECP/LTDEWIKKMWHIH TTEYYSA
10576	24477	A	10659	358	1	ILAVFCFCGSAPGFEGGKLTFFFNNGRE TFLALVKTPPPGKARGPVFISKNKKIPE FKQPPNPNPNSFFFFFETESHTIARAG VQWHNLCSLQSPPPG\SSDSPGRWSLQR TEIAPL
10577	24478	A	10660	2	235	KRDLIRHYPKEDIYMANXYILK\CSLT MHTETLIRTTRYHLILIKVTIFKKTND MTAVGVHICNPNTLTGHRGIA
10578	24479	A	10661	9	538	CVTVRIPSRPTRPLSSDRSNPGRFLSTS NSSLY/EKDKRNKAYFTK/RSPVNDII ST
10579	24480	A	10662	374	38	SPLWKLHLRGAPGCIRCQSA\LLGGVSQ LGYSQVRDPLEEAVCPFDLKPAGRTT TLFKAVRQGRSLQKFLPFVOLCPAAR GGVYRGRQASLSCSGLHPVRASRPLCSR R
10580	24481	A	10663	268	47	ALIPLSSLTISAFHLLLTSTVSTSSPKM ECSGAITSHCSFNLDPSSPSPTSASR/V IGTIGARHQQLMFIYFC
10581	24482	A	10664	64	451	FSSERKSHMSLTNLQKLEMIRLSEGLS KAKVGQKLVRHLQTVSQVDAKEKLLKL IKSATPVNIGMIKQHNLIADIEKFGMIW TDCQTSRHTVLCQRLIQK/ALTFLNSM KAERGKEAADEKLEVRRG
10582	24483	A	10665	355	474	ILFYFIFFFETESCSVAQAGVQWRDLGSL QAPPPG\SRDSP
10583	24484	A	10666	317	481	GHTCPWQTFFFFLFRDRVLLHHPGWSAV TQSWLTAALT\FGPKRSSCLNLLNDWD
10584	24485	A	10667	57	329	VKNTQWGKDSL FNKRV\FKNWASTYRRI KLD/LTSYAKINSKWIKDLNVRLEIVKV LQVEYPSFKILNGSVLDFVFFYSYGIFA LHLMGEHP
10585	24486	A	10668	86	468	ENYKIPLMGGKNFLFSPIPPYFFFFSR LGLTLLPRLKCSGDHCSLQPRPPGLKRS SCL\GFPKCWDYRNEP/CVPR
10586	24487	A	10669	254	25	GSHICKVPAIYSNTCTSSHEGDGGVVG GCSSGSTTHSPVADSFVVVETVSL/S VTQAGVRWCDLSSLOPPPPGI
10587	24488	A	10670	206	3	YGRPRKLCNIGLKSGLDPTHWGQHRVI SFFFIMETDSRSVAQAGVQWHNLSLHP PPPG\SSDSPAS
10588	24489	A	10671	20	355	GFTSQSELLYSIDPITRPTDQVTTIGISA

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10607	24508	A	10691	240	406	DGIRRLSFFFFFFFETKFGFVA\RLGR GTIWNVNHLHLPGRDSEASASQVAGIT
10608	24509	A	10692	343	3	QVPLNLSLHLKLGMLFPGCINGSLSQFL QFFAQISPYQTGFPSFYKTSIYHNSLHQ YSLSLPYFIFLFFFSFFFFLQKSHSVS \RLECSGMVSAHCNLRLLTATSTTQVQVILV
10609	24510	A	10693	196	3	YDAGHTKKTLHFPTVYPFVLFVCWWECKM VQPRWKIVRR/FLKKLNTKLPYDPAIPF LSVHQKELRT
10610	24511	A	10694	245	391	KTDYQPGAVAHFGRPRREDHPRLGVDK PDQLEKPVSTKNTKLW/SWWL
10611	24512	A	10695	252	389	KTGGKVLFFFETESRVAQVGVQWRAL RSLQPP\QPGTSDCPASAS
10612	24513	A	10696	385	1	PPNKAAMTSSKDNKLNHWGKDTLLNKWC WESWIVTCITMKLDSHSPYTKINPKWI KD/LKTIKILGENIKKTVDIGLHK\NM SKTSKAMTKILDLIKLSFCPAKEIISR VNRKSTEWKVFASYLN
10613	24514	A	10697	296	430	KHIQARRGGS/CGN/RQHSRPRRADHL RSGVREQPEQPGKPHL
10614	24515	A	10698	280	468	DYLC/SLSIYLSIYLSIYLSIIHQFIY HLFYIHLNLSISIFFTKWLS
10615	24516	A	10699	15	393	RSVGVLGPVRCQA\LGSDSQLG\SGQ SGVRDPLEEAVCRFPYLQCTGRTTALF KAVRQGHLSLQRLLSF\VLCPAPIGG AYRGRQASWSCGGLHPVRA/SMLCLPK EAWAMAGAPPPASLPPLS
10616	24517	A	10700	176	1	DWTNTFTFLYNFKPSSIMPYLSHLFKT LR/MWPGAVAHARNPSTLGGRGGWIMRS GDE
10617	24518	A	10701	494	80	FNKKDIHSDTPSEGHQLQRPNVETLKKM GRNQCKGENPKNQNASSPKDHNSSTPR EQNWMKNESDELIEVGFRRWVITNSSEL YKG\DVLTQCKEAKNLNRLGKVLTRIT SLEKNHGGLMEVKINIAQLCEASAGWR
10618	24519	A	10702	264	410	KKGPLFTPPGGGGG/PQKPPGPLNPGG QRDSSFFPPGGGNTGETPPGG
10619	24520	A	10703	125	3	NRGNKGQV/QWLMVPVIALWEAEAGRSP EIRSRDQPRQHGETL
10620	24521	A	10704	184	2	RLRVLAPCRHLPRAPRTWPKRPFFFSFF LFFPQTQSHSVA\RLECSGAISAHSNLC FPPTRP
10621	24522	A	10705	187	406	LFLWKFCRLRGVPGHVRCQSAL\LGASQ LGSSGVRDPLEEAVCLFSDLQLRAGRTT TLFKAVRQGHRLRLQRIIL
10622	24523	A	10706	82	410	ILRGKFGKHYFNRIWREALRQSLSLFN FIIFSNFLASLHKPEMETELKGSFIELR KALFQLNARDASLLSTVSDSDFSCRKFS R/CSKCGQ
10623	24524	A	10707	390	2	SKDCRTAKIAACSFLWKLRSRGAPARCK PELSCMRCLSA\LLGGVSQSGGTGIRDP LEEAVFPLAELERCVRSAALFRASRQE HLSLLKMHPQLPLPSGALSQADGSFIYK PLTGASAFLEMPQERR
10624	24525	A	10708	229	392	YSWWRQMHSVAHAGVQWCD/LVSLQPQP PG\SSDPPASASLAARTTGAGHNLQIF
10625	24526	A	10709	193	2	RYLCYQDHYILLLLLLLLFLRWSLTLSL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RLECSGTIMAHCSLDS\SSNPPTISASQA AGTTGACYH
10626	24527	A	10710	180	11	LLFFFETRS/HVSQTVVQCGMISGHCNL RLSGSSDPPLASRVAGTTGKHQNIWLS R
10627	24528	A	10711	234	408	MKLIMLKVILFPQIHLQIQPNFYQNIFF FETELCSVAQSGVQWHNLSLQHPPP\G SSD
10628	24529	A	10712	312	470	TGPHCVT\RLECSGAIATAHCSLDFAGLS TSPTSVSQVSGTTGTWMKLETIILS
10629	24530	A	10713	64	392	PKMVIRISSETSLYASLPLQMKGRQK/ CEPQPKKKKKKKKKKKKKKKKKKKAR G
10630	24531	A	10714	169	427	NNQKTNNKMVGVSFYLSIIILNVNELNA PIQRHRVAEWIKKEKKKK/DPGICGLQ QTLFFYEDP/HDPLRLKIGGW/RKYYP S RGTQIK
10631	24532	A	10715	176	410	ARSSWGLHTAVPVAFSLRFLLEIFLDR DTRCSPPAAFFFETGSCCVA\RLEGRGA ITAQCSLNLGSSNPPTSASRVA
10632	24533	A	10716	234	389	NSGNMDRYKDVQNTIQNPICWPGTVAHA CNPSTLGGRGQIL/RQGEFETSLA
10633	24534	A	10717	190	2	GPFPHPGGFLRGFFVPNTIPPTFFFF FFLRRSLVAQAGVQWCDLSSLQPLPPG P\SNSPCQ
10634	24535	A	10718	201	1	WPLFLPKMFFFFFKRFPHMGPSPVWGAQA KKKKIFFFLTGSHSVT\RIECSGTISAH CSLNLPGPSH
10635	24536	A	10719	195	419	EYHTSLVTCGNPCVYRSNNKLNQTSRRK VITKIRAELEIETEK/LQSGETKIWF FEKINKTGLELLGSSDPPVW
10636	24537	A	10720	218	407	GKKNLAFKKKKRKEKKRKSQSNMNS AKIEARTNIKLVVKHGWKNCEIIDA\LQ KAFGDNA
10637	24538	A	10721	231	409	GTQLHLGGFFFSEKELSFCFWF/MFALF EMEACSVT\RMECSGTVAHCNLRPLPGT SNSSA
10638	24539	A	10722	40	401	PLCPSESSGNTLMASSDPSTPAVPPNT THPPLCLSKSHLPLRPKQGLPSGNLLQL PLTLIPLLGAPVACWQLPQQCTLSTFF FETKSHVPAQAGVQWCCGLSLQPLSPG\ SRDSPDSAC
10639	24540	A	10723	210	14	HVMGLLLLFLNKLTVNNFGWLAGFWCLG FFWFFSFETRSGSVT\RLECSGMISAH YKLCIPGSSH
10640	24541	A	10724	347	462	TFFFFFFETKSRCDIQAGVQWCDLCSLP PSS\PDSSDCP
10641	24542	A	10725	169	386	DKKQAKTIKWGKNSFSNKWCWNNCIATG KRMKLDP\YLTPYK/INSKWIKDLSI
10642	24543	A	10726	257	54	PLFFFFKRQGLTSLPRLECNGTVAHYN LKLGSRLDPTSASP\SAGITGISNPAR LFTYLNPTHLQT
10643	24544	A	10727	2	401	NNYDRAETQIYQYMCLNPTFYCLQETHL TCNDIYRLKVKGRREIMQIENKRVGVAI LVSDKTDKPTTVKKKLHYIIKGSIQPE DLIILCTYSPNIRASRFIKRIPDLRKEI A/HTVKVGDFSISLNLRSRQNT
10644	24545	A	10728	154	1	PMCSLLGLSKGGIIFFFFEABFCSSVAQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AGVQWRDLGSLQPPPPG\SSDS
10645	24546	A	10729	34	151	PRPPVPSLLDRGRLQLWRQRLRHRAHS NGFIGGKQKIMKLLKNYVRPVG/VAVA IMFDPDPYPRSWIEDDFNYGGSVASAT VHIRMGSLVENNKS
10646	24547	A	10730	2	408	VFLLTVRTLICRSVGVWWRSTPDLVCLG ISSGGCRTANIGLYQMLLPDHSSGSFCL RGVPGHVRCSQA\LLGGPSQLGYSRVRD PLEEAVCPFSDQLHAGRTTTLFKAVRQ VHLILQRFLRFVWLCPAPRG/GVYR
10647	24548	A	10731	274	89	ENIPVFNPPVCSPLLPQPE/CEYPKL CKLCLKLHKHRVYF\FLFFFETEPHSV ARLECSG
10648	24549	A	10732	251	1	TFQMMQKCFSHRKIFHNLLDKASYKIVY KEDPFPSSLSSSVSLKNNFFLETESC SVTQAGVLWCHLSSLQPPPPG\SRDSP
10649	24550	A	10733	375	1	AFEPPLWVRGSPFSPFVPHPKLPPL AEILGFFKERKWSIRKPCLFKVKKLVS VWPGLELQIFKFIGEFPFSPSLVGRKP NFFLGPVFFFFFEKESRSA\RMECKGT ISAHCNLHLPGP
10650	24551	A	10734	82	398	SFLWKLRLRGVPSHVRCQA\LLGGASQ LGVLGVRDPLEEAVCPFSDQLPAGRTT TLFKAVRQGHNLQRFLLPFVQLCPASR GGVYRGRQASLSCGGLHPVRAS
10651	24552	A	10735	2	341	TFCAISWLESGVEDGPRSRISYRISTFF FFFKGAPEPKEVRGRPKPLAPTSPLGA HGTTLGSGWTTPSIGGWQPPPPPRENPK GEHPPAPVAGDTFQ\PKKPPILKVFFP K
10652	24553	A	10736	171	1	RVFYLLAFALFVDTGSPFVSQAGVQWCD HSSIQSQTSG\SNDDPASAYRVAGTTGV
10653	24554	A	10737	190	1	EKTTVRKIPKMEEMADSGSNMLRIIIF LFLFFETKSCSVT\RLCN/GSISAHCN LHLPGSSNS
10654	24555	A	10738	252	413	GLLGLQNFYSYKVLTKAHLKKCSWLDV AHAYNPITLGGGEW/IQEFQTSNTV
10655	24556	A	10739	101	249	AGSTSRCI/QELSDLLEHLEQENCLNPG GRGCSEPOSCHCTPAWVTETQKK
10656	24557	A	10740	185	403	LGLPVHTMKSNYHYHLCHHHHHLQH HHHCHCHYHS/HHNSQHPPPPPPPPP HHHHHHHHHLP
10657	24558	A	10741	119	425	IKFHLHSMERTHLFLWNCWAHKQRNCFK ADFVITDDIKQLCPPQSWWTRAGKLPLG AGRGGSHMLSHFWRPRHADILYLGVL DQPGQQGETPSI/LKNTKSSW
10658	24559	A	10742	112	2	GETFFFETGSSSVA\RLCSGAISAHCN LHLPGSSKSP
10659	24560	A	10743	188	3	PPPLFFFFFFFFFKTGSGSAT\RECTA HCNCLPGSSHPTSAVQVARTTDCNH AWLIFV
10660	24561	A	10744	176	3	SLYSKNKNPSHLLFLPIPIKFFFFFFET EFRSVAQAGVQWHDLSLQPPPPG\SSD SP
10661	24562	A	10745	250	1	GPRIFFLKEFYPRFVGKNPAPGGFFS GGKKPGPFPPNRPPIKFFFFFFETFRS VAQAGVQWHDLSLQPPPPG\SSDSP
10662	24563	A	10746	155	3	PPHPFPNPLPIKFFFFFFETEFRSVAQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AGVQWHDLSLQQPPPPG\SSDSP
10663	24564	A	10747	157	1	TPRPFPFNPPPLKFFFFFFETEFRSVAQ AGVQWHDLSLQQPPPPG\SSDSP
10664	24565	A	10748	157	1	TPRPFPFNPHPIKFFFFFFETEFRSVAQ AGAQWHDLSLQQPPPPG\SSDSP
10665	24566	A	10749	153	2	PPPLSVVTPAPLRFFFFFFETEFRSVAQ AGVQWHDLSLQQPPPPG\SSDSP
10666	24567	A	10750	157	1	PPPPFLFFPRPLKFFFFFFETEFRSVAQ AGVQWHDLSLQQPPPPG\SSDSP
10667	24568	A	10751	155	3	NTFPFFFTPLTPKFFFFFFETEFRSVAQ AGVQWHDLSLQQPPPPG\SSDSP
10668	24569	A	10752	86	406	SFLWKLHLRAPGCMRCLL\LLGGVSQ LDYSGVRDPLEAVCPFGPKLHAGRTT TLFKAVRQGHLSLQKFLLPFVQLCPAPS TGVQEGRQASLSFGGLHPVQSSR
10669	24570	A	10753	364	469	GQFLHSLD/SHWKKSEDFCLWFPHSEN VSAIHQDH
10670	24571	A	10754	250	61	GEKKKKKPRVFFFFFFETEPGSVT\RL ECSGVLSAHCNLRLLPNPNDSPASASRVA ASAKLG
10671	24572	A	10755	66	446	SFLWKFCLKGVPVCVRCQSA\LLGGASQ LGYSGVRYPLEETVCPFDLKLHAGRTT TLFKAVRRGHLSLQRLPPSVCLCPAPR GEAYRGRQASLSGGLHPVRASRPLCLP TQALAMVGAPPPGSL
10672	24573	A	10756	252	482	RLPRQPVRKWWAGVRGCCVWGVVSKSLQ RSTTLDWQGPQRGGPILFFFFFFETLCH /TRLEGNGEISAHCDLCLPGSN
10673	24574	A	10757	205	488	PLESLRSPGLPLSWRTASSVSPVICIYY IYIYIYIYTHY/HIHTHTHTHTHT QYIFVCVFLKDRVLLCHPRQSAGARSW PTRTSASQRQEM
10674	24575	A	10758	272	471	YSYVLFFFIFLGIESCSV/AFSAGVQWHN HSSLQLQTPGLKQSSHLSLP/ASASPVA GTTGMRYHARLIF
10675	24576	A	10759	17	342	GTLSSGAQVLIGRIESTVVGLKPWALG GCPSPRAVHWLLASSDWRPSLDGAEWG KKGEANGNHR/GIAVISDQIDFKTKTI KGD\KKSHYVMKGPQQBAITINI
10676	24577	A	10760	42	498	EFRRGREKEREKERKTEERMEDRERKA EREREKERQEGRRERERERERERERKR ERERKRERE/RHEPGSL
10677	24578	A	10761	1	305	ASWDDPAHNNFNHIPPGGVVAHFFFCRL DCPPWAPRPPAPR/VLL/TPAAAAAAA AASRPEKKRAENVGATPPRKRPPRWEE RRGPRKGSAPPGRGAGRAR
10678	24579	A	10762	364	2	FPQKQNGQYLPLFPKPTGLCGKGKTRLG FFLNIFYGKKKKRGRELGFPPFCQIWGT SIYRGSMDYFFFFFFWRQVSLALLPML C\RMIRVHCSLDLVGPSNPSTASQIA RTTGTCMCHH
10679	24580	A	10763	152	484	RFVCSSTIKVLRDLSSDRSNPGRFLSTSN SSLY/EKDKRNKAYFTK/RPSPVNDIIS T
10680	24581	A	10764	208	420	SFLWRFPLRGVPGHVRCQSA\LLGGASQ LGYSGVDRDPLEDAVCLLSDKLKAGRTT ALFKAVRQGHLSLQR
10681	24582	A	10765	319	85	GKLLNNNRFCGSKFQGIMFFFGETESPY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						ITQSGVRWHDGSLQPP\PPGSRDSPAS AS\RGITGARKHTQPIFLLVSNS
10682	24583	A	10766	122	3	KFFFFFFETEFRSVAQAGVQWHDLSLQF PPPG\SSDSPSL
10683	24584	A	10767	240	86	RAPPPFFEMESCSIAQAGVQWLSLGLL QAPPP\GSCHSPASASCELMFSKI
10684	24585	A	10768	244	85	RAPPPFFEMESCSIAQAGVQWLSLGLL QAPPP\GSCHSPASASCELMFPKI
10685	24586	A	10769	35	296	EVKSPSARQPPRLGSEHLRPAAPSGR EVGGQPPPGQPPCPGGEG/PPPPGSPDW EVRSPSARQPPRLGGEPPSSLRTHGDDD GGFV
10686	24587	A	10770	260	484	MDEELLLMNEQRTWFLVESSPGEDAVS I IQLATRDLEYDLNLVEKGAAG/LERKH YSFERSSTVDKILSHNTACY
10687	24588	A	10771	248	393	TQEGKKLINWPGTVAHACNPSTLGARGG RTTRGQLETK\LANKIKPCL
10688	24589	A	10772	239	2	SFLWKFCRLRGVPGVRVRCQSA\LLGGASQ LG\SQSGSVRDPLEEAVCPSSDLQLRAG RTSALFKAVRQGHLSLQRLLSF
10689	24590	A	10773	158	455	LFFTLCPSLLQHIAMVLELGLKGPKSTIQ PIFWVFLQTEP/HFLVTPVR/CCLPLL KLFCLLVFCMESPSVPHAGECSGVISAH CNLCLLGSTDSSASPSRV
10690	24591	A	10774	166	403	KKTFLGEPLFWGGAKKKKPGKKNPGFFP RG/IKPRVFFSRFFFFGPPPKGFPQKS FFLKSLPGFFLFGGCPPPFFFFFFFEM ESCSNTRLECSGVILAHCNLCPLGSSDS P
10691	24592	A	10775	208	1	RLCFFYFRKALLGKAQIKNIAFFPRKGS FFFFSETESRSVAQAGL/LDCSGAISAH CKLRFPGSRQSPAS
10692	24593	A	10776	192	29	IFRKEFPCLNFFLLFFETESRSLAQAGV QWRDLGSLKAPPPG\SRSPASRDTGV
10693	24594	A	10777	275	490	KPGFFLLQMAKVYMIFFFFEMEFC\VA QAGVQWHDLGSMQHRPPG\SGDSPSCLP SI/AGIPG
10694	24595	A	10778	340	3	LKVPVGKPRSTLLGVKKVPFFGNKRKKF LALFFFPRLPPGEGFSTAFLAQKTPRV VPALGFPKNQSPSPFFFFFFETKSCSV TQAGVQWGLRSPQMPPPG\SSDSPASC L
10695	24596	A	10779	313	1	ANPFGGPGGDPFSSRVFPPPGPKNETP FFKNKTATKKTGNKGWAPSPHRGGPK KGPALWDKKGKNLWPPFFFTESHVST\ RLQCSNTILAHNCQCLPGS
10696	24597	A	10780	116	422	ILEDNIQTITETLLAIREVQIQTTLRNH FTLTGMAL I /RKTDNNKCWRECGKIETL ICCWRECKMLCNEVGTALEIVWQFLQSL NIELSYDLAMPGFIIFPRE
10697	24598	A	10781	120	418	TQTTGAPQLHLASRWLSRSGGLTSSPQE IPKLFWSIESPLGSSKHLQVFCLEFV CSFVFEMESCSVARLECSIVISAH\CTL HLWGSSHFHASASVA
10698	24599	A	10782	134	1	SSFFFLCQTESCFGVQWHDLSLQPSTS RAQA\LSLPSSWDHRR
10699	24600	A	10783	2	435	CSHRGDSYSYQLSGIRAGDLGGGGKDI FRLLPPTLNIFAGKESYDVVCVTHRMIC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LC/SCLFIYMCLCMCVHV/HYTHEACVF MCLCL
10700	24601	A	10784	432	161	FSRAGFH/RVSQDGFDDLPS\CLPPLGL PKCWDYKREPPRPAPKLMCRQVHRKCTW LFIQIGSTLFKTNGLSAVAHAYNPNTW GGRGERIA
10701	24602	A	10785	270	442	NVRLRLGLALSPTLECRGTIMAHCRDLF PGLMQSSHLSHRVAGTTG/TCHHAWLIF KFL
10702	24603	A	10786	12	424	LIQLPRLECSGALICARNFTY/SLGSGD PPTSASQ/VLKTTGVCHHAQL
10703	24604	A	10787	350	3	DSSSVQTNKGIPGQVLSLSCAVKASV LVIIPLHNALSSWLVPALFLWKSQVQVK SQQAHSVSGLC/MHYRSHTHAHTSPH RHRHTYTYARAHTHHTQML SAYLPSKQ PSGSL
10704	24605	A	10788	155	3	HAFFALCIRNRLECNVLAHCNLC/RL LGSSDSPVSASQVNGIAGACHHAQL
10705	24606	A	10789	188	2	RRDLSSLQPPRGGQ/MRGCIYTHHTHT HTHTHTVHWGWGKRHHVPKGMKSANG ESGRAK
10706	24607	A	10790	19	405	IRPTISRVERGINSLVASEGQRLPWDGI ACSQGLVVQQTWGPPLGPFPSLLGMPHR PTFRDLNSEPAPGVANVSGTLSTPLPGA SHGLLVFFFETESHFVAQAGVSWGDLRS LPPPPPG\SSNSPVSAS
10707	24608	A	10791	157	1	KPGPPFPYFPGPLKIFFFFEFETFRSVA\ RLECSGTISAHCNLHLPGSSDSP
10708	24609	A	10792	157	1	QPRPFPNRPKPPKFFFEFETFRSVAQ AGVQWHDLSLQPPPG\SSDSP
10709	24610	A	10793	83	387	SFLWLKHPGGAPACMRCLA\LLGGVSQ LGYTGFRLLEEAVCPSELKHAGRTT AVFSAVRQGLSLQKFLLPFVQLCPAPR GGVRG/RQALLSCHRLHPV
10710	24611	A	10794	204	419	KGVYGHSGSFSPAPLACFRDKTLFPVS LWKEFVHSPWCKCTLPQPLWKTWVRYLK NFKME\IPYVPEIPLG
10711	24612	A	10795	207	2	RRGFTMLVGQNSLDPSTSRSAHLSLPKC WDYRCKP/PAPS/LREGFSYLLHSLHP TPAPGSHHLWAALIC
10712	24613	A	10796	2	237	FFFLRERILLALSPRLECS DANMSHCSL NLPG/FSQSFCLSHP\SRWDHRHMPYP VKFFGI FVGDRVLALFPKLISYII
10713	24614	A	10797	342	40	DRVFFCSPRLECSGAT IARCS/LRTPGL KQSSHLSLPKCNHRCPPRPARCSLNE SHSAKKWPGQSTDSSACEVQPTSPFPT VPYPTLLSPSAGHGRGR
10714	24615	A	10798	209	2	CSVLAVILNPECIYVVPWLELLAHDPIP RLVCPSKFFFEKFCFSAQAGVQWHDLG SLQPPPPG\SSNSP
10715	24616	A	10799	142	2	IFFFFEMESRSVARPGVQWSDLGSLPP PPP\GSSDSPASATPSPMQS
10716	24617	A	10800	276	2	ILPIIIRNTCCCFLLKESRSCSVTQARV QWHII/GSLQPTPG\SSNPPASAFQVA TGAHHHTSLIRNTLIIINWEKTHKLSG CTSMHFRFL
10717	24618	A	10801	12	364	LHHYKTVSGIYKCLCVLNGPPTFFPDF LPPLGLPYSLRHNNIEISPINNPIASK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						YSRERMSCISLTNLQTLVMIKLNEESLL KANSDHKLCLLR/SVYQVNVAYEKFL
10718	24619	A	10802	235	3	HRPSEDLDFFPHWAVMRAPQYPSWDTRE GGPRSFLFLFLFFEMESYSVAQL/EGTI SAHCNLCPLSSSDSPTSRLCSL
10719	24620	A	10803	349	1	NQTPFFFFFPGGTETTTLCS\YGLLI LLKYPEVA/ESASQRDPWEAAVWRWLE GPGSAQPPSAPAKGQELDPVVGQRPVPS PDDHVQWPYTNVAVLEIQRFISVVKRTL TLDTRY
10720	24621	A	10804	365	3	IDVCNVCVRKQYRGFCQKYRAWISPVY PHKCGWHRVYNTPTPHCETEWLWVILHA QEH/TFSLTGRHTHTHTHTHTHTSKL APPASRALFGVAHVEAQKALASPSSGRY LAITMFVQPCI
10721	24622	A	10805	406	96	CPPEFSEESPRLLKFRVGGYLTPOVSKC GLGVVRIFKVFFWSPPKVQTSLFFFSKT GSHSVT\RECGDTILAHCDLCAPGSGD PPASATRVTVVGLPPCPAR
10722	24623	A	10806	58	369	FFFFKGDRAQNN/SGERCLLNKGYWDI WISTCKMKSTPYLTLTKISSKGLKDL IRAKRIHLKKYIGINLHDLGLK\DFL NMTPKTLATKEKIDTLDPIKIK
10723	24624	A	10807	126	1	KEPFFFFFFFETESCSVAQAGVQRCLSS LQHQP TG\SSDFP
10724	24625	A	10808	204	415	HLGFDLSLTICISLSDGLKYKATVFLVFF FERESNC\AVWAEACNGPISVNCNLRPLG SGSSPASPSRGVEIT
10725	24626	A	10809	168	2	KISKRPFFFFFFFETGSHYVA\KLECSGV ITAHCSLDLPGSSNPPTSASWVAGTTGT
10726	24627	A	10810	97	389	LAVSPSLSLSLSLSLSLSYLGLPYSLRR SNIEITPINTPAEGSVCSSEKGHMSLS FNEKIEVITLSAQDMSNTKIG/RKLDLL CH/TSQVVNAEEKFLK
10727	24628	A	10811	24	416	LEYIARRYLGVVWLFFFFLNRQGEKSR GPFKFFPRGFFSTRNGAPGGPWGFLP WGGGPPVGFQKQGGGAP\PPKNRFPK GGPLTQPNLEKPTIENPKGPPTRGFFPS GPPPKKGAGPPPIFRVGE
10728	24629	A	10812	60	435	KKRKNFPQKKISPYFYPLKWFKTPPLWV KNQTPPV/CCFFEAPFLKPPRGLKKG /WGKNFPPPLVPQKKKKDTAGVAILVS DKKDFNPTKIKKDKGHYIMVKGSMQQBG LGCPDAWVPS
10729	24630	A	10813	618	1519	FWFGVNCKSVCPFLPVLFCFVVCWCER GVLSQRSMGQAQSKPTSLGTMKHFKKG FKGDYSVTMTPGKLRTLCEIDWPALEV WVSEGSMDRSLVSKVWHKVTCKPGCPDQ FPYIDTWLQLV/YRPPPY
10730	24631	A	10814	179	15	KVKRLKTPFFFFFFFETRTCSVAQARVQW HNHSSLQPQPPGPKRS\PTSVSREAGT
10731	24632	A	10815	61	422	NCFFLKGPPLFFFFFFFLLQIIVFI YKFFAFLQMEFRSLPRLDKCNCAISAH CNLSLPSSWDYRNLPRLANFFLFLVET RQPASA/FLTCWDYR
10732	24633	A	10816	170	440	RQGLSLLPRLECSSMTTAHCDLKLSSS NPPISAPHIALG/LTGLCHHTQL
10733	24634	A	10817	322	443	FIFIFYFFETRSHAVAQAGVQWRDLALL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QPPPP\GSSDSPA
10734	24635	A	10818	134	3	KKAHLPFFFFLEGTESHVA\RLECSGT ISAHCNLCPLGSSVSV
10735	24636	A	10819	76	245	FLLRKGTRQGGPLSS/LLFNIVRDVLAR AIRL\EKKIKDIQIGKEAELSLFADMI IF
10736	24637	A	10820	233	440	FFFGALKKWKSMTHKKVERGKRTTLNG GGIKAATASLKKHLQGWGKVMLMANKL LRGERAW/FPPRIRG
10737	24638	A	10821	293	402	RNPFFFLTEPHSVAQGEVQWCNLSLQ PPP\PGS
10738	24639	A	10822	168	1	PLRGLSDSSLGIMKRMATDLSSLQPLPP G\SSDSPASASRVAGITDSHHHAWVIF
10739	24640	A	10823	97	405	LCVNICFNFPWLGVEWLNHIIGVGLTFF FEMESCVARLECSGAISAHCNLL/LPP SFGSSDSPASVT
10740	24641	A	10824	186	2	EPGTISLVALKLQKWPRR/SDHLRLAVR DQPGQHDETPSLLKNTKISWAQWQAPVI PALEPV
10741	24642	A	10825	199	1	KKTQIGGAPGGALFFFFFFETGFPFVA\ RLQCSGTNQAQCSLNLSSSNPSFPALQ VTGTPSACP
10742	24643	A	10826	252	381	GQQEFFFPCSVPOAGGQWCNLSLQAPP PG\SHSPASASRVAG
10743	24644	A	10827	77	427	IPQVHCPMSPPVPMACIPRVSSFTSWVF HNLLPPSECPGLPLVPASSHPRPCVCCR PCTSW\CPLWPRPPCSNSPV/TCVPCL PCLCISEIPSCVPWP/WTYSSLCPMSHV PDSPCPLP
10744	24645	A	10829	20	518	SFAFSLLOHLTETSFAINSCSEATLLFL SVFL/RAQTLTAPCQTRGPRRGKDRGSG SSSPSGPKATKESSVERRKSFDSWGHFR AA\QRLMDNQAERESEAGVGLQRDEDDA PLCEDVELQDGDLSPEEKIFLREFPRLK EDLKGNIKLRALADDIDKTHKKFTKAV
10745	24646	A	10830	351	3	LHFSPPFLQHRQNIKVWLMRASMQRHSRT HGAFPLHQDEIQTRPRLRSAASSGPSLL SDHILSTLPAFTCANLSSRFCSSSPCSC SCLRA/CCTCHFDLSTLIHAHTRTHHT HTHTMY
10746	24647	A	10831	8	376	GMLPAHLADVLRHNSVGRPKHMRVMAGA LEGDLFIGPKAE\EHRG
10747	24648	A	10832	336	38	GVATEGVGEAAQGGEPRQPEQ/PPPQPY PPPPQQQHEEEMAEARQA/AGAPMDDG FLSLDSPSYVLYSDBAEWADIDLVLQNV GNPNVVQIYSDKYTLWK
10748	24649	A	10833	206	1	TYFFPPPPGLFFIAGIFFFFFFLETGSH/ SSLRLECSGIITASCSLNLDPNDPPAS ASQVAETTCATMY
10749	24650	A	10834	226	376	RISQAIISFYFYFLFETESRSVAQAGAQ WSDLSSLQPPSPGV\SDSPALPS
10750	24651	A	10835	213	1	DRVLLSPRLGCSGMITAHCNHLPLWFK RFSCLCPPE/SSWDYRCPLP/PPRLTSV FLVETGFHHVGQAGLR
10751	24652	A	10836	351	447	RENLWLTVPVLPALREAKAGI\LEPRSSR PAWAT
10752	24653	A	10837	71	472	SASTAPMAPVKKLTVKGG/K/KKKQVLK FTLDCIHPIEDGIMDAA/NSTNYEQFLQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ERIKVNRKAVNLGGVVTIERSKSKLTVT PEVPFSRRYLKYLTKKYLKNNNLCDWLC IVANSKESYELRYFQITQDKEEEK
10753	24654	A	10838	37	382	SRCIMAFYLYGIRSFPELWKSPLYLGVGP GHSYVSLFVAGRCGVRNQQRRLCSVKTMS PONTKATNVIKARYLRKDEGSNKQVYS VPHFLIAGAGKERSQMNSQSEDHK/LA/ PVRNAV
10754	24655	A	10839	313	617	AFFLIVFQYVARERERSRS/VNCGLYQ HCYFRTL
10755	24656	A	10840	309	511	WEQGSWEHVLQAPCSLIAPRITHAYTHT HTHTHRYTHLYPH/APTSIL
10756	24657	A	10841	269	450	TPWPLKKEFFFLKWSLALVAQAGVQWR DLGSSDSP\LQPSRFKQFSCISLPSW DYR/PC
10757	24658	A	10842	420	1	LERGENGTRDRRKGLSHCHQPMDSVLP PLCHPPPLVMTMEETIMLFIDIGSSMY KAGFAG/DDASRAMFPSIVRCPWHHGVM VGMSQKDSYVGDEAQTKHSILTLKYP IKHDIIITNE\WDMMEKIWHHTFYNKLHVAP CI
10758	24659	A	10843	431	1	GEHSWASDLAEDVTKVTRGPLGLFWGL CSGNLSFSGCVPGLPAGAVPPWVPVFPQ GGA/SWVWKGPSPTLHLLLRTWGLAGG VGGRSLGRWRAWPGNPGSQGQGAAPAHQ ATGTPRSRTGSTGGIETVTILEGSHVSG MGIR
10759	24660	A	10844	55	297	QRWPGTLLGVQPG/APPDSTSASGSGGA RGGPVPTLEGNTGSRKWDPCWGSQNS PSSDGSKPPPGPLTSKVCDLSE
10760	24661	A	10845	109	427	QTGPSAAGLLEFARGPLQTLFAWVPAAV AAEQQIFVNRECCCLIVLEFCLRGVPC CVRQSA\LLGGASQLG\SRGSGVRDPL EGGSCPFSDLQLHAARTALFTA
10761	24662	A	10846	17	416	SFLWKFCLEVPGRARCLSA\LLGGASQ LGYSGVRDPLEEAVCPFSDLQLRAGRRT TLFKAVRQGHLSLQRIILPFVWQCPAPI GGVYRDRQASLSCSGLHPIRA/SRAAVP TQASAMAGAPPDLSLPPCSLSSN
10762	24663	A	10847	265	429	LSGASCCFLSLPIVLFALLLSVLSFSF CAWCVPWSLSPTLFLTFVLHFL*RFIS CF*VNSNPKNLTFMVNFQGGKMGKIGLAL ERICICGCSLVFPEAILETSCQNLFCY ACAGVLSSVYDYLALLAVSFLFL*FFSL FFFFLYLFLFALGASLPGLYLLLYFLL LCCISYSLF
10763	24664	A	10848	12	462	QTLGTRMNEGLFATFIAPTILGLPDALL IILFPPLLIPTS*YLINNRLIITQH*LV KLTSKQMITIHNTKGR*SLILISLIII IVTTNLLGLLPYSFTPTTQLSINLAMAI PL*AGAEVIGFRSKIKNALAHFLPQGT TPLIPILVII
10764	24665	A	10849	2	462	TTLHAFGTMKREAFITLLCLFTSANSRG VYARDAHKSEAAHRIKDIAEKDFLALVL IAYAQYLQCCPFEDHVKL*NEVTEFAKT CVADESAETCDKSLHTLFGDSLCTVATL RETYGEMVDCCAKHEPVRYECFLQHWDD CPNLP*VVRPEVD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10765	24666	A	10850	164	1	RGFQVRGE*NSGRETER*RERE*KLARE RAIGQEREREKSREAGRERERKKE
10766	24667	A	10851	417	100	MMLVVGNLETRLWSQAQTIPCTKQRSSL FFPVLNAAIFRSKSKVLNCLFYFLGNTL FSWDLIPEILFPLSHYHHYHHHHNHQY *KS*QWSASNTRFQGILDKNSY
10767	24668	A	10852	339	3	ETTHSEARRGRSAAASCRGSALRRGRFP ESRRGREAAPVCPRHVL*GAQSKQAAV AGKRSGRTHASRPWPKSLFPTPRRRISLK RALHFWQQSADPSPSVSRIPPHGVGSS
10768	24669	A	10853	1	373	LQQKGMKRKAGQSEMAPAGVSLRATILC LLAWAGLAARDRMYLHPHFLVIHNEST* EQLTKANAGKPKDPTFIPAPIQAMTSPV DEEALQDQLVLVAAKLDTVDKLMAAMVT MLAIFLGFRIYG
10769	24670	A	10854	1	423	VSCSFLKLTMKHGLLLLLCGFLLKSQG VNYTEEGFFRARGHRPLDKKREEAPSLR PAPPPITGGGYRARPAAATQKKVER* APDAGGCLHADPDLWV*SPTGCQLQAL LQLERPITNTVDELNNNVEADSQTSSSF L
10770	24671	A	10855	343	3	RGCEAHPLPRSEGPAGSALAQPVMYCTI FAGTLITAISSH*FFT*VGLEINMLAFI PVLTKKINPRSTEAAIKYFLTQATASII LVIAILFNNILSGQ*TLTNTTNQ*SSSI I
10771	24672	A	10856	147	1	TRTPTGQCVSPKSMFLGAVAHSCNPITL GG*GRRIT*GPEFDPPLANMV
10772	24673	A	10859	189	422	NHTMDDFERRELIRHKREEMRLEAERI AYQRNDDDEEEAAR*RRRRARQERLRQK QEEESLGQVTDQVEVNAHNSVP
10773	24674	A	10860	90	273	SHQEIEQNSAMAPRKRGGRGISFMFYCL RNNDQRYMT*RL*SGIGWMLLSSGRMGY ALPG
10774	24675	A	10861	25	411	APCAKPCGDWRSRGLVWAMSGCNARKG DCCSRRCGSHL*N*IPTDWPLN*FPLTS AKVKECFPKESIYSQTVY*SPG*KM*T *DKEHPRYLIP*LCIQFYHLCWVTGTGG GIILKHGDEIYIAPSGV
10775	24676	A	10862	33	302	SRRATLIYVDMENGEPGTRVVAKDGLKL GSGPSMLALNGRSQVSAPRFRGRTFNAPP SLPIATIRALGTVNRATEKFVKTNGLR Q*QPRS
10776	24677	A	10863	1075	1521	YCHTGKGEQLGERFCEGVSRRGPAERGS DSQTPWPWPLCAAAGTSAGTSHSGSSSG AFSSWPCWTAEEPAARKRGRPAGSWSSP ATGAPGRCRHRIILSRGAGGSAGFVCSGL AESGL*ESSSPGRSQG*PQGQRHPQPNG LPAPPSTSV
10777	24678	A	10864	245	418	TSKLAFPI SIPVIYANKVCP*FSKKKKK KKKKKKKKKKKKKKKKKKKKKKKKV FFEGPGFFF
10778	24679	A	10865	132	398	LNMKGDPKPKPRGKMASYAFFVQT*REE HKKKHPDASVNFSEFSKKCS*RWKTMSA KEKGKFEDMAKADKARYEREMKTYIPPK GETF
10779	24680	A	10866	115	455	LLTRNMDRLILLAGMPGLGQGPPPTDAP AVDTAEHVYISYLALLKMLKHGRAGVPM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EVMGLMLGEFDDDDYTVRVIDVIAMPQS* TGVSAEAVDPVVIQAKMSDMLKQTGKPEM D
10780	24681	A	10867	64	483	QGERPAAAMKI*SLTLLSFLLLAAHVLL VEGKKKVKKGLYIKVDSE*KDTLGNTHI KQKSRPGNKGKVFVTKDHTNCTWAVEQE EGISLKVECTQLDHEFSWAYAGNP TLCL KLTDEIVYWKPVARNLRLQNDIMIYSPQ
10781	24682	A	10869	229	1	DTTILKLGRLLIILQWLLSEGKSHMSFTL NQK*EIIKLSKECMSKAELSQKLGCFQ VGSQVMHAKEMLLKEIKSAT
10782	24683	A	10870	934	515	KKVLLCLPGLGCGGVILAHGSLALPGSS SLHLSLQSSWGLTGM*YDARLIFVYFPR EMGSCHICQAGLNSYNSSIPPTLVSQNV GTTGVSHRAQLAPVFCFCFVTLVDVKAL HFGKQENRIFFFFI LFPGGSRD EDRVA
10783	24684	A	10871	373	424	EFKTNLANMG*CLKSQHLGRPCANEMR LGVQNQLGQHGEIPFLK
10784	24685	A	10872	1	469	RSRSGDSLPAACDRPSGASALATCETIFS AISCFWDLPAAPSLRLTPSCQPTMSSQIR QNYSTDTEAAVNSLDNWYLQASYTYLCL GFYFDRDDVALEGVSQFFRELAEENREG YDRFLKMQRGRALFQDIMP AEDD* GKTHNAMTAAMGLETK
10785	24686	A	10873	244	2	NIYSCKETFSVPLLAHVHFLVGRGGS QGTEMLWHRVDLRYREQAGHSGSHL*SQ HFGSPRQVDQLRYGVSDQRGQHGE
10786	24687	A	10874	83	427	ISLNMIRIAALNASSTIDDDHE*SFTRH NTQTKEAQEAKAFALYH*ALDLQKHRI EESAKAYHELLEASLLREAVSSGDENEG LKHPGLILKYSTYKNLAQLASQREDLET AME
10787	24688	A	10875	94	1	KSQKACNPSTLGG*GGWIT*AQEFTTSL ANT
10788	24689	A	10876	2	413	GVTRGFNMRIEKCYFCSGPIYPGHGMMF VRNDCKVFRFCKSKCHKNFMMKRNPCV RWTKAFRKAAGKELTVDNSFEFEKRRNE PIKYQLELWNKTIDAMNRVEEIKQKRQA KFIMNRL*KT*ELPKVQDIQEVQLN
10789	24690	A	10877	65	417	RFAGAGATPEARAWPTDVHAAEEEEKEMD LPDLASRVFCGRILSMVNTDDVNAIILV QKNMLDRFEKTLEMLLNFNNLASARLEQ MSERLLRHRTL*DMKPDLSLFRPIRT LEWKL
10790	24691	A	10878	4	442	APTPDAMGHFTEEDKVTITGLWGKVNV NAGRETLGRLLVDYPWTHRRFDSFGNLT SGSVIMGNPKVKAHGKNVLTSLGDAIKH LDDLKGTFA*LTELHCDKLDVDPENFKL LGNELETDMAIHFGQDFTPEVYAYLQNM VTVVAN
10791	24692	A	10880	1	419	GKHIRQYHEEKETGQRINIEHYLGNML AKNLLFEKEREAEKEKSYEIPTKNIQG QMTPIYPVGMGNGTPCS*KQNRPRSSTV MYICHPESKHEILSVAEVTTC EYEA VILTPLLCSHPKYRFRASAVNDIFCQSLPG
10792	24693	A	10881	54	335	REIFTMSGALDVLQMNEDVLKNLAVIT HLCCTKTDSPEQIIYGS*TEYIYSIKL NRT*QNLMLAVP*NYDI*NHDEVMTVF

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						NNTLQMFEF
10793	24694	A	10882	216	3	MSIKSMSICCLRKKKGKHFQIRGK*NSG RETERERERERKRERERARGQERERQKT SEGGRETERERERKKE
10794	24695	A	10883	3	390	GELKCSKEKQCSMSAKSRTIWIIGAPFL KGQPRGGVEEGPTVLIKAGLLEKLKEHE CDVNDYGDLPFADIPNDSAFRIVKNPRS VGKASEQLAGKVAEVKRS*ISLVLCVN LGGGLECLCGHAKVYSR
10795	24696	A	10884	3	375	STMRAWIFFLLCRAGRALAVPQQESLPD ETEVEETVAEVTDVSVGANPVQGEVGE FDDGA*ETE*DVVAENPCQNHCKHGKV CELDENNTLMVCQDPTSCPALIGEVEK VCSYDTLTFYSS
10796	24697	A	10885	95	2	KCTQGPSAVAHACNPNTGRGGWIT*G QEF
10797	24698	A	10886	1	114	MGFHHVSQDGLDLVTL*GACFSLPKCWD YRREPTHLAH
10798	24699	A	10887	1	368	EPTMELTTAEKTNGKAAWRKVGAGAGEY GAEALERMFLLFPTT*TYFPHFDLSHGS AHVKGHCCKKVADALTNVAHVDDMPNAL SALNYLHAHKLRLDPVNFKLSSH*LLWT LSAHLHVEFT
10799	24700	A	10888	336	9	FRGQVIPAIFFPPFQTTSLSYFQTGPQN* TPFFQKILKLTRGGGKLLDFQTPGRLRQ KREDPLFPGV*NCN*P*SHPWWGTKQNP VSKKKKKLKTSSIFVHRVSMSP
10800	24701	A	10889	3	362	GFLIAPLEMQELGTPMNRILQLTTAEQE TFLTPALLLPIPHQTYSTASAVPLAKPD T*PKDVGILALQVHFPAQYEDQTDLENY NNVKALKYTEDLGQTLMGFCSVQEDINS LCLTVEQP
10801	24702	A	10890	66	333	TLPGNIGISFVERVMEVLRPQLIRIDGR NYRKNPVQEQTQHEED*DFYQGSMEC ADEPCDAY*VEHTPQGFRTTLRAPS*LY TPIVG
10802	24703	A	10891	405	49	IPWMGTERTRASAQRDVAGPARNPACPL PEQCFPGPAEWGTPLTPPGSC*LRPGER ERHGPCWGPRERLSSGQTHPPSPQGC NTCPCHKHQELLAGGVAVFYKLFYRYG NSPKWDL
10803	24704	A	10892	2	197	PQPLRVLWTAHLAAMAPSSRTSLLLAF LICLPWLQKAGAVQTVPLCTLFYHAMLQ THRAHQVIDTYQELEETIYPKDHKYSF LHDSQTCL*FSDSIPTPSNMEETQQT SNL*LPDIPAPGFCPDLPALASKGWCRPNR SAMHAFLPRYAPNASRAPTGH
10804	24705	A	10893	3	334	DQLPEPLKVLWTAHLAAMAPGSRTSLP PYALL*LPWLQEAGAVQTLFVSRFLDHA MLQAHRAHQLAIDTYHEFDETYIP*DHK *SFLHDSQTSFCLPDSIPTPSNMEET
10805	24706	A	10894	3	341	LLTPGVSDAICYILDSGYIIMSDTFTAY VIG*RFEVNG*HATVRFAAVVPVALPW LGV*WDNPERGTYDGTHEWTVYFKCRHS TGGFFIRSNKVNLTDFVTADKNLYVLD Y
10806	24707	A	10895	25	351	AMIQTRDLQGGRAFGLLKAQQD*RLDEI CTQLLDDLKYSNDEDLPSRLEGFKKYM

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						EFDLIGNGHIDIMYLKLMYKLAVPQTD LQLPRSIGEVYSGSGETISYPDFLM
10807	24708	A	10896	364	38	FSQFKIAQFLKKIPFPGFSPFFQNGGNF LKFSKFFPNKRGFFPHPPFF*KRGPFFCP KWGPQGHIGAHGPPAPQGGKIPFPQVPK KMGIKGPTPPPGFFFFFFFFFFFSW
10808	24709	A	10897	136	3	STLKHR*RPGMVAHACNPSTLGRSGRI T*GQQFKTSLTNMVKP
10809	24710	A	10898	193	269	GNKYCLTILLLLLLLSFKRQSLTLLPTL ECSG*TRTPGPKGSSLLNPS*VAGHGGV CL*SQLRRLRWEDHLSPGV*GHSDPRL HHCTLTWATE*DSVS*KTTTTTTTK
10810	24711	A	10899	316	374	CCCCCCCC*CCCCCCCCCYKETNFE QQ
10811	24712	A	10900	38	206	VYCVLVFTICTLLCNTSLGLFHPEFFFF ETESCCVAQAGLQWHHC*SLRLLPHRII
10812	24713	A	10901	364	2	DYQHISPEKHCRPEGSGMVYLMCRKKK RKKKNLSTKILNPQPSFIL*KPRNSARK S*QKEITKIGADSLIENRKRIEKIYIN ETMSWFIEILNKIDQPLARLTMIERKDS TKFRNERG
10813	24714	A	10902	132	3	ATSSPWGYSAVRVAILLFLYFSNKLAF T VLYGFV*NYFLQEI
10814	24715	A	10903	234	352	NFCFFETGSCSVT*AGVIMAHCSLDLPG SSNSLTSVSEE
10815	24716	A	10904	250	356	TMEMMLDKKQI*AIFLF*FKTGDAAET TLNINNAL
10816	24717	A	10905	280	322	QT*SLILVSLIICIATTNLLGLLPYSFT PTTQLSINLAMAIP*AGAVVIGFRSKI KNALVLCSTPLPTSTMLPVHMDTSSD IHPKI*SIR*QTCIQHRLLLWLKC
10817	24718	A	10906	271	365	KWRPGVVAHTYNPSILGSRGGWIT*GQE FKT
10818	24719	A	10907	135	358	LRYKLTNPKLTLTCLGLIFLKGNIVNIG QCNGVHM*YQHFGRPQDCLSPGIQQQH GQHKESLSL*KSLKISWS
10819	24720	A	10908	107	212	IKNEGMGQVRWLMVPVIALWEA*VGCTP EVSHSWL
10820	24721	A	10909	165	383	PKNRPIIPLKRSSISNPGDFQKSLRPGL TPMGPHFKRGNYSYDENLENLCPVGGNK GPGSH*GLLTCETCRGF
10821	24722	A	10910	119	291	GGYRFYVKDTF*K*GFWPLTLFIILKPL AGHGGACLSWRMLRLK*EDHLSLGGRG CSELWLC*TLA*ATE*DPVS*KVRLALN FVYNTKTFPSRAWWCMPVVLATHEAEVGG SLESGRSLQ
10822	24723	A	10911	283	2	SDNTTDTFLPFYKYIFPITWEQGETWK KNPRNSRLKKTLRSETIAQIPLKCNLWP GMVAHACNPYTLGD*GGWVT*GQEFETS LANMARPSC
10823	24724	A	10912	1	360	PHAFGTMKWVTFMSLLFFLSWANSRGGF RQNA PKSEVAHRLKDWGKKNFKAWG*MA LAQNLKQGPFFENHGKLGKEVPEFAKPGV ADDAEAENGDKWLNLTLLGNYPVAAVRE TYGERAEC
10824	24725	A	10913	270	361	SKTWPGTVAQTCNPRTLGSQGGWIT*GQ EF
10825	24726	A	10914	157	1	VFFQLSRLAWKGFSRFFVFETESHVA

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						*AAVQWRDLGSLQAPPPGFTPFSS
10826	24727	A	10915	1	357	LEEWGPEREFAEEKEKNTKKKKIKNS TPPKKPARKGEEKPGPFKRAITTFVAR IPLFCLKGFLWPS*IIGRSSPTPGSKG HTGAPNCPPLAAFPKDVFNPNKPMVE AVKNPIL
10827	24728	A	10916	102	471	PSTPIILTSSYPHYVKSSVTSTFIISLF PTTIFMCLYQEFIIISN*HLPTTQTTHLS LSFKLDYFLIIFILLTFLVTWSIIEFSL *YINSNPNINQFFKYLLIFLITILILLT ANNLFQLFIG
10828	24729	A	10917	2	138	REPTMVLSPADKTNVKAUVGKVGAGAG* YGAVVLFWTWLTNLNVIDS
10829	24730	A	10918	178	393	LVLCTVLLMWRFFHFDLSILKAQDVTE NLSNPTVLRGETGPSAVAHTSNPSTLGG *GKWITQGGQEFETSLA
10830	24731	A	10919	278	124	TAWADWGSNETPFLKLKPKKLT*GGGVC LEFQVLGRVRPKNPNFLNQGFN*PKFR PWTSTWGAQN*FV*KKKKKNKKNKP*NS RHTPPP
10831	24732	A	10920	221	243	IIIGSPLIDIKISKCFKLIVAFGQAQWP VIPALWEAEAGRSPEVGSPPA*PGSLK VHVDNNWESIN
10832	24733	A	10921	33	292	GTMWLEIRHAVEVQCVLVSELVIPTSGD KPBQC*DHYLIT*YLILGKWGI**ISGA LEKKKKKKKKKKKKKKKKKKKKIKITGG FI
10833	24734	A	10922	108	3	KLAVYGSVCL*SQLLGRLR*EDHLNLGH GGCSEP
10834	24735	A	10923	106	2	KLAVYGSVCL*SQLLGRLR*EDHLNLGH GGCSEP
10835	24736	A	10924	195	2	ASLFKSQLNRAFIYLFYVFIFETGSL* PMLVCSGVITAHCNLHVLGSGDPPTSAS QVAETMVL
10836	24737	A	10925	127	2	YVCILKNLKGKPGMVAYACNPSTLGGQG GWIT*GQEFKTSL
10837	24738	A	10926	639	282	FFLSIKGWVQQFMPIIPTPWGLKQEDHL RPGLRDQPVQNSKTPSLKI*KLARRGG ACL*SQLFRKPR*ENCLSTGELKPKGGI FIRLVQNKIPTTRGEKQKQSHTGSYQCP KIKKKG
10838	24739	A	10927	1	363	ALLTQALTCRQAGAEAPHAGATPSLMPP SLPQGFDRDCSPSDAAYTMENTIDKKQNG VIILFKFKMGHKAQTRNINNAFGPEI ANKGTVQWRFKNFCKRDESREDDE*YAQ PSKVATDQL
10839	24740	A	10928	53	379	TEAELLTLYLLPNALLNHFTSPPLMFAD RRLFCTNHIDIGTLYLLEGA*AVVLGTA LSLLIRAELCQPGNLLCNDHIYNVIVTA HAFVIIFFIGLPIIIGRGN*LFPL
10840	24741	A	10929	180	350	EPMAKGKTESPGPKRCGP*I*WVISQRG TLRFRGAGLFFMGEFLRLGENLLEIPRG A
10841	24742	A	10930	361	379	RRYWWLG*VQWLMFVIPALWEAKAGRSP KARNL
10842	24743	A	10931	121	543	HRNTGSTHASAHAYHIVHTNP*PLTGAL SALLMTSSLAMGIHFHSITLLILGLLTN TLTIYH*WRDVTRESTYQGHHTPPVQKG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						LQYGIIILYIT**VFFFFAGFF*AFYHSIL SPTPQLGGHWSPTGITPINPLKDPDLLNT S
10843	24744	A	10932	227	339	VGGVKSQVQLLLNCHFSSR*MKKKKKKKKKK KKKKKKKKKKKKKK
10844	24745	A	10933	64	409	DQRNKS AHLRAHLKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKRGEL*KKIN WAFFLPLLKRKFVGENFLKKNFFWGGNI GGQISSKKYRGGGK
10845	24746	A	10934	2	362	NKLSGPYPPEKVGYTLPVLMNPLAQLVIY STIFAGTLITALSSH*FFT*VGLEIDML AFIPVLTKKINPRSTEAAIKYFLTQATA SIILLIAILFNNILSGQ*TITSTTSQYS SLIILRAM
10846	24747	A	10935	154	3	GCPLSPLLFNIVVKVLVRAVMQEKETKS IQIGLEVK*SLTDNMILYLGN
10847	24748	A	10936	250	363	TAWPGYLYSFSFLY*ETTKIWLGAHAHA CDPSTLGGGR
10848	24749	A	10937	199	339	NVLGILLVFRIIVEIYKCGRLWLGTVAH TCNPSTLGCQRGQTT*GRE
10849	24750	A	10938	130	240	KNEQDPRDL*DNDKWPNIHVIGVPPEEDK DNGTERVFD
10850	24751	A	10939	35	235	FILVENTKKMCICPLLNMIIYAILYLFVP SVFL*EENKQ*GITEKKKKKKKKKKKKKK KKKKKKKKIKPGGL
10851	24752	A	10940	179	12	DQPGQHNTKTLSDQENKNKSSWVQCCV*P QLLGLRLRWEDCLSPGGRSCCEPCSHSG
10852	24753	A	10941	297	278	INQDNELTLINQSSKQIKHKNNINQTLRT KMENENLFA*IIAATILGLSATVQIILFP PILIPTSKYLINNRLITTQQ*LILKLTSK QMITIHNKTGR*T*SLGGD
10853	24754	A	10942	3	318	FGGGRGVRNYPDAFVLSVLLPSRLLFPH LFPHLFPLPPFLGLAPYCFRTL*YF*K* *LYYSQSIIFFFYREMKNKLLVFWAINL FFLYYYNYMEMWTLCYWKN
10854	24755	A	10943	190	3	KLSHKQSVYFKTFPI*KNHVLFK*KNLW VYPNDKFFFFFFESLALSPLQCNGTIL AHCNLR
10855	24756	A	10944	281	1	KKWLFSSSYSSLYGNGLFLIPPFLRVSGF GKGFWKKFFFLRARGALFWGSPKGFPL GFFWVFFFFFF*DGVSLLLPRLECNIGIISA HCNLRFPGS
10856	24757	A	10945	169	319	NGVEDAFKNMVLGWAQWVTSVIPALWEV KVGGSPEVRSFRPTRPI*KYGFRLGTVG YICNPSTLGGQGRRI*GQEFQTNPANM VKPC
10857	24758	A	10946	312	1	FARPGLLKSQWDFQP*PLDPVWGGFFKRF PENWLEFEIFPFLIIMAKRKKLSKSLFP FPFLG*FKD*GQKTPFFFTVSLLLPK LECNGAISAHCNLCPLGSSD
10858	24759	A	10947	208	329	IFTGDRSRNNRIG*ARWLTPVIPSLWEA EAGGSLEPKSLR
10859	24760	A	10948	116	374	FYFGYLLFFFCFFEMAPCSRG*SWSARG QSFCNLI FPGSSDLYVSAFRVARITGAR DHACIIIVFVDGGCVDTTITSLAGWL RG
10860	24761	A	10949	264	434	QLAFCTDTLTSVREQCEQL*KCVKARKR IELCDEQ*SCRSHTD*CTDELDFDLHA

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10861	24762	A	10950	226	429	T NFGFRLDKTVFFSKIRINAWAQWFMPVM PELWEAKAGGIT*AQELETSLSNIVRPW LYKKFKN*VWWC
10862	24763	A	10951	188	433	YSAEWKIDLGIEVFWVGKMTYKQ*FFWF VFKFLFF*RQGRTLSSKLEWMSVITGHC NLDLLGSRETFASAFQVTWTIGSCHS
10863	24764	A	10952	298	445	LFSKCSSKSIKEEGPGVVAHACKPGTLG GRGGWIT*GSEFESSLANMVK
10864	24765	A	10953	244	1	KTPQGLVVFCLFKKSPKLGKGVSMGVL ICFFLKSRINLNFNPRGLGQRKNFFFFF ETDSYSVAQTGVQ*HNLGSLQPPSC
10865	24766	A	10954	199	3	QETKKEQNKENKQIK*STRKKHRQGTN KTKERGERQTPPVGNRQPTPLGIHARPR RRATTSPRA
10866	24767	A	10955	157	3	YSYTFSTFIITTSILIIQTLSGHGGACL* SQLLGRRLRQDNHNLNLEHGGCTRA
10867	24768	A	10956	263	357	GLSLKVLQTQWLGAHAHACNPSTLGGRRG *IT
10868	24769	A	10957	333	2	KWKADMLIPLVIKSFFLGIFFKMFTNSK RYIFLLQLLAQHSSFFSFIRCMEL*WPY PIPLCYGQSNQPSV*LAYCRDLFNELIF FFFFETEFHSCCPGGISAYCNLCLSC
10869	24770	A	10958	130	228	GSSFLGGSPSVAQAGVHLPDHGSLQ*DK SPSVQKMSKWIGCSGACL*SQLLRRLRC QGRISP*GQACSEP*SGRCTPAWATEGD PPKLLPYTTDS
10870	24771	A	10959	250	3	VQACSITGALYQRRNADEPQTARPISG FTTSIAMRLMLLTCSGHIWVPVADLAFSG IMP*GLFFPSRQNLALSPRLECSARA
10871	24772	A	10960	199	326	VLGRMWSNQKNYTLARM*KIK*NNTR CWGGCGATRRIHC*QECRI*KCQPQSL WRTV*QFLNTLNIR
10872	24773	A	10961	323	3	LLFFHLPDNWQH*YVFCHYNLSFLQFYI N*IIQLVVFVWLLSMSIILKSHPCFHS K*LSTVTFFFRQSRVSRLWGSAGISAH CNLCLPDSSDSCASAS*VAGSC
10873	24774	A	10963	120	3	PPFFFFFF*EMRSCFVAQARVQ*CDQSSL *PSTPGLKQSSC
10874	24775	A	10964	168	441	LTPVIPALWEAEAGRSPPEVRSSR*SPP
10875	24776	A	10965	19	207	APLKLNVAMELSLGQWDVSRNSLWEIPL KKGDTGRVQWLTPVIPALWEAEVDRTPE VTSVTRC*PLKLNVAMELSLGQWDVSR NLWEIPLKKGDTGRVQWLTPVIPALWEA EVDRTPEVTSVTRC
10876	24777	A	10966	209	1	TKSALSNNMVTTHIGLCKNFCIVL*DRV SVTQIGVQWHDLSLQSLSPRLKDPPTS ASRVAGITGMHLV
10877	24778	A	10967	109	1	DYLRSGV*DQPQGHGKTSSLLKIQKLAR LVGPIISC
10878	24779	A	10968	141	2	GLAMLPRLENIIFRPGTVAHACNPNTLG GRGGQIT*GQEFKTSLSLSC
10879	24780	A	10969	175	348	LVYECKHILCVFNTSLFFPH*TCYK*RG VLWLGEVAHACSPGTLGGRGGWIMASGD RD
10880	24781	A	10970	108	2	KTKKLHMRSGVVAHTCNPSTLGG*GGWI T*GQDSC
10881	24782	A	10971	184	2	SFLWKLHLRGVPGRVRCQSAPTRGASQL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GYLGVDRDPLEEAV*LFSDLKLCAGKTTT LFLV
10882	24783	A	10972	245	339	SQISGPGTVAHACNPSTLGGRGWEWIT*G QEF
10883	24784	A	10973	295	340	KRVFF*ARKKNPFLSPLWGLTLENPLGF RFLNPFLGLKISQFFFPRI*PLAFFF WGTLPRLNLKFGPFFFFFFFFFFFF*DG VSFCCPGWSQARRYIEINISLSTCPRA
10884	24785	A	10974	186	340	RPYLTIIRFKGHPNPEIQ*SFFVLFYC FDTESRSVTRLECSGSNSAHCNL
10885	24786	A	10975	253	491	FLECTSLLRQRVHPGQHSKAPPTKELQ TTGRGGALLQSHLLRRLRQEHCLGPGVG SYSEP*LHCTPAWVIEGDSSKK
10886	24787	A	10976	141	1	SFSFFKFSPTGDMIGFF*HFFFFLRRSH SVAQAGVQWCHLSSLKPRA
10887	24788	A	10977	3	138	HEETGFHLVSQDGLNLLTS*STHLGLPE CWDYRREPPPGREGDF
10888	24789	A	10978	186	323	YESRSATQAGVQWCELGSL*PSTSRFQ* FFCNLNSTWDYSGLAPS
10889	24790	A	10979	183	3	IKILFPFFFLRLSLALLRLECSGTFS HCNLCLLGSSDSAS*VAGITGTTTSPM QLV
10890	24791	A	10980	309	55	KNFGPNWVKFLGGKGGEMAFLGKFFFP FFFFEKESWVFQ*MQWGDFRSLQGP PGVTQISRLGKIGGPLFPKKKKKRERGN M
10891	24792	A	10981	637	838	SQHLGRPMRVDQLRPGV*DQPGQH GEMP SLLRIQR*AGHGGTHL*SQVLRVRQDN CLNSGGGGCSE
10892	24793	A	10982	275	2	RNRTLKMEFLSWFWGFWNWLNMIRPKN VKDSTSKSMENDTSPWHELFKELGKINA FDTPLSLVRGKFSDSIHNTFDHM*RTK EYNEARA
10893	24794	A	10983	98	346	GHGHATLRGLCVLTFSFHITALSVSGTN DAEDCCLCETQKPCGYIERNLLYLLIK DVCRVPAVV*VVERVYSLISRYSLWRD
10894	24795	A	10984	30	410	LPEFTGRPKRTRTRGFSTNHTDIGTLYL LFGA*AGVVGTAVALLIRAEALGQPNLL GNDHMYNAIVTAHAFELIFFIVLPIIG GFGN*LVPLIIGAPDMAFPRINNICE*L LPPSLLLLLASAIAE
10895	24796	A	10985	141	360	QTLRTKMENLNFASFIAPTILGLPAAVL IILFPPLIPTSKYLINNRLITQQ*LI KLTSKQMITIHNTKGRT
10896	24797	A	10986	3	347	HELRTKVNHELIASFMGPTSLGLPAALL IIL*PPLIPTSKYLISNRLITQQ*LI KLTSNQMITIHNTKGRT*SLILESII I IATTNLLGLLPYSFTPTQLSINLAMAI PL
10897	24798	A	10987	46	317	KSMTPIRKINPLIKLINHSLIDLTPPSN ISA**NFGSLGACLILQITTGLFLAMH YSPDA*TAFSSIAHITRDVNYG*IIRYL HANGAS
10898	24799	A	10988	245	1	VSCLEGLTNRKDIHTKNPSVHHHHQR PKVDKTKMGKKQNRKTGNSKKQTASPP PKK*SSSPATEQSWMENDFDELREE
10899	24800	A	10989	255	1	SCLPWANWISVQNHKKTFLVIRTFPI GSFHVT*LLGPPLILISPPRIFFFFETG

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						SFTVARAGVHSGAISARCNLRLLGSSNSA
10900	24801	A	10990	166	307	GEKPGWGLIWGGLVGRSSWASCQVLELL*EMVFRHVAQAGLKLLSSSNPPASASQSAGITGVSH
10901	24802	A	10991	109	330	TNQFKTKKEREAGKKKVKELERERERGKKRKEQRKNEKERR*P*NMD*RRIRERNHSFDVYEFLICGLLNLLHV
10902	24803	A	10992	244	326	GRYLKGWLDGPA*AVVLGTALSLLIRPELGHPAILLGIDLISSVIVTAHAWSIILVRVIPIIIIAGFGN*LVPLIIGAPDMAFPRINSISF*LLPPSLLLLLPPI*QMRAGVGEREVVR
10903	24804	A	10993	101	2	KTFWARFVGTCL*SQLLRPRQEDHLRLGGRGC
10904	24805	A	10994	177	1	TPSLLFFVNIICFCLNPGGGGYSEQKLC LCTPAWVTE*NSISRPSQNNRQSRQVNHLF
10905	24806	A	10995	214	326	KEERKNPRAIRVV*PWGFFFPFLKEISLFLFVFRFWHGYPFGAFFSTQKWLVF*TMVLFFFFFF*VSLLPRLCSGVISAHCNTFLPGSSDC
10906	24807	A	10996	184	379	LCCMVYHFPILLSLLYL*CKLFFSPKLEFSSCCPLECNGTVLAHRSRLPASGDSPTSASRVAGHGGTCL
10907	24808	A	10997	136	3	GRVDGQHIMTHQSHAYHIVKPS*PLTGALSALLMTSGLAM*FH
10908	24809	A	10998	274	363	PWAYAEPLTLHDATYST*SLIRASFTLFIA*TTLRLLP*SFTPTQLCMNLAMAIPL*AVAPDIGYSSMITNALSHLLPQCTPTPLISILGIETVSLLIQIPITLGVRRTANIT*CHLLMHLIGSATLSISTI
10909	24810	A	10999	305	1	NLHTTPSQIPLT*PLPNINIHNLHLTTTQ*IKYLILIPSNLPHNKNLKTAYSVPPSPNLHLPSSSNPASASQVAGNAGARHYAWLIFVFLVETGYSLV
10910	24811	A	11000	154	2	IVVGILQSRRCGRSRL*SQHFGRPRQADCFTPGVPDQYFTLLPEVVFFLV
10911	24812	A	11001	142	367	GVCLYQRISYIKKTKKLSQGLFYFLLL LLLF*EGGSHSVTKLECSGGVSAHCNCLLASSHPPTSSSQVAGTTG
10912	24813	A	11002	60	385	GNTLLSHTLRAHLIENLHAEFIDRTILGLPAA*LIILFPPLLIPTF*YLINIRLMA NRH*LIKLTSEMITIRNSIGRT*SIILVSLIITIATANLLGLLPYSITRTT
10913	24814	A	11003	214	83	SKKSASPLTFNIVFQVLNDSVREERTRYTEMEKEEIKLS*FVD
10914	24815	A	11004	241	368	SYLL*PSP*PLTGALSALLMTSGLPMRFHFHSITLLILGLLTNTLTIIYQ*WRDVTR ESTYQGHHTPPVQKGLRYGIILFITLEVFFFARFF*AFYHYSLAPTQL*GHWPLTGINPLNA
10915	24816	A	11005	3	396	HEPHALGMPLTADLPMSASCSTSLLLL LHLHLPLWI*EARAYQAACSKLFDHAM LQAHRAHQLTIDTYQEVEETYIPEDHKYSFLHDFQTSFCFSDSIPTPSNTEETYQKSNLELLRISLLLIESWLEP
10916	24817	A	11006	156	335	FGCCCCFLFF*LVYCCYVMMLYIYVLI

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						SFGFYF*YWIM*YFYRLVYNIYLVLFYLYMS
10917	24818	A	11007	107	2	KCSSSKHFTKEDSQITNKHIEKCSS*LLVREMQII
10918	24819	A	11008	129	412	KTRSGFKKTPGQKGKTPLLKKTPKITGPGGGALKPPFSGGFRPENPLNLRDKGSSGPKTPTFFSPWGKK*NFFQKKKKNLLYPGKIFFFWMKNI
10919	24820	A	11009	63	268	CTFKFNHCSTIQSTT*LDRSEKKKKKKKKKKKKKKKKKGGPL*KNPSLKGK
10920	24821	A	11010	154	422	NEFSFFFFFWKPKPPFFAQVGGQYRNWG*LKPRPPWLKNFSGGFASGEAGITGGVPHPG*ILVF*VKAGFHIEENLVWNSETGNQACASQ
10921	24822	A	11011	23	375	TRYLTKIKKKKKKKKKKKKKRGAFFLTPWGAFFFPGSAIFIFFFFGGFF*TPLGFFWETLFFWGKILGHLSPKILPFWGKKNFFWVKGGKNLLNSPFLKIFFLGVFFKKFFPPG
10922	24823	A	11012	151	361	ACTTTPSSFFSNIDTVSLCCPG*VPGHNSSSLNFPSPFLRSWYYRHAPHPAHFFPILIRSRYVAQAGLEFLALRDTPISDCPCTVHYPPSLAN*SVFFFFLTQSFVSLPRLKRK
10923	24824	A	11013	146	378	NFVVSIEFLHICY*IYSFICLIKVFL* *KKKKKKKKKKKKKKKKKKKKGENLKGAGGKKFLGGGKNNSFFRNGGCF
10924	24825	A	11014	82	264	TEFLYTICNWSAAILYLC*RNKVFLSFINTEKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKIERKI
10925	24826	A	11015	381	2	GRTALFTLLKGPIHRPQMFFTPLRVFPGSYTGISIRQSGFFFIKRVIFRL**KALFLLPFLLPFFSFFLKIGTYSVAQECNGMIIDN*NFELLGRNPSTSASQIAGNTSAY*HTQLVFLCEDGI
10926	24827	A	11016	1	251	PNCIVHSLRTGTNLNFIILLLCFTFE*F LNKNLIFESQKKKKKKKKKKKKKKKKKKR GAPLKKTGGPKFYPPASKKKISPQKGG
10927	24828	A	11017	234	1	DINIKGSWVGKIPKPSVLSLQLFCNSKIFPN*KLIKKNPNEPGVMVHCNPSTSGGRNGQMA*GOBFKASLANMAKP
10928	24829	A	11018	107	342	FQLCIGAIVHCFLFMKQHSSEYKSTDHRA SSKCHTVQGSQSLSTSAPFKQK*THKKKK KKKKKKKKKKKKKK*KKKGASF
10929	24830	A	11019	264	1	CFKPLLFKYPGIIKAVNLVSTASATFH KF*YVTFSS*KKFLCVGGKTGSHSITQ AECSGTIKAHCSLELPGPGDTPTPTSRV AARA
10930	24831	A	11020	1	288	RTRGTSSRSRAATLFFFFFFPKGGFFNG NLPTTFGKLGNNKFPNLNFPGGPPLPHG GLKKGPGAPQVPPLFLKKPQTSP*GLR EGPPPLKKFYLF
10931	24832	A	11021	115	287	STCBISFGCSRGCCWDYLMVWEFSHFYF *FLETECCSVA*AGVQWSNLSSLQSLHP E
10932	24833	A	11022	186	1	RPKVDKTAKMGRDQSRKA*NFNQKASS PPKEYNSSLAREQNWMENEFELTEVGFR KSVITN

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10933	24834	A	11023	180	353	IFCFCTFSRDGVSVCPGWSQSPELMIH *NTKIS*AWQRPVKIPATQEAEGESLE PG
10934	24835	A	11024	155	1	PQARRGGTCLQS*LLRRLRLRQEDRLSP GV*GYSEL*SCPCTPAWETERLV
10935	24836	A	11025	22	325	KLILLYDPQLTFIFLNTRAVVAHCAFC WPIHFVFGNYGFVFSCLFTFIFVYSGKA DLFFKPKKKKKKKKKKKKK*KKGG RGLKNSWGGPIFWGFPK
10936	24837	A	11027	127	259	GQVQWLTPVIPTLWEAMVGGSTKLRSR PFFSTP*PCIVMILYG
10937	24838	A	11028	37	408	IASGALFFFFKAAGKRGRDFKTEGAYQRO RTIFKNKKRARREKTGRENLRGNYKNMG RGLKTPRGALGGPYLDKKGPLRGKGPFO GGTLLGGGPKIKIQGTL*IRRNYWPYIR RYNRFKKRQKNM
10938	24839	A	11029	146	3	LLVLKDLPRIMVRSAPTYIYIYTYLYIY IYIYTHTHTHTFIT*VLFC
10939	24840	A	11030	268	435	LMCLRNETHN*F*KVE*WLGAGHTCNPK TLGG*GGRIA*GQEFETRLRNIVRP
10940	24841	A	11031	322	2	KLPHLQQQCVKVCYKPFLLKNGKIGHGG VCL*SQPLRRLRQENHSNPGQCTSAWVT QRDSVSKNKKRKMKEYFSSVRQNKPVK HTKRMSPTKADTKSTHCGGGRV
10941	24842	A	11032	251	380	HKRLHTIYFVPLKKMGPGLVGHTYNP STLGGQGGQIT*GRE
10942	24843	A	11033	64	324	FWFFFFFFFFFLNPPGGGKKKKKPPPL GKKKKRKGKGGKKFFSPPPRGGGGPKK ISLKRVLKFF*NPPGGTKGGGPFLLIPP GSP
10943	24844	A	11034	420	534	CPGVVAHAYNPSTLGS*GRQITIDREIE TILANMAKPH
10944	24845	A	11035	196	1	KNGHSLPPGPQKGTFFPKKKKTPKINLS ELGKSKAYSWPGTVVHACNPSTLGG*GG WIN*GQEFE
10945	24846	A	11036	10	248	PSDR*LFSTNHKDIGTLYLLFGA*AGVL GTALSLIRAEALGQPGNLLGNDHIYNVI VTAHAFVIF
10946	24847	A	11037	32	405	DYVSKRKEKREKRNIVLETSSISHLVE WMLCSRYHPLIKKRSSVRILIALCPQK VRDMS*GIGSKKQWDSWLSIWIKMESD PFLIPYPKINA*RLKDLCEINLKIIK REYLHDYRVKKV
10947	24848	A	11038	337	448	KNPRGFFGKNPFFWGGPFGGPPPKKMG FGEKKKF*FKRSKKKKKKKKKKKKKK KKKTG
10948	24849	A	11039	307	415	RFVCSTIKVLRDLSSDRSNPGRVLSTSN SSLK*KKK
10949	24850	A	11040	213	403	VHRGIKYYFLNKLPDFPQTFKK*G*RL GAVAHACDPSTLGG*GGWITLQGTFFETS LTRMGKS
10950	24851	A	11041	104	2	SAFFF*ETESCSVAQAGVQWCDLSSLQL PPPGFK
10951	24852	A	11042	177	3	AYTAYICVCIHIYLYK*MYICINHVCK ITYLYIYKYLKYNATYLIHIGFFSFLHTI S
10952	24853	A	11043	314	395	TVYILNLSINSVQSVLLSVFHLRLHQPR GRVQWLTPVIPALWEAQAGGSP*VRISQ

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						IKTPA
10953	24854	A	11044	310	403	RGKGGKKPRNPGGGKS*ALTKKKKKKKKKKKKKKKKPGGALKKKPRGGQKKTGGGKKKFLPKRGAKKKPPGDFGKKNQIGGGEKRGKTPPKKKKKP*GKKKNLKGKGGKKTpkSGGGKKFPFRVV*KKKLPPGG
10954	24855	A	11046	181	3	EGPLSLSLFFFF*RISSLLRLKYSGTIIAHCSFKFPSSRNPPTSASQAASTTG VHH
10955	24856	A	11047	392	41	KESRSLSQGGREKGPFFKFLAPPAPKFKRIFRPHPLKKGPKGPPSPS*ILSLKKKGGPPILARWFNNSCPQGFPPPGPKRLGFKGGPPPPPLF*KKKPPFLGGENQVKNF FFFF
10956	24857	A	11048	147	307	TVIFVFLLRKGLTLLPRLESGMTMAHLKS*PPGLKQSSCHSLSSWDYRRRRRG
10957	24858	A	11049	118	1	HGKIPSLQ*HK*TAGYGSACLQSQLLRLRWESRSISI
10958	24859	A	11050	54	284	RKIRRGGLHLWSNLLGRRLRWEDLLGRRLRWEDRLSPRRGGCSEPLCHCPPAWATE*DPVSKKKKSLFVEKPQGGG
10959	24860	A	11051	130	340	HNMHFAAHGSRINFDFFFFFFFFERRGFPFCPPVGRAGTHFGLLEPFPSRV*KQYYWLGTVAHVCNPSTLGGHVGES*GQEFKISLANIVK
10960	24861	A	11052	140	337	NIIMFFFFFFETVSFLLGLLEGKGTIWN*NLCLPG*GDSPLGCS
10961	24862	A	11053	197	428	IRSINNPTVASQYSSEWKSHIPLILNQNLDMIKFSEEGMLKAKIGLLRQTVGQVVNAKEKFLKKNQSATPLSI*IRK
10962	24863	A	11055	180	1	AI IALLYSRLGDYARRFHLRRKKEQWQGMVTHVYNPSTLGGQGGRTA*TQEFKSSLG NIA
10963	24864	A	11056	158	426	FFPLPLPLPTVSLFPRSPSDAEPKLDCTAAISAHCNLP*FSCLSLPSACNCRRAPPRLTASASRGAGIADGVSTQCSMVPRLECSGV
10964	24865	A	11057	220	421	YALHLNMKNNSYF*MRKKKKKKKKKKKKKKKKKKKKQNKKDPGGA VYKKIP
10965	24866	A	11058	162	464	SCSVGLKLFMSKTSLSLSYCLLLLLTLHYYYYYYYYY*SLVFM
10966	24867	A	11059	1	134	APENRVDPVRKTLVPLILPITITLANPCKKD*YPYVKISIAIC
10967	24868	A	11060	382	273	SSCL*PQLRLRLRQEDYLS*GA*GCNEL**CHCSPA WTEQDPVSKNIHTYIHSQSINYGSMIGYIHEQKGIADHKPIIAEPE DSTYPRDHT
10968	24869	A	11061	298	378	SCSASPCSSRHGWSPCG*QTCLLLAIALRCLPWLREAGALHTGPGCRLFDHAMLQAHKAHQLVIDTYQEIGENYIPQDKNSFLLESHTSFCSDSITTPSNMEETQQKSNLKLRLISLLLIETWLEPVRFLTRIVANN
10969	24870	A	11062	39	486	RPTRPDAYHIVKPS*PLTGALSALLMTSGLGMRFFHFSITLLILGLLTNTLTIIYQ*WRDVTRESTYQGHHTPPGQGLQYRIMLFITSEVFFFAGFF*AFYHSSLAPTQQLGGHWPPGTITPLNPLEVPLNTFGILAI GGSIT*AAH

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10970	24871	A	11063	269	429	ATWQKLP LQIQKNYPGLGLVAHACNPST LGGQGGRI T*GQEF LNQPANMVNTH
10971	24872	A	11064	248	65	IIEGQAQWLMPPVIPALWKAEEAGGSPEVG SSKPA*PCDEPPASASQAGITGVSHRTQ LILNS
10972	24873	A	11065	176	1	LFPPPKKVPPWGNTQFKSICLYTTNFFF FETESRSVARLECRGTISPHCKF*LPGS RE
10973	24874	A	11066	2	397	MVLWTAHLRAMAPGSRTWGLLTFALLCL PWLQEAGAVQTVPI SRLCDHAMLQAHRA HQLAIDTYQEFKETYIPKDHKYSLLNDS QTSFCDSDSIPTPYNMEETQOKTNLEVL RMSLLEIDS*LRPAQSNKR
10974	24875	A	11067	172	399	QILYL*KYAYTVTMQHLSHPI L*KKKKK KKKKKKKKKKKKKKKKKKKKTGG
10975	24876	A	11068	192	3	PKLTPMLKLIVPHIILLPLT*LSKKHII *INTTTHSIIISIIPLLEFFNQITSNLFS CSPTFC
10976	24877	A	11069	204	345	DKSGEHSKTSSIQKNLRLGAVTHTCNPR TLGGQGRWTT*SQEFQTSF
10977	24878	A	11070	3	416	HELPQPLRLVWTAHLGATAAGSRTSLLL DFALLCLPWVQEDGAGQTV*SR LFDHA MLQAHRSRLGIDTYQEVVETIYPEDRK LSFDDCHTYFCF*HSIPTPSHLGETLL TSNLELLRLICLVLIDSWLEPARILTS
10978	24879	A	11071	108	2	PSPFFFETESCSVT*AGVLWRDLCSLQA PLPGSSC
10979	24880	A	11072	400	278	KVK*LRQENQWNSRGRDCSEPRSRHGTL PWTTEQDSIPKNKTKPKYKIS
10980	24881	A	11073	139	3	KLACGGRHLSFQLRLRLRREDHLSFGG *GYSEPWSRYCTPASRA
10981	24882	A	11074	17	421	DHVGQPRWLMPPVILALWEAEPGGILLEP KVQDQPGQNCCKSLSLTITKKRRENFPG RGGTQLCSQLRLRLRVGCCIDPKLHNCL PAWMTERDPTFKRE*KKNDVLEAKNFFT ILTFMNTTKEKMVAQRIGSLFHG
10982	24883	A	11075	412	1	QFFFLGVCCPTQIFGVGKKGEKKKKRG FPPRVFFFNPQIFSPFFFGPFFFLGK FPPFFGERFLFFSKSKFFFGVFKRGFP FPPKNFFFF*RIF*KWFSPDKPFFFFF FFF*DRASLCHPGWSTVAQS*LTSC
10983	24884	A	11076	279	410	VFCCVAGRDGAPGVKAHFFAAQKPWDGG FPGP*SAGVGPPPIPR
10984	24885	A	11077	12	386	IAHLLLSFYHKDTGTLYLLFGAGAGVL STALSLIRAE LGQPGILVGNNDHIY NVI VTAHAFGIIFIIPIIIGCYGN*LATL IIGAPDMAFPRINNISFGLLPTSLLLLL AYAIVDAGARTGW
10985	24886	A	11078	412	3	LAILSLSLSLGFPYSLRYKNIKIRPINN PTMASKSSKRKTRTSFTLNQNLMLKL IEKSTAKAKRLKVRPLVPVSQVVNAEEK FLKEIKSAIPLNIQIMIR*QTS LIADMEK VSVL*IKDPTSYNIPLSQS*IHSK
10986	24887	A	11079	78	443	RHRLPSDTCLTAAP*PCKGSKKKKKKK KKKKKKKKKKKKKKKKKKKGGGFKKNS GGGQNFAGGKKIFFFFGGGVFKNPLWIF WKKTFWGGKISGQLSQKLSLWGEKKI FWGCGGETSF

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10987	24888	A	11080	395	2	KRVPKKKPKKNSPPGGRKGGSP*SPPF GGPDQPIF*VGGFDPPWLTPEPFFFK KNN*PGKGMPLILKSLGGWKKKIFT GGGLPKN*KETPPPPPGGKKKIPFPKK KKKKKRAAARDLELVPTRP
10988	24889	A	11081	24	182	TVSTTKCFSLIPYYGRKDM*KI*TIQ KKKKKKKKKKKKKKKKKKKKKKRGG PP
10989	24890	A	11082	173	3	NNVICYILYIPSVPKYKTTLNMRGSAFF FFFFFI*DGVSICHLGWSAVARSWLTA
10990	24891	A	11083	284	391	SVAHACNPGLGG*GEQITRGWEFETSL TNMEKARL
10991	24892	A	11084	257	3	TKKLREVNMLGWLYYMREEARPVDYVHW RGPEYSSLTKTIRNVIVKGHQHY*KASA GRGGSRL*SQHFGRRPRADYLGSGVRDQ
10992	24893	A	11085	42	171	ARRMRAGIHRVSQEGDLLTS*SAHLGL PKCWEDRREPLRLA
10993	24894	A	11086	176	325	FKRSKKKKKKKKKKKKKKKKRGGAL LKKF*FKRSKKKKKKKKKKKKKKKK RGGALLKKFLGGPQISGGGKRFFFFF
10994	24895	A	11087	67	379	KKKKKKKKPKTKKRTGPVRQNVWRGSL SPGRAPAEGPQGGSTESPLLVGRCIL GLREPGVPPAAYGRFLRDYMNISIQKLE KQRQP*GLPSLTGAELKH
10995	24896	A	11088	128	326	KKKSGGGVFFFTIGGGGHFFGGGRFFFF FFLGGFFFLKFFFF*EKFFFLGGNLVKH SSKKSSWVGW
10996	24897	A	11089	109	2	KTHSRPGTVAHTCNLSTLGGQGEWIT*G QEFETSL
10997	24898	A	11090	52	347	DHSLLELQMKLYASAQAATKCHRMGGL NNTFLFLFLSLFFFFLKQSLALPPRLK GRGPILVN*KLPLRGKRDSPPSPQCVG ITGLAHPRLILFF
10998	24899	A	11091	386	48	IHLQPPLQICTLKFFTNKNPHLFTGCP KYALIFLCFGLVKTGFHHVQAGLQIV PLCPDRLGLPKCD*RREPPHPAKKQFF IDRVMLCYPGWCPALGINPSSPVGLPKR
10999	24900	A	11092	164	3	VYSLLLRCPPS*ALTAKFINRCTYIHVC MYMCEPYAYTCLYTSTHIVCMYIY
11000	24901	A	11093	148	325	CLKLQPFGLGVVAHACNPSTYFISYQ*L SPVIPALWEAKTGGSPVSRSPARP
11001	24902	A	11094	162	3	LLGLKRP*IFFFWGGKFFFFFFFFFFEIES PSVAQAGVQW*CNLGSQPASGRV
11002	24903	A	11095	259	358	LRPGTVADTCN*GQARWLIPVIPALWEA KAGGSLEVGSRLRLAWP
11003	24904	A	11096	254	2	SWGFIPEERERENRYWDRQQGHAI VSN IVINAFLYRYTEREKPGVSLSPRVECSG MIVAHCNLSLVGSSHSPPAAS*VAGTTG
11004	24905	A	11097	132	3	KKKKRQPRVVAHACNPSTLGGCGGWIT* GQKFRTSLVMVKP
11005	24906	A	11098	2	455	LNLEQLIEPLEVLWTAHLEALDPSSRTF VLLAFALL*LPWLQEGAGVQTVPLSRFL DHAMLAHRAHQLAIDTYQEFETYIP* DQKYSFLHDSQTYFCFSDSITTPYSMBE TOOKSNLELLRIYLLLESWLEPVQFLM SMFGNNLEYDT
11006	24907	A	11099	2	375	QLPEPLMDLWTGDLVAMAPGSRSTSLLA FVLLWLP*LQEGAGQTVPVSRFLDHAM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LQAHHRAHHLAIDTYQEFETYIPKDQKY SLLHDSQTSF*FSDYIPTPCSMETQOK SNVELLRICLLV
11007	24908	A	11100	1	359	LQLPKPLTLVGTALHPAMCLAYATALIL GCALLCLA*VE*ARAAQTVPQSNF*DHA MLQAHHRAHQLAIDTYHEFEETYIPQDQK YSFLHDYQTSFCLSYSIATPSNMEETQQ KSNLELL
11008	24909	A	11101	1	370	LPEPLTDLWTAHLVPMAPGSRSTSLLLAF ALLCLPWLQQAGADQVP*SWLFDRAML QAHHRAHQLAIRTYQEFETYIPKDQKDS FLHDSQTSFCF*DSIATPSNMGETPQKS NLELLPISLLL
11009	24910	A	11102	2	361	AHLAMAPGYRTYLLLAFAILLCLPWLQE AGAVQTV*SRFLDHAMLQAHHRAHQLAI DTYQEFETYIPKDQKYSFLHDSQTSFC FSDSITTPCNMEETQOKSNL*LIRICLL LNEWMMEP
11010	24911	A	11103	8	366	PLRALWTAHLAARAPGSRSTSLLLAIAL CLPWLQEAGA*QTVPISRLLDHAMLQA RAHQLPIDTYHEFEKTYIPKDKHHSFLH DSQTSFCF*DSIATPSNMDETQOKSNLE LLRIFLL
11011	24912	A	11104	3	341	EPLRDLRTAHLVAMAPGSRTYMLLAFAI LCLPWL*EAGAAQTAPLFRFLDHAMLQA HRAHQLYIDTYQEFETYIPQDQKYSFL HDSQTSFCFSDSISTPCNMEETHQRSNL E
11012	24913	A	11105	240	329	RNWPGAEAHYYPSTLGGGRGRQIT*GRG FE
11013	24914	A	11106	2	316	HEERERERERERESAIVRQIHTQGEGLT ELVFPYRRPAPSGLKFTFVYVQEHILGV GGNGLSPLQIGVILRDGRGLAHIRCGR NKILRILKSQGRAPDLS*DLY
11014	24915	A	11107	169	1	EDGHHSGHLHKKQKQPAWPSMVHTCNP NTLGGRGWIT*GQEFETSLTMEKPCCL
11015	24916	A	11108	192	355	GMSLTGHSNYIILNLNFWPCVVAHTCN PMTLGGQGRFT*GQEFENNLAYRGK
11016	24917	A	11109	145	383	EVNKDKGKYHVSQGIQSFYSYVAYVFRK LIYTMMTIVNSALLYTELVICQGRRLV FDFGF*FWFFETESCSVIQAGEQ*CDLG
11017	24918	A	11110	199	400	TRAGFFPPFKKFLKGPFGPAPPFNLF GGRGGGFF*IPKKKIYPLLLPFLKVQKT PSKPPFFFFFLRQVLLCCPGWSAMAR SRLTRA
11018	24919	A	11111	373	177	QFETSLGTMSGPSFYLKN*KSARCCHTC MRFQLLQRQSREDHLSSGVHRCSNP*LH RCTTTWVTK
11019	24920	A	11112	204	399	NHFWDVVYHFSPPFFFFFEKNLCSVPR AEDQGMNLS*LNPLPPGLKQFFA*PSQE AGIIGPGHH
11020	24921	A	11113	192	16	KKTENNR*RGYGETETPAHCGRACKLG *PLWKPV*QFLKKLKMCLPYDPTIPLPA IFS
11021	24922	A	11114	113	369	AGGQGPNFLQKPGPPGLKGPPIPLPG GGNYGGGPPSRGIF*FFEKKGGGVPKV GPNLRG*RDLPAPPSKGAHPLNGGFFSR N

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11022	24923	A	11115	250	387	ILCDVEHSLWPGVEVHAYNPSTLGGQDGR IA*AQEFETSLNNIARL
11023	24924	A	11116	192	1	VCDLFWKPSPHALTRRRTSVFHLKR*FS WLGAVAHTCNPSTLGG*GFWRIT*AQEF ETSLGNMV
11024	24925	A	11117	289	202	VFYQC*KFIRKKKKKKKKKKKKKKKKKK KKLSKKIKKMDQQKLRSPTIK
11025	24926	A	11118	412	421	RA*PTEQVTLGITEQSYSRGHINNRVHD LDVGS*HPDGAAAIKGSFVQRLKGY
11026	24927	A	11119	16	472	DRLKPSATHAFADAYHTGKANP*PLTGA LLTLMTSGLTM*VHLHSITLLILGLLT NTLTIIYQWREVTRESTYQGGHTPPVQK GLRYGIILFITSEALFFAGFF*AFYHSS LAPTPQLGGHWPPTGITPLNPLEDPLLN TSVLLASRVSIT
11027	24928	A	11120	304	346	GLWHATGITP*PLTGSF*LLMTSSLAM *FHYHSITLLILSLLSSTLTIIYH*WRE VRESTYQGHHTPPVQKGLRYGIILFIT EAVFLARFC*AFYHSSLAPTPQL*GLWH ATGITPLNPL
11028	24929	A	11121	174	420	FISALLKSAIQRNAMFSTYYALTCTVG TAVSWSSVS*PQRNMMS*VHAPAMAGR LVCHYIRVYRRFEHVCKRAVHGQYP
11029	24930	A	11122	299	466	IFILHEICTTFFFEETRHFCH*AEVHWCS LGLLKPPPPGLRCDPSTSPSRVAGTRPS
11030	24931	A	11123	138	1	NPFNEKNPPPKGPGPKNAFFFFFEMES CSVAQARVQ*HDLGSLQP
11031	24932	A	11124	241	499	NQRERS*HLYLLYNTVCLTHGLPIIIY SAYQLAIYDLLLRDALARLQADLADRR RGLQPKKRFAFKTRRKDAASSTKVDAAP GI
11032	24933	A	11125	252	391	PLSLDLQSNASLSHFTSPPLMFADR*LF STNHKNI*TLYLLFGAWA
11033	24934	A	11126	45	459	AFLKNHPLET*SNHSFIDLPTLSNISA* GNFG*LLGACILQITITGLFLAMHYS PDASTAFSSIAHITRDVNYG*IIRYLHANG ASIFFICFLHSGRGLSYGAFLYSQT*N IGIILLATIATAFIGVLP*GQISF
11034	24935	A	11127	109	301	QDSLMRKKSKNRSPSHER*RSKCLERKR SGDKKKKKGGPPKKKIGGFPFGQMELK PFSILGGF
11035	24936	A	11128	322	2	SCHHVSSLGDRARPCIQKEKKKKERKKVG DFNTPLSMDGYQHWYQARKIIIMDGT TK*KITRK*KIRNQ*DLTDVYRTLHPRVK YTFLSLAYGTFSRTHIRGQAI
11036	24937	A	11129	182	2	FLPRGFQPPPVVVPGLGFLFPSSRD PGFSPMPFFFFFFFETESCSVS*AGEQW RNLG
11037	24938	A	11130	138	1	GWVFFLVVFSFSLFFFLR*GLSLSPTL ECSGAITAHCSLKLPLGLS
11038	24939	A	11131	304	83	WKKTDPRKGRNSASRLPSDSNCNSSL LSLQGLSLLYRFWTYHVTGKGSQSRPQEQ VLGYHARKNSR*VHRVK
11039	24940	A	11132	247	225	KNFWGGPPLRGKKNFFFFFGGYKK*L LLCLVNMYI*CV*YI*HKRIISDPKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK K
11040	24941	A	11133	242	3	KKKKIFFPPRYFWAPPYFFFLGPPPPFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFFFFFFFFFFFFFFFFVF*TFHLS PRLECSGTSAHYNLHLPGPSDC
11041	24942	A	11134	361	2	ASQSAGITGVSHRTRPETHGFKDT*RKPA EEVVTIH*I*ITLMSCNIESPEKVCADL IRGAKEKNLKVCRPAGTPIKASRITTRK TPCEGSNTRDRFQMRIHKWLTDLHSPFD GRVGGRV
11042	24943	A	11135	1	370	IRQTFFQKREIVGIILCYWNVGYSQLH *SSRMLWIFHFYRVYISVKVILVILVPH EKKKKKKKKKKKKKKKKKKKK
11043	24944	A	11136	273	2	GGRAGQQILFCRGITWLGPPRSCQCTFRS PPGLAL*PWECSLPPALKIRFSPFLPF FFEMEFSLSPRLECNVTVAHCNLRPLP GSSNFP
11044	24945	A	11137	130	354	GQLNKLSGPYPENVGYTLVVLINPLAQP VIYSTIFAGTLITALSSH*FFT*VGLEI NMLAFIPVLTKKKKKGGPL
11045	24946	A	11138	366	2	LVEMGFLVRQNGLYLLTS*SARLGLSK CWDYRREPPCPASDWVILTSPLIHALD GKEHTHTHTHTHTHTGLGICQSSLGKQS GGWGWLSANRGQFSPFAVCLVVSFLPEV PVVTSALFT
11046	24947	A	11139	228	1	CRAGRGLPAAVLIILFPPLLIPTSKYLI NNRLITTQQ*LIKLTSMQMIAPNTKGR T*SLILVSLIIFKATTNLLG
11047	24948	A	11140	157	337	HIPTPPHTTCPERPSIRHNSIYYLKRYC LLRIILSLPLQTS*PLTGALSLLMT SGLSM*SHLHSITLLALRLTYTLTIYQ *WRDVSRLHSTYQRHTPPVQKGLRYGII VETTSKDIVFSGLF*AFYHSRLAPTQQL *CHWPPSGITPLN
11048	24949	A	11141	188	3	IPTPGGPPPLPPQKVLFPKNPRAPPGV FFFFFFETDSRSVVRLECSGVI*AH*NLH FRGSR
11049	24950	A	11142	224	3	SVSSPCISNTHKVDVRSSALLQESTSSR EVMTGHFHYLIYET*LRSLAQSAALAC SGTISAHCNLRPLPGSSN
11050	24951	A	11143	262	371	SYCGPGVVAHAYNPSTLGGRGRRIT*GQ EFETSLTN
11051	24952	A	11144	244	379	TIGKQRCAGIEEVSDDSQAPWLKPVIP AL*EAEAGGSLEPRSLR
11052	24953	A	11145	1397	1565	DRLESLEMHIPGVYPNQWNTNFYLFYI FEAESHVAQTGLQ*RHLGSLQLPPQV
11053	24954	A	11146	284	1	GRGRQGGDSSGKEGNGRAMDITGGLVGK GQGAGEAFVEVWEKELRGFKVEGEDMD KERVVD*GL*GGRERERERERERERE RERERERESLV
11054	24955	A	11147	64	286	THALAWTRNQIRSGHGAMCLYSHLLRK LRQNDHLTPGV*KCLEL*LHH*TPWT KPTAKAIFNLKKKDSWD
11055	24956	A	11148	230	358	VSVSLIIFIATTNLLGLLPYSFTPTTQL SINLSMAIPL*AGAV
11056	24957	A	11149	81	367	QTLRTKMKNVVASLIDPTILGLPAAEL IILFPPLIPSCKDVINRLMTTQQ*LI ELTWEQMITIHNTKGR*CLILECLIMV IATTKLLGLLP
11057	24958	A	11150	257	2	SVCAVITKYLRLLGCFADAADTQRPLPPA TVKLTMFNFIATHGEPLGCI*LFVDKV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PKTAENFHALSTGEK*FSYKGS CFHRI LP
11058	24959	A	11151	257	1	WRCGEKETLIRCWWECKLVQSLGRVTWR FVRELKLELFPNPAIPLLG IHPKEKK*L DPCTCMFIVALVTIAKMWNQPKCPSMDL V
11059	24960	A	11152	17	367	NHKDGKKTEEEKQSTSPQKDCSSSPAM EQSWTENDELFDEEGRFRSRYELQEEI QTKGKEVKNFEN*DECITRITNTENCL KELMELKAKARELCEECRSLSSRCQLE ERVSA
11060	24961	A	11153	213	2	TFCHFFFFFETESGSAVQPGVWRCDLGS LQAPLPGFPTPSWRQRLQ*AEIVPLHSR LKLHFKKKAGVFSC
11061	24962	A	11154	1	347	GTSNHFPFLYTYQVHNSTDYPRNRCCLN PSLRFHTSSKPLPARPHIMTHQSHAYHI VKPSP*PLTGALLALMTSGLAM*FHFH SITLLILCLLTNTLSIQ*WRDVTREST YQG
11062	24963	A	11155	223	3	YSTNLKILRNHFILFF*DRVLLCLPGWS AVASSRLTANSASCLSLPSSWDYRRAPP HPANFCTDRFHHVGVQVG
11063	24964	A	11156	143	1	RGFLNQCPSONFFFFFETESCSVTQAG MKWYDLS*MQPPPPPRFKLV
11064	24965	A	11157	149	355	LQPLPPGFKRFSCRLRLTSWDYRKDVDS ALLSNYVT*KYISKTLCRHQSP EIVREF LTAMKSHKLT KVG
11065	24966	A	11158	156	370	RSDGCQKIPRNM LGGWSVLHHTVDEQ*G PNRYIKKCSASLIIREMHIINTVRRCLT PATMATVRRKTT SVG
11066	24967	A	11159	298	4	HFOVVIMWRQLVKGR LQAQKNAAFTDSH THLCYLKCVYFCVCVCMCICVFCV*SR AL**SLYLF LCIKAVKAGHSVSGLESQH YGR LRQADHLRSGV
11067	24968	A	11160	364	285	NSWGKIKILKGK*PPPPKIFFPKYPQS FFLSPP*KKKTNFPHPRKYLSPGIFLK APPPLIFFFFFFFFFFFFFFFFFFFWG
11068	24969	A	11161	198	406	KSVYMTLKKKRGSFHERGDVPAICNFFF *IHIYMCVYIHC VYIYIYTHIYIYTH QIYIYIYIYIYIY
11069	24970	A	11162	95	376	KIITKHNIARTNPYTF CIMN*LEITLQG EPKLRPPKPDKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKRGGGGFKKKPGGGP KIRGGEKIFFFFLGGD
11070	24971	A	11163	343	391	WR*LSSTNHN DILTLYLLFRARAGVLR AVSLLILAEQGP GNLGDDHIYSAIDP AHAFAMFFIVIPMIIGGFDN*LLAVRN GAPEMAIPHINNISC*RLPPSLLLLLAS AIVEAGAGTG* TAYPPL E
11071	24972	A	11164	1	158	QPMTPNRGPLSP*PLTGALSALLKTSGL AM*FHFHSITLLILGLLTNTLT IYQ*WR DVTRES
11072	24973	A	11165	265	466	KLLTSLSFNLLRETNQVGLLELSQAKY KKT PRLGTVAHVCNPSTLGGQG WIT*A QEFETSLANMA
11073	24974	A	11166	204	458	KRCLLP LFPDSNTQSSQCRREQIGRAIR KILTFETQNIKRLKTEKQLLKLE*SGK ITAHCNLDLP GSSSPPTSASQSAGITAG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11074	24975	A	11167	256	3	S KILFFKPGVLSPPWGGVNFQLMFPQGG PPKKKRGPPLSPPKKGPFFFFFF*ESR SLLPRLECSGAISTHCNLCRLGSSRTRG
11075	24976	A	11168	1	457	HRTPSVRTPNCRGDPVRVRSSTNHKDIGTL YLLFGA*AGVLSTALTLLIRAELEGQPGN LLGNDHIYNVIGTAHAFVIIFFIVIPII IGGFGN*LVPLIIGAPDMAFPRINNISC *LLPPSLLLLRASAIIVEAGAGTG*TVYP PLAGNYSHPGAS
11076	24977	A	11169	343	428	GR*LFSTNHKDIGLLYLLFGA*AGGLST ALSLLIRAELEGQPGNLLGNDHIYNVIGT GHAFVIIFFIEIPIIIIGGFGN*LVPLII GAPDMAFPRINNISF*LLPTSLLLLLAS GIGEAGAGTG*TVYPPLAGNYSHPGAYV DLT
11077	24978	A	11170	91	2	PRQDPSFFFFFF*TESGSVAQAGVQWCD L
11078	24979	A	11171	219	1	IFKSKILCLPPPEPNFFFFFFF FFMRHGGACCSPSYLG*GERMT*ASRV AGTTGVCHYAWLIFVFL
11079	24980	A	11172	292	365	RI*SLGQAQWLTPVIPTLWEAKVG
11080	24981	A	11173	251	1	ICDLQILTHGITTVCVMGLTTLFVSGIT FLIHSLAIKFGV*KNPS*LGTVVHTCN LSS*GGRGRIA*AREFETCLGNIVRP
11081	24982	A	11174	200	407	KIFETDVYVKCSNLCWASISFSNYFG GPFYLN*FLSYFSFLETESHIVAPLE CSGMILAHCNLCL
11082	24983	A	11175	11	155	STNFFLFSETGSGSVLQAGVQWPGDLL ASSHSPASAS*VSGTTVDAA
11083	24984	A	11176	140	1	PSTFPDVAMRRVSCSKGDKGQV*WLT PVIPAIWEAKAGGSPEI
11084	24985	A	11177	210	1	TDEELLMDQQRK*FIEMESTPDEDAVN IVEMPMKDLEYVINVD*VVAGLKRDC SFERSSTVGKMLSN
11085	24986	A	11178	133	148	STSTR*LFSTRKDIGALHLLFGA*AGV LGTAVSLLIRAWLAQLGSNKEA
11086	24987	A	11179	236	1	KFWKKDPLTKGGCPLKKGGGGIFSKKK KNVFFPKKKFKGGKKKNNFFFKKKKKK KKKKKNKE*LFISFAHIAVHL
11087	24988	A	11180	210	1	QSLGQENLQVFFPLFGP*PNYLDKGEKW IRVGKIWGHLEFFETESRSVAQSPRLE CSGAIAHCNLCPL
11088	24989	A	11181	292	348	KKGALFFSPGG*KKNFPPGGKKKGPLFS KKKNPP*KKPGEKEKTRFPFLGGLGG GFPLAPGGKPPRNRVLAPPNPGGKKK KTPFSQKKKKKKK
11089	24990	A	11182	168	3	KPEASMLRMDFFFF*EAGSHSVAHAGVQ WYYCSSLQPTPELSDPLAPSSKVGGIT
11090	24991	A	11183	87	351	KGIKWSLNIQRGVQPHLSYNSYFSSFF S*DWVLLRLECSGTTTAHRSNLPGSSD PPTSASQAAGTTGMHCHTRLIF*ETGFH HAVQ
11091	24992	A	11184	55	344	TSLNLCFFFFFFWGEKSPFLPPGGDEGPL FGQLDTRPWGIEKIFFAPPP*KGKRGVP PGGEFKNPPAPKGEPLS*KK*NQPGQ GAPPCYPFLGGGAKKIFSIQGRVSN* PKRGPSSPPGGKKGDFSPQKKKKQRF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EV*PNSPSGAP
11092	24993	A	11185	344	190	LVETRFHRSVDGLNHLTL*STRGLGP KCWDYRCEPPRPANTANSLNPFPM
11093	24994	A	11186	135	3	IFPKVFGGPPFFFFF*ETESRSVAQVG VQWCNLSLQAPPFGFT
11094	24995	A	11187	305	14	IMLITSIRRSRLSSTAEGKILSRLRICG RVAKYLINNRLITTRE*LIKLTSKQMIT ILNTKGR*SLILVSLSVVGYHFL*G* FD*SLLLY
11095	24996	A	11188	198	1	LEQTFNMFPNPKSIISIPSGFLFKIS FPFLFFF*DEVFLLLSRLCNGTILAH CNLCPLGSSD
11096	24997	A	11189	352	3	QLCNTPLPKTNHAMLTSNANTLIYRRS AIAAASSPPIFPASKILNSRLITPHQ *LIKLAQKQMIAPNTKGR*SLILVSL IICFEVSLISHCWVVISRLLMRYLEVGI NRGG
11097	24998	A	11190	270	137	CIINRLYVCVYIYIYIYI*YFYMYV YNILCILGHRRESGVI
11098	24999	A	11191	18	342	ACRKRKMSSKFALRATGNCYYSCTFCSI SFPHPK*MPCYQKKKKKKKKKKKKKK KITV*K*SKTKNIKGLGAR*ELSLA*L LGEPPIFAKGHPLMLKNVETCKRP
11099	25000	A	11192	169	3	ERSGIIRVYQD*NQCLAWSLA*KIHPW LAAVAHTCNPSPSGGRHWIT*GQEFK
11100	25001	A	11193	407	1	KRACFRWLTLTLSTLWEAKQENCLNAGV HDQPGQHGETPSPQKIKKSAWHGGPRL* EVRWED*LSQGG*GYSEPCSHHCTPAWA TERDPV*KQKRSIPWKELASERKDSGR RWLVREMPSCQASVIQVRRISF
11101	25002	A	11194	110	412	VCGFRLHSPAILMPLMPSYFRRHSNT EIKPISNPTVASKRASEKSCSLTLNQ KLEMIKLSEAT*KAEVGQKLGLLHQKV SQVNAKEEFLKEIESA
11102	25003	A	11195	34	155	AWHEGMHHSVDGLNLLTL*DACLGLPK SWDYRRKPPCPA
11103	25004	A	11196	289	453	NQPGKSFMSSTFHFMMFETLVHAGV*W LDLGLLQPPPRFKGFSLHLPWGDR
11104	25005	A	11197	177	432	KWEKQAQTLGGGNFPKGPKTRVGKNFEK LKGNNPFLCL*KRGRKGDTPWKKPAPS GERGIPGKKGKTGPPGFGPMEKIKRG K
11105	25006	A	11198	139	3	AMVSLSPRLECSSMIMAHCSLGLSGSSD PPTSAP*VARITGMHHP
11106	25007	A	11199	150	492	GDPLPGHHPV*EVRRPFARQLPRLRSEE PLRPVATPSGK*GASLSGSHPIQEGGGG GQPLPGHLPHPGWRSGVKPPPGQSARPG GEGHLLPATPTGK*GGPQSGQPHLSGGR RE
11107	25008	A	11200	239	64	YQKYYYYYFF*ETESRSVARVKSSGLIS AHCNLHLPGSRLQLCLFPTS AVFGQESH IT
11108	25009	A	11201	31	396	ILTMREIVHIQAGQCNGQIGAKFWEVIT DEHGMDPTGYHGDSDLQLDRISVYNE ATGGKYVPRAILVDL*PGTMDSVRSPPF GQIFRPDNFVFGQSGAGNNWAKCHYTKG AELGDSVLDV
11109	25010	A	11202	85	407	VLLPHSEALEGADTMPHSYPALSAEQKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						ELSDIALQIVSPGKGILAADECVGSMAR RLNQIGVENTQENRRLYRQVLFNADDRA KKRIIGGVIFFHETL*QKDDDGVT
11110	25011	A	11203	302	115	THLDHVAIYLSIYLSIYLSIYHLSIYHL SIYLCRF*LID*DRVSLYFSGWLQMPGL KPSSCF
11111	25012	A	11204	130	348	GNAYGGPCSVLVQRT**IPALTFPSTCL DSKFQRDVLVTLRDFSNFTSNTVAEIQAL LTSQGESGLDGALGWGQ
11112	25013	A	11205	232	62	ISARNEGFTNLN*RTFFFFFSSHCLSR LECGGMILAHCNLQLPGESLEPGRQSLQ
11113	25014	A	11206	161	2	KKKGFLPLIEPFCIQEIQLRLGAVAHT YNPSTLGGRGGWIT*GQEFKTSLAN
11114	25015	A	11207	251	3	PNHLPKAPSPNTLRIRFQHLNFRGAQQ TFGLQHKLTSKQMITIHNTKGRT*SLIL VSLIIFIATTNLLGLLPHSFPTTQL
11115	25016	A	11208	145	287	GFRLLK*INQKYSFLKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKK KKKKK
11116	25017	A	11209	436	110	ISGRGEQKFKFYFSPAPFFRGINPPPLGG E*NQNLKPP*KKIFLGSPKVPKKKGGPQ KILKKGPGGGPPLFPPPLGGQGQGFPE SQGFKTPPGKKKKPPPKKKKKKKK
11117	25018	A	11210	217	2	DKWSVLHINYNILSSSLVHVLFKYLEN* K*KKNLWPGMVAHACNTNTLGGQGGRIV *AQEFETSMGNTVKC
11118	25019	A	11211	146	3	QKVSHAQYRCLSWGYFFFFILFLETRSRS IAQAGVQWRDLGSL*PPPA
11119	25020	A	11212	187	384	GLICFYLTCFYFIFYFILFYFSLLCYVM LCYVLCYVMLCYVMVCYVMLCYVI*DRV SFCHPDWSAA
11120	25021	A	11213	373	482	MIKLRHRLGTVAHTCNPSTLGGRGQWIA *GQEYKTS
11121	25022	A	11214	64	362	ITGVSHFTQPLPFIGGLALSPKLECRGM IIAYCNFELPGSGDSCHLSLPSSWNYRY MPCMPS*LKKNF**RQGLTVLSRLEKDY LL*DFSALRSFPWGR
11122	25023	A	11215	181	368	CDSAVPLLDIYPTFEFKADLKKIRIPMFI IALFAVAKR*KQPTYPSIDKWKKLWAG CGGSRL
11123	25024	A	11216	268	369	TTRPDMVVHTYNSSTSGGQGGTIT*AQQ FKTSLT
11124	25025	A	11217	90	3	IGQAQ*LTPIIPALWEPKSGGSPEVRSL
11125	25026	A	11219	277	272	SLTAPGL*SQLRRLRWEDHLSLGQSSF SEP*SCP TPAWVTQ*DSVSKKKEKKKE KKRKEKEKVNTPKATESPGQALIGSHS LQVQKRVYAHPIIL
11126	25027	A	11220	19	343	LELEVEPEDVSELLQSLDKNYLSCFLKR FLENKYTPGEDVVNTIKMTTEDLKYNTD LVDKAAAGLERINFNFEGSSSVGKMLSN SIAWYSEIFYEROSQFMWQT*LLA
11127	25028	A	11221	266	356	FFEMESHTVA*AGVQWCDLGLLQSLPPG FK
11128	25029	A	11222	105	2	RFVCSTIKVLRDLSSARSNPGRFI*TSN SRPRKS
11129	25030	A	11223	145	350	RKGRQLLD*DLGWV*WLTPIIPILWEAB LGGSLEARSSRPAAW
11130	25031	A	11225	155	348	PLFFFCFHRNTFY*KSVCRFPKKKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKKKKKKKKKKKKKKKMEGGGGGANTKFLY GENRKPPPLFFFF
11131	25032	A	11226	271	3	NFLSVFNFRICLGMCFLSIFLLIFGGS LKYQLFLAQGFFFFFLHYFFTSSIHSSLL Y*MLDFLDLFFLYLFCNFNFVSFLFCI LSKFF
11132	25033	A	11227	3	413	SPAEPHRSYTMWNVKGVNGFGRIERLV TRAAFNSGKVDIVAINDFIDLNVMVYM FOYDSTHGKFGHTVKAENAKLVINGNPI TIFHERDSCIKRGDAGAAYVV*STGVF TTMDNAGAHLHG*ATRGIIISAPSAD
11133	25034	A	11228	48	413	VFVLVSCGFFFFFWEKKICFFWPGGKK RGKIGGTGTGPGKKGNGFRGPPPKNKEK GGPPPPNNFGLKKKKFYQGGQGG*KT RNFGKPPAPNPPKGGDLGGGPPTQGQNG FLKKKKKQKK
11134	25035	A	11229	172	404	EFENS CSPGWQRRGMIPGVTVEDMNQQ EFIRALVALLKKSRLKVPPEWDTTKLA KRKELTL*DEKWFT*AASTT
11135	25036	A	11230	247	2	QPKKKS VSKKKKKELPCDPAIPLPGIYP KEKKSVYKKNLHLRVYCRAVFTIAKIW NQPKC*SGDK*IKKI*YIYTVDLRR
11136	25037	A	11231	1	372	TETTVEVAVCELQDRKLTKSERQRFKEE AEMLKGLQHPNIVRFYDSWESTVKGKKK IVLVTELMTSGTLKT*VHQYYS*PRSM REFDFLNRSTSTFLVQPKKGTVLPTV TVLAYFLAHKVL
11137	25038	A	11232	311	464	KKATPRNLCKWPGTVAHACNPSTLEGRD GWIT*GQEFETSLTNMVP
11138	25039	A	11233	64	418	VPVASRRRRRCGRVGGGKAMADLDKLN DSIIQRLLEA*GAKPGKKVQLHENEITG LCLEPREIFLRQPILL*LVAPLKICGDI HGPPYDILLRLFYRGLPPKSNYLFLEDY VDRRQH
11139	25040	A	11234	233	421	PTTSNMRSLRLRGASS*KKTAGPQQRNL EPALPRRWGGRSADNPPSGSLRKS GKNM QKTPGTA
11140	25041	A	11235	343	1	NNTHGLSHSSVGRNPGAVGSGSCMSGIK LSEGLRSLLEAVCISRAAVIKCHSWVAS NNRHFFSPSSGG*KSEAKVWAGPCSL*R RVPSLPLPASGGSRLCLVCGCVTPPSAF TW
11141	25042	A	11236	122	419	RTPRGPKPNPGLQRKTFLLIGGRIKTYL GIFGKDLYFWGGKNWDTLPKI*RSREN KNF*REKWNLPYPGCLKNGARQQHFA HLLILRDTKTYMLAF
11142	25043	A	11237	1	379	AFNHLHAGHGLSGAAMKSLVLLCLAQ WGCHSSPHGPWLIYRQPNCDP*TEEAS LEAIDYINQNLPGWKHTLNHIDEVKVW PQ*PSGELFDIEIDTLETTCHVLDPTPV A*CNVRQLNEHAVQ
11143	25044	A	11238	1	397	QTMTPNRGLCPSKDLRSSHVISLPLHS ATHTRPTNQHTNHI PMARRSTRKHIRR APHTTCPKRPSIRDNP IYYLRNFFLRRI FLSLLPLQSPYPPIRRALAPNRHHPAK SPRRPT*PLTGALSALLKTSGLAM*FH FHSIALILGLLTNTLTIIYQ*WRDVALE STYEGHHTPPVQKGLRYGIILFITSEIF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFAGFF*AFYHSSLAPTPQLGGHWPPTG ITPLNPLEDELLNTSVLLASGVST
11144	25045	A	11239	267	3	FVSVRITPIYASAAATWLSYVWVWASSPN VCPGDRVALSPRVECSGTISAVRNLR PGSSDYPASA*PADGWAPPQYRCPPRL ANF
11145	25046	A	11240	391	31	VFFFFFFFFFFFFFFFFFFFFFFFFPPPF LKNPFEPNPPNFFFCPKF*ILFLN*I*F *IKF*I*KIPGFLLNPPFPFPFFFPF GALFFFFFF*EGVLPSPGWSAMSHLLS EKRKLTPRMSYN
11146	25047	A	11241	371	491	KIFLCWARHDAHACNPISIFRGQGGHIT* GQEFKTSANMV
11147	25048	A	11242	1	221	HRIDPLCRNSARAFFFLSTGCHRVSDG LDLLTS*SAHLGLPKCWDYRCKPPRAL NCFRTISQLLNLCIKD
11148	25049	A	11243	382	333	TYKIKDKFTF*RWFHPNISRVEAEKFL SRGQRGDFLARPSSESPGGFTLSVR
11149	25050	A	11244	169	477	TQKDEKESTTTTKNAENSKGQSAYSSPS DCNTSLARAQN*EEAEMDELTEVGFRRL VIMNFVKLGHIITQCREAENHDKTLQK LLTSITSLAWNINDLMELK
11150	25051	A	11245	200	462	SLIYNELCTIHILYQYVA*QRS*CFQQ LMSFY*RTLKNLKESELCKVALLYPSFLK WKRGLGTVAADT*KPSTLGGQGGRIA*A QEF
11151	25052	A	11246	484	301	IFCEKKGL*FQLRRVRWEGPFNPGNQG CS*LLSSPCPPGWITE*DPVSQKKKERK RNQVMELVSAQENKNKPRSVGLQACARS MLAFSTTPR
11152	25053	A	11247	226	458	NTVAVDWGPRCFFSLLLSHAENCDMWFT KIELFIFTNHLKQDLEMLW*GQAHAC NPSTLGGRGGWIT*GQEFETS
11153	25054	A	11248	304	436	SPSRCRK*KIG*AQWLTPISTLWEAKV GRSLDPRNSRSATWY
11154	25055	A	11249	216	451	THKYLFFYLGYNPMLYIERETGSCSIA* AGVQWYSHGLLHP*PSGLKRSSQVAGVI CLANFFFFFFLKKWSLVVLPRLG
11155	25056	A	11250	260	474	DKYFLLYPLKALNVVLGAHINI*KVSKI MC*K*DKNMYNFFFSF*DGVSLLLPRL CNGTILAHCNLCCLPC
11156	25057	A	11252	193	496	MTSCYSFYL*IKDASMVKKKKKKKKKK KKKKKKKKKKKKKKKKKASSSQAQDYS KADYK
11157	25058	A	11253	348	478	DLGWLKLGTVAHYNSSTSGGQGRIT* GQKFKTSANVVKPC
11158	25059	A	11254	174	475	MHHWVLIQDIDDNT*NCNLHFLCSQL KSIQKEKKKKKKKKKKKKKKKKKST
11159	25060	A	11255	292	48	LPLTCHRPVSHTHLAFSNPTAGITIF* TRSSWNAGTFIIFKIVTFFLFFF*ER VSLKLTRLERSGAI PAHCNHLPEF
11160	25061	A	11256	347	16	TQSADWCIYNPPARHKSSPSPHPTQ*PS WLHLVDPAAPGPWVELPTSPAPSACTPQP LGSRWDPQPSQKGQCPSGRLGPQGSPPQ VGLGKAGWRSQALPVGLTRSIESHWW
11161	25062	A	11257	238	590	APGAYIFPQQHNPTDSQVIFSLTASHLL ICSPLCISVLHFNMGNIIDENRNAHVHA RACAHATHHTHTHTHTLYLMNYRETL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						MLLKTRGRATGSHARCIFS*SLQACP
11162	25063	A	11258	310	461	LSFGDVLQLESDRPGAVARTCGPSTLGG*GGWIT*GREFETSLANMLKPR
11163	25064	A	11259	461	174	MGEHRVSQDGLDILLT*SSAHLGLPKCWDY*CEPLRLAPVGKLFKCVGYKLVLCCHGS GYMSMVIKIRMPGLIWSLEGGSAAVVHR YWSIWEISFGC
11164	25065	A	11260	343	472	LERRRLRQKDCLSGGGQCSEPRLDYCTPAWVTK*DPVSHKQE
11165	25066	A	11261	229	3	VKMKLQ*VPVKVKI*KYTPLLGIYLKELKAGFGRNTCTLMFIAALFTIANRWMQPR LP*IGECVNNM*YIHTMES
11166	25067	A	11263	163	399	KLLPGTRNLHAMEHPIFGWLRNPHATAQG*HPLSQSSSLALHGRADHICYPELCTSS SSCIIAGYPN*EGMFASQHRVH
11167	25068	A	11264	316	427	TNKKHII*IINTTTHSLIISIPLFFNQINNLFSCS
11168	25069	A	11265	184	418	KTPPGFFFEKNPFFWGGKKGPPPPKPNLP LGKKKKFLRGKGGKTFFFFF*KIGSSSS SPPPPPGGEQAPPPPPKSPRR
11169	25070	A	11266	219	13	KFFFSLEHQNFGGGGVPLFPPPKGEGFLPKPKQGFTTPLLKQKIKPPPPGGYSGPP RVL*KGPPHIFYK
11170	25071	A	11267	3	173	SHHARPETGFHRVSQDGLDILLTS*SACGLPKCWDYRREPPRQARKLYCLGMRTNE
11171	25072	A	11268	157	2	PVDITHVKTTVGLGMVAHACNPSTLGGRGGRIT*ARGSRFLLPHTSEL
11172	25073	A	11269	291	468	ISEGKRSLFVILHFIFFETGSCSVAQAGVQWCDLDSL*PHIPGPK*SSHLGLHTGACH
11173	25074	A	11270	29	478	GWNPNQQDIGTLYL*SGARAGVLGTALCIIIRAEELGQPDLLGNHIIYNVIVTAH AFAIIFFFIVTPIIIGGSGN*LVPLIIGAPDMAVPRINNISF*LLPTSLLLLLASAI AEAGA*TG*TVYPPLAGNYSHPGACVDLTIFSLHLAGV
11174	25075	A	11271	61	474	PYNQGGNDAAHAWPHLTKWRSGQTTETC REPEGAWQRPSQPRHLHGRSPGQLRALS QNLPSYSGGSHLLSAYVVPDTISKHFIN TIGWLGTVAHACNPSTL*GEDRWIY*AQ EFKTSANVL
11175	25076	A	11272	277	478	KIYQPVKIHGPRPGAVAHTCNPSTLGDRDGWIT*GQEFETSLANMNSPSL
11176	25077	A	11273	350	11	KEKTAGQARWLTPVTPALWEAEAGASPEVRSSRPA*PPP
11177	25078	A	11274	138	3	NYINLYANLGAHACNPSTLGGRGCGWIA*AQEFKTSLGNAKP
11178	25079	A	11275	359	219	FVIKMGFPQVGRDGFNPLAS*SAPLGLPKWWDYRHPRLALFFFF
11179	25080	A	11276	262	3	FCMSLVHLFSSHQDNYFTSFSL*IFNIPSGPFLFAFQDTLQ*P*DFIYFYFETESP SVTRLECSGAISAHCNRLRLVSSNSPASAS
11180	25081	A	11277	285	1	VKKGDSVSKIFRKKKKRKDKIRLHFMITTVNNLGIENLNLNMIKEYKNPTANIIL NGERLKAFSL*SGTRMSFLTPTFF*ILVDTQQVYIFMSH
11181	25082	A	11278	160	3	TDKEVPLINAQRKWFLEMESIPGEDAMN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IV*MTTKELQYYINLVEKVLARPE
11182	25083	A	11279	334	488	PLNTCGY*NLN*NFQPGSVAPACNPST LGGQDRWIT*GQEFETSLANMVK
11183	25084	A	11280	527	356	FFVFLVETAFHHVAQDSLDTLTS*SSRL NLPKCWDYRHEPQRQAKNVGEFSETRSI Q
11184	25085	A	11281	486	248	VRQLFSLLLPRLECNVISAHCNLRPLPG SCDSSASAS*VARITGASGSQAVVLQVQ CLQPVPQPGELLRVDLFQLVVLQR
11185	25086	A	11282	38	157	STGLHHVSQDGVDTLTS*STLPKCWDYR HDLRPPASQRL
11186	25087	A	11283	474	339	FVFLVQMGFHHVGGAGLELLTS*SACLG LPKCDW*RHEPTDPAK
11187	25088	A	11284	2	462	LETTRTARWNSVIALRHHNSCPYKMANL IDKVCSDYSKDWPFPIFLPLLRPPYCL RHNMMETRSINPPWPSPKCSSEKTNEEG MLKVEIG*KLCLLCQTFSKDMNAEKKFL KEIKSATPMNTSMIRKQNLIDHMEKVL VIRIEYQASHNIL
11188	25089	A	11285	65	280	SRAVEFNLLTT*SACGLPKCWDYRCEP PHPASP*FSKLLSSNLKTYLSSL*DSHS GFYSFVCSGLIILI
11189	25090	A	11286	244	488	MRLGRVPSVLFYVVRMQREGIILEAENK PSPDIESVGALILDFTASRTIRNKILF IIFPG*GILDSPNVP
11190	25091	A	11287	345	445	KRPGTVAHACNPHTLGG*GRWIT*GQEF WTILA
11191	25092	A	11288	223	500	SPGTRPKVLECCSTLGRQATLLLGEGWL WGQSHRLGVQSQCCLCVLWDLTCSLSCS FQIIKLR*RPGVMVHTCNPSTLGGCGGR IAQGQEFK
11192	25093	A	11289	157	22	LSCQEVKGEIGEAETCWAQWLPPITPAL WGAKVG*SPEVRSSKPA
11193	25094	A	11290	305	497	KLVNCIYFKGVSFVRELYCNKIV*WLG TVAHIYNPSALGGACGWIT*GQEFETSL TNMAKPRL
11194	25095	A	11291	478	1145	QHVQACPERPQMMGTLERSRAVASKIGH SYSLDSQPARAVGKPPWQQACTRVTELT EATGKLIRTSIHGKPHQSFQPAATQK LRPASQQGVQMKTOGGASNPALQIGSHV MCKSSQFKSDQSNPSTVKHSQPKPFHSV PSQPKSSQTKSCQSQPSQTKPSPCKSTQ PKPSQPWPPQSKPSQPRPPQPKSSSTNP SQAKAHHSKAGQKRGK*HANSRDL
11195	25096	A	11292	352	468	TFFPGQHKGIPSLLLKIQLAGHGDACL*S RLSPR
11196	25097	A	11293	295	24	ENIQGSKKNERQHMHNGVGTWNSNPGFV STWVYRNCLACLDISFSFIKWKSHKDT SMGMFTAALFTIAKT*NQSTCPSMVDWN STTRTS
11197	25098	A	11294	274	429	ECEPVQTLWKIRKFLKLIKIELPSDEAI PLKGINLKEVKSVP*SDTYTPMCI
11198	25099	A	11295	168	469	PSLGNKSETSPKKNLFLGFPYFREK LVGILLKTVLQKGAGGVFFGPKNPPEKN PDEPLDSPKTFRRLGAFVKTFPKGLKA AVVFPALV*PQGQMG
11199	25100	A	11296	37	348	IKIFNKTLKYFKKKKTIKKKKKKGGGGL KRPRGGPRIYPDGARKNLPHIGTAKKHW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GGYWEKNPHGGGGNTGPTPPQKTRPLGG KNNLKRVOGGEKPRPRLGGGKTRSQLFSC HA*P*VQGEKPRPRLGGGK
11200	25101	A	11297	93	388	DEYASDNCCYFPGSSHDSQVKQIGSQFT TQIQAHNLAKPRRAL*NHS*PMEMRSK CLLLAYKKKKKKKKKKKKKKKKKKKK PKYLSSRGKDH
11201	25102	A	11298	61	243	YYIHRTTVFMCMN*GLKDNVDK*TIDL LCKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKPQGGGA
11202	25103	A	11299	250	341	IYMSLTGLQNL*EIHLLTHKDSHLQVK GWKNIFHANVNQKQTGVALLISDNIDIK ATTVKKKKKRENPTILNIYVPNTGAPKF MKHLLNLKNERDGTTVLG
11203	25104	A	11300	3	285	DAWERKKRSQMNQKTTNKVAGVSPYLSI MAWNVNELNFLIKRHRVA*CIKKTSMI CYLQETNFKDTHRLKIRGWKKIHPHNR N*KLAVVY
11204	25105	A	11301	175	407	AENNPDLVLQKA*TSRGTFMP*ILLRVK RGSNSRNNRCWQGWRTGMLLHC*QECK LVQPLWKTVWRILPDLESEIL
11205	25106	A	11302	75	280	YHLNLVLYPHPPKNRVC*KKKKKKKKKK KKKKKKKKKKKKKKRGGLKKNLLGGP FFPGGKKKNFF
11206	25107	A	11303	299	3	IHASFLFRGCITLAFTVRCSHRSITSSE TSDLTHYYYYYYYYF*LASQSVALAGVQ WDQLGSNHPPTSAS*VAETAGASHHARL IFNFFVEMEVSLYC
11207	25108	A	11304	137	323	FFTVMNGRHRKEKKSNKDQLNLGLHDFLD NPLLLF*KYLGREKKKKKKKKKKKKKK KQKKKK
11208	25109	A	11305	64	481	RPTRPHVYHIVKPI*PLTGALSALLMT CGLSM*FHFHSITLLILGLLTNTLTIQ *WRDETRESTYQGHHTPPVQKGLRYGII LFITSEDLEFFAGFF*AFYHSSLTPTPQL GCHWPPTGITPLNPLEVPLNTSVLLA
11209	25110	A	11306	142	330	FFTVMNGRHRKEKKSNKDQLNLGLHDFLD NPLLLF*KYLGREKKKKKKKKKKKKKK KKKKKKK
11210	25111	A	11307	259	440	RPWIRDNPYYLKSCFLRTIFLSLLPLQ PRPYPPTRRALSPPNRHHPAKSPRSP*PL TGALSALLMTSDLTMLGHFYITLLILG LLTNTLTIQ*WRDATRESTYQGHHTPP VHKGLGYGIIILFITSKVFFARFF*AFY HSSLDPTPQLGCHWPPTGITPLNPLEVP LLNTVRL
11211	25112	A	11308	433	3	FPPPDIRHSRSLGFPPSFGAGFLNFAF SKGQEPALPGGFYYPSPKKNLAFCSPP LFYWGKFGSKFSLGVGLFFP**SPKSF CQFLENKGFFPEKSFFKFFPPAGGCVFF FSEGGFPFCLFLFFDRVWLCHPGWISV ARS
11212	25113	A	11309	2	423	GRVGDR*LFYTNHMDIGTLYLLFGA*SG VLGTALSLLIRAEQGQPCNLLGNDHIYN GIVTDHAFDIIFFIATPIIIGGFGN*LV PLIIGAPDMAVARINNISV*LLPSSL LLAYAIVEAGAGTG*TVYPALAGNYSH
11213	25114	A	11310	234	1	TFFGKFPFCLKFKPAQRGGENTPGFPFP

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						LVFFFFEMESRSVAQTGVQWRDLLGSSN SETAS*VAGTTGACHHARLIF
11214	25115	A	11311	406	211	LSLFLHSLISTHGARPDPVGLVPTQDG LDLLTS*SAHIGLPKCWDYRRAPPCPAC GFDLHLPND
11215	25116	A	11312	379	398	KT*NFTVRGSIPLLNIPMASMTFSKKK KKKKKKKRGGLKKNPGCAKFNNGGRKRK IFSLKGGEKKNPGGILEKKPFPGGKKKG ENPPKKNKGLREKKKF*RGKGGKKPQKG GGKKMGSSSAKTPTWG
11216	25117	A	11313	390	489	RYRLGVVAHACNPSTLGRGRWII*GQE FETSV
11217	25118	A	11314	286	434	ILWYMNYSIKLLKIIYKLGAVAHTCN PSTLGGRGGWIP*GWEFETSL
11218	25119	A	11315	322	3	FTFYGCRQFQVF*IVTKNDRIIFSSYTK NLLKIYLGly*FYVPLLRKTSKKTGTS FESNLSFK*VFLWSGTVAHTCNPSTLGG RRGWIA*GQELETSLTNMERPR
11219	25120	A	11316	251	389	TFFFFEREHFVPQVGQGGSLGSLQAP PPGSHSLA*ASPRCWDGG
11220	25121	A	11317	313	80	EYICPRCLSPGFRD*PGQHGETPSLQKL QKSAGCGGAHLRSQLLRRLGDRVRHCLK KRIYLSLFSNLVLSNNRFQII
11221	25122	A	11318	145	410	APKTLKVALTSAAAARESTICQLGVDEL VIFLELNRSTDQRPGAVAHTCNPRTLGG HGGWIT*AQEFKTNLANMVKTC
11222	25123	A	11319	393	3	NFFKIIFTLSPPLPLIFTPPFFFFFKKI PPKPLFFGVFHSQTCPIQSFFKNFYPPFL FWFSNPFFLLFSPSRKGPFPFSRFFFFK VGNPLFFLFFFFFFFFFG*EGVSLLLPR LECNGTISAHYYLRPRV
11223	25124	A	11320	135	1	HRDVKLEYAIRKMEVRPGVAHACNPST LGRGGWIT*GQEFETS
11224	25125	A	11321	282	2	NSESVLIKEKGDDEEKVLSFLLFSKRKV LESKTFPTLHSGCKKRSYFLKITSSFL *PRVECSGVIIDHCKLKLGGSDPPTSA FPVARTTGM
11225	25126	A	11322	149	30	WGGGQVRWLTPPIPALWKAEGGSPEV RSS*PVWPCLY
11226	25127	A	11323	316	399	STLGGRGAQIT*GREFETSLANMPNPIS
11227	25128	A	11324	223	397	IIKAYQ*DVNREQIKTIIYFQNKLKCI KKMIWPGAVVHVYNPSTLGG*GGWIT*G QE
11228	25129	A	11325	3	396	NYSTAALFLRGIHWGRWGTLYYGSSPI YCRGLNSTLGLYPLNASSNPHPRKLCKP KIYTHIAKCPIGHKIIYPYANTPIH*HH THTHTHHTL*DSLLWPGVVAHTCNHNT LGSWGRQIT*VQEFKTSIA
11229	25130	A	11326	113	442	KRYIQIRAHSEVLCGHELWGTLHNPVQT IQTWEPFPYLPPLCSRVTSGKSHRFVPL LFHL*NRNNSHHHHHHHHHHHRNPC* ECCRAHSDSYAVWSDKVSQEPVAAAM
11230	25131	A	11327	145	3	ELDIKPPNPFCHTGVQ*CDLGSPQLLP PGFK*FCLSPSSWDYRCA
11231	25132	A	11328	189	1	KTNLLLTHSKLRHLQSSVFQC*SKSEK SNVCT*CAFSCLPKLFWLGKVAHACNPS TLGGRGG
11232	25133	A	11329	193	405	ID*QTLTKKKKKKKKKKKKKKKKKKK

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						AYTSKKKT
11233	25134	A	11330	209	11	GKRGTPPTINNIFNFF*EKGSCCSS RAC*CNGEI*AHCPRLRPGSSNSPAAAS RVQETATTPS
11234	25135	A	11331	38	390	VDQSTVCKMGQSAGCGWGS DKG I KAGCL K*QRQKKKKKKKKKKKKKKKKKKGGG LKKKLFLGPGGEKFFFFFWGPPFFFGGR FLKRGGGKKPGYKKNKISGHPPPFLGGG KKKKR
11235	25136	A	11332	38	326	VDQSTVCKMGQSAGCGWGS DKG I KAGCL K*QRPKKKKKKKKKKKKKKKKKKNRGGG FIKKIFFGPGGEKIFFFFWGFFFGGG FKKRGGEEKNLF
11236	25137	A	11333	1	234	RTRGKNWMAFIKEGWVPTGRMGGSFIKH SFLESKNTWLGKKKKKKKKKKKKKKKKK PHDKIKDLFDPV*NKKQNISIP
11237	25138	A	11334	244	398	INHLYSNKNDLIFLLVFLFFFP*RRPG EPPLIKGWLPLYLGGVNLNRKDPL
11238	25139	A	11335	174	1	HQVYPYVKQEHYKQDSCQYIKYMNWVP DAVAHGCNPGTLGAQGGWII*GQKFERT RG
11239	25140	A	11336	148	411	LEFFPHCYLLNAPSILYLNPKVVYNLH LCVSAVCLLPVHSPHRTCLY*KKKKKK KKKKKKKKKKKKKKKKKKKKGGAFK KLLF
11240	25141	A	11337	237	453	GQRPLLSFREKGSFFFLLETEFCFAPQA EGQGHNLG*LQLPLWG*SNLSVSSSQEV GITGAGHHPRLFFVF
11241	25142	A	11338	65	347	VCRVDDFVPEARTRFFKSI*EAWNKNKI KPLLSTFSQVPGSENEKCTLDQAFIGI LEEEIINHSSCENVLAISLAIGGVTEG KYGSVLFCLK
11242	25143	A	11339	158	393	VPCTHSEGIRKGRKCLPKTRENAREERD KKIPPGLC*AGKLFQKESSTWPGKVH AWNPSTLEGRGGWIT*GLEFKTT
11243	25144	A	11340	117	3	GIRPGAVAHVCNPSPLGG*GRWISRDWE L*TSLANIR
11244	25145	A	11341	292	60	SGQGLRLRGAFRGKVQAKBWMPIPKLGC LVKDMKIKSLEEIYFFSPPIK*FEIIDF FLGASFKDEVFFLVCLFVCF
11245	25146	A	11342	149	30	TQIFPPPPPPGKKKKFFPKKKKKKKKK ERKKDRKNKQK*KGPGVGVSPLPFPPLG GQGGGFPGGLGFKTPLAPKGKWPFP*KT QKFPRRGGPPKIPFLGGGGEKKPFSPG GQGSNKPFFPPPPPRGKKKNFFSPKKK KKKKRKKERKTEKTNKK
11246	25147	A	11343	120	504	GVHDCRLWDDMTRRPPAAAATACPAGRP PPRREEHSQLLLISFQGFWD*QQDVN TPNLDHLAREGVKAKYLMPPLVMTSPS HFTAITGKRHSAHFTRCPSNPQRPSFPV IRSKSSVSSREVEA
11247	25148	A	11344	213	399	ALVIHCLTTTIQVSGLSGSKYLMRQGMV AHGCHPNTLGGRGGWIT*SQESETSLAN TVKPCL
11248	25149	A	11345	308	3	NPTPRSGDLWVEEGSPGAGNWGCLSEQT LRAIIKATTSYSFYCYFFETGSHSVAWA RVQWYNPGCSICGSSHLPTSAS*GAGTI GMHHHAWLIFLFFVENE

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11249	25150	A	11346	189	433	GHCRAGTSLTLTHLGGSAMLELIHGLCLGRMKFIHTTCIILFFLFSATQAGGQGDLS*LQPPPLGFKQFSCFSLPRSWD
11250	25151	A	11347	257	3	KWGELCFLTIKEERMGFPLAKKRKIKGVF*FGLFFFFETESHVPAQAHCNLSLSDSYSPASAS*VAGITGACHHNQLIFIFYE
11251	25152	A	11348	159	434	LSPSCRDVGTYSAHAHPHTHTRVRAHTHACTHVRAHTHTHTTAHGSHLTKEQPGLCTLPGSSW*PGLGGRAIATAQAWVHCAGITTAHPP
11252	25153	A	11349	240	406	AFKKLAKNNSMGVNRSLSRPGVVAHAWN PSTLGGRGRQIT*GQEFETSLANMVKP
11253	25154	A	11350	163	360	PQLQLMKFLQN*LLERLRPQNGNLNLEG LACSESRSPCAPVWRTERDSVSSPQPR PGAGGRPSFF
11254	25155	A	11351	145	406	PLNSGAKPTLPPWSPRRPELNADPPPPPG EKEFFFFLGRGFLFAPQEEAGGENIV*G KPPPPG*REFFAPPPGDDGNKGAPPPPLFL
11255	25156	A	11352	122	337	ILWVLLLVRESLKFFFFLLLLFFLFFETDVA*AAVQ*SDHSSRQP*PPGLRGSYTS AFRIAGAIGICHHL
11256	25157	A	11353	325	416	KCVYIMGWA*WLTPVIPALWEAGAGRSL EV
11257	25158	A	11354	260	415	LEELQNTACQKLEPFLSRTETKQGCLLS PRLFNIVLEVL*AVRQEKEIKGI
11258	25159	A	11355	160	2	ISEISTKRNNYFLKNWLGVAHACNPST*RG*GGQTTRGQDFQTSANMVKP
11259	25160	A	11356	160	3	ENLKLYNGSPFLKI IWLGMVHTCNPST LGQGGRIP*AQEFKTS LGNVRRP
11260	25161	A	11357	235	408	GQPLPAALFFYQWHLHFKELLAHPWGKT VWRFL*PLKKEGPHDPAIPLLDIYPKNK KW
11261	25162	A	11358	11	393	QTERTPTPKPHLYVSFPNPSQDPQLQGG KLINRKNHTKTPSVCHHHQRPVKDKTT KIGKKQSRKTGNSKNQASPPPKECSSS PATEQSWTENDFDELREEGFR*SNYTL KEEVRTHGKEVKNL
11262	25163	A	11359	283	475	FMVSVSIKVYFFIFIFLFFEMESC SVTQ AGVQWHDCLSLFC*VLASSPGNSSPVR
11263	25164	A	11360	266	407	LEIHHSKTL*FWLGIVARACNPSTLGG* GRWIT*GQEAIIILANIVK
11264	25165	A	11361	93	1	DVLSILLPRLECNGAISAH*NFRLPGSS NSS
11265	25166	A	11362	131	377	MEEMIKGRGLSKPPALSSYLTLKSS*LK RVRARRRLFLKSRFSLDLQVAGFFVCLF VFWDVSLCHPGWSVVQSRSLTAALT
11266	25167	A	11363	212	392	QAEECAPLFIGVKEPPKNLTHWLGTVAH TSNPSTLGG*GGQITWGQEFETSLANMA KPCV
11267	25168	A	11364	141	3	NELWLNHQNVLEWLGTVAYTCNPSTVGR WIT*V*EFETSLGNMVK
11268	25169	A	11365	215	384	ANFNIRPEISLASKCPSEKRSRTLLPLN OKLEMI*LSEEAISKARTG*KLGLLHQI
11269	25170	A	11366	48	373	EPWTRKEVLKISSSLKIHCVLSILCLIL MPTLECTAAIMAYSNLPLPGTSCPTCA S*VAGTTGACHRAPTVLKIFLRDRIFFF FFTNVTPWCHTPADPAIFKANAR

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11270	25171	A	11367	310	2	GLICLNRENAYFFVIRQISMSCLEKEKP ARYSSPYAKSVTRGEKRRQFFLSRAP IPFLFFI*IV*AESRSVAQAGGQWLHFS SLQTPP*RRSDSPASAS
11271	25172	A	11368	303	50	MFALTNRGVQGSPIVFLGVFLISKMGFT CFKGFSRKFVLVFFLGVFPSSFFFLRAR VLLCCPGWSPITLGIK*SSCLGLPQCIVLT
11272	25173	A	11369	109	419	QSNASLSHFTSPPLSVADR*LFSTDEKD IGALYLLFGA*AAVLCTAISLFILDWLG QPCNLLRNDHIYVIVTAHAFARIFFIG IPIIIGGFN*LVPLIIGA
11273	25174	A	11370	112	258	GGRFKGSNFTSAGMQRNIFFMGPPK*NS RAGV*QRGEGKNPGVTKLNRL
11274	25175	A	11371	823	1078	SQHFGMPRWADHLRSGVDQPGQHGETL SLLKIQKLGRGGRCL*SQLLRRLQEN CLSLGGRGCSEPRSHHCTPAWATQ*DSV S
11275	25176	A	11372	184	420	IKQOKNFLALVKELVQLLWKTVMQFLK KLNIELLCDPAILLGLIYPRELKMVYHT KTCT*MFIVELFIKSKK*KQPTC
11276	25177	A	11373	234	44	LATITDRLLALSDSAIPPLGIYAKEKKS VYQKDNCTYIFVAALFTVAQI*NQPKCP STRTRGS
11277	25178	A	11374	73	456	PPIGSPLVPYIPSPALSSPOAPRMGSH CLIPSASCHPPLETDFLSLLPTHFCLAV FTKERFSPPPSPYPRF*KFLRS*KFSF FLPPFLFFGGTVLLCLSGWSAVAQSWLT AASLGLSSDPPTSTS
11278	25179	A	11375	43	456	EFFHHVQDGLDLTTS*SAHLGLLKCDW YRREPPRPASDGHY*TDATGSLPSSGTT *IRTKPSQAPASWGLWNLAHHPRSHPS CPMANLICSTLSSFDGSGPGTGPWWCP LGLSGSPARAVFKDSSCSLHPLATGI
11279	25180	A	11376	288	484	EWVLSAVGGSQYGVCLPFLHCFIFETE SRSVAQDGVQ*CDLGSGLSLPPG
11280	25181	A	11377	129	1	NFNALNLRAGAVAHAYNPSSLGGEDGR IA*GQEFETSLSNTA
11281	25182	A	11378	307	1	DSEIPLGLAKFWNHRREPPCLALFTL NQKLEMIKLSEEGISKAKTR*KAGFLCQ RVSQDVNAKEKFLKEIKRATLVKTQMMR HQNSFIADAQKVVMAWMK
11282	25183	A	11379	200	397	CISLFSHYKDLPETGSFIKKRGLIGSH WLGAVAHACNP SILGGQRRIT*GQEFE TSLASMKPC
11283	25184	A	11380	167	1	SNGLYSREARMVQHTHTRPGVVAHTCNP STLGGHGRIT*AQELKTSLGNIVRPC
11284	25185	A	11382	12	395	AHSSFLSLDLVVFATCPHRAETQTGHR FSTLLPLSALYPK*DYFKKKKKKKKKK KKKKKKKKKKKSGGGA
11285	25186	A	11383	160	2	TMEMMLDIK*I*EIFLFEFKMGLKAAET TQNINNTFGPGTANEQTAQRWFNK
11286	25187	A	11384	274	389	GQAQWLTPVIPALWETKAGGSLE*GQAQ WLTPVIPALWETKAGGSLELKNRPSLG NMVKPP
11287	25188	A	11385	389	37	WSYESSWSFIFKSFLFSFMISAYDM*YA SQILFTPKLYRTHPYFLVLFLILSILV ILETGSRFVSRLECGGGSAYGSK*LG SGNPPAAASLSSRIPIYVHQSCWSDLA FN

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						PEFEM
11288	25189	A	11386	214	374	KGGRFRFGSKFTSPGGGKGNFFIGAPK*NSRAGV*KRREGKNPGVTQLKKGVG
11289	25190	A	11387	142	410	RFVCSSTIKVLRDLSSDRSNPGRFLSTSN*KKKIKKKKRGAPFKKKNFYRGGGGKYFFFGAPKINFLGRVFQPGGGENPGRSPFKGAWG
11290	25191	A	11388	144	1	CLSNEDSIKTPKGLGTVARTCNPSTWGGRNGWIT*GQEFKTSANTVK
11291	25192	A	11389	167	2	RNISSHLNMAITKQTNNNNCW*GYREIITHIHC*WEFKMMQLLQKLVPOKVKHT
11292	25193	A	11390	2	412	SDQVQDAGRLISSEASLLGLPTATFLLC LPTGFALCTRVPGVFLLRSTVILREGP TLVTSFYLYNLLKDLVSIQSHWGLGLQPMNFGETQFSL*QKLV*KEKESMPGMVAHACNPRNLGGQGLIT*GQEFKTILA
11293	25194	A	11391	1	206	TGRLAGHRVSSLPPIRGRAEAPLTSRTGRLNQDGLNLLTS*SARLGLPKCWEYRRQPLRLAVISGFLT
11294	25195	A	11392	262	388	VSK*KKKKKKKKKKKKKKKKKQ
11295	25196	A	11393	78	414	ICFFLRAPPFFFFFFF*TKIFFFFPALNSMANFFFWTPPFLGGIFLPPFFLEGGGPGLASPPGGAFFF
11296	25197	A	11394	238	11	IKWETAGRSSACL*S*LFERLRRENPLNPGVHG*DEI**HHCTPAWVTVRPLSKYINKNKK*ARLAARCGGSR
11297	25198	A	11395	340	1	KHILVPPFVSEIQRYSLV*HLLFVGV*NLFFFLFLSFKKPVLCM*IICHEIISP SKPKCKASHLSFV*KKNSNLWLGAHAACNPGTLGARGGRIT*GWEIETSLTNMEK
11298	25199	A	11396	363	245	QMDLNRHLSKDDK*MANQCMNRCLTSLAIRQMCIKTIMI
11299	25200	A	11397	292	2	DPKKEAGRGAQL*FQLLRFRKHETHLNPGG*GCSESRSHSSPPAGATK*NGVSKK K*Y*APKEERHPRPVLVEPRVPQVPSPGSQTYRQDHSR
11300	25201	A	11398	121	321	KKLYTHKSKSDVMIFLKIETVSWLYCPGWRVMAHCDLKLGGSSKPPTSAS*VAETSGTCHHARLIFL
11301	25202	A	11399	118	394	QALPQPIPVILLQFFFFF*GTGFCFVAQIGGQGGHYG*LEPPIRGLKPSSRRTL RGGWD*GGHHNAQLILGFFFEKTGSCFVVQAGLKALA
11302	25203	A	11400	273	379	AEPGVVAHSYNPGTLGCRGGGIT*AQEFYTS LGNM
11303	25204	A	11401	360	38	KIFGQARWLTVPVPAFWETEVDGSPVEGRSRPA*PS
11304	25205	A	11402	254	404	GPAGHDFHMITPSKSTETGLGAVAHVCN PSTLGGRGGWII*RQDLETSLA
11305	25206	A	11403	161	3	ILTPTLQYIKINLRGAWWFTHVIPALWKAK*SGGLELRSLRPAWVIEGDL
11306	25207	A	11404	1	170	MGVSLSPRLECNVISAHCNCHLL*FTFK*FSCLSLPSSWYRCVPPCLATTFLIY
11307	25208	A	11405	249	3	NAKSRIQVISIWVFTVKFFHLYLNCNFSQ*NEMAGQSI FRKKHLDFSLEHSGMMTTHCSLDLPSSDPPNSASSVGGTRH
11308	25209	A	11406	70	401	CGKHGVNLIITHSFLNHLKYLLLLQMANL

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						FISQFLLTCVSEPLLF*YCHQITKVGRL HEVKQMRGTTKKQEKMFPPYWNNDKNVCPG VPAHACNPPTVGG*GGWIT*GQEFNT
11309	25210	A	11407	257	389	GGSLQLQKYLRLVAFLLSFFFFSFETES *SVVRLECNMISAHG
11310	25211	A	11408	364	420	SQFFGRPRQADCLSSG*AQWLTPVVPAL WEAKAGRLLELRLR
11311	25212	A	11409	312	413	TSGMGPGVVAHACNPITLGGQGGWIT*G REFETS
11312	25213	A	11410	283	425	HGHKDYVHWLGAVARACGPSILGGRGMW IS*GQEFETSLANMVKPCL
11313	25214	A	11411	389	3	CRIDGLFFNLVFLRLVVKF*VIFFLSY FSFLVILQLTYMLNCTFF*QILNLF ILVLLTKILNTLLSTENYCHFSLLYCLE FWFHPILKHMYNLFLI*FILIFILRQS LARSRLKYSGTISIH
11314	25215	A	11412	267	3	QBFQQEDTSELDLEIRSLCKRKGGLKQG DTKDNLKRVVETDKGKAAWPGAVTH ACNPSTLGGQGGWIT*GQEFETTLNRC PRV
11315	25216	A	11413	3	281	GAWSCRIPGEGSLASQAIQPFSLYPVN PQ*ISLSARKKKKKKKKKKKKKKKKKKK KKKGGGVLKKIYFPPRGEKKFFFFWGP PKKTGGGGF
11316	25217	A	11414	275	2	KTAHFQLFNSDFKFPGRSNPGQSWSPRA KQSFCQALLKYFLK*NMENKLNKSRSG AVARTCNPSTLGGQGGWIT*GQEFETSL ANMAKPR
11317	25218	A	11415	319	1	RNLGVQVYEVVLVYKCVSSNNMKMN KRDLLVI*VPGIVIHLYRIKENPELY ISLFIYSMRSLKLTYPGAVAHACNP TLGGRGGWIVCSQEFETSLGNM
11318	25219	A	11416	121	428	LSCDKWGNRDMTKMLSKELKKKKKKKK KKKKKKKKKKKKKLGDDEEDKE*QSSW GGGALIKNLFPSPRAAGFFLSLLKYK KLGAAYIILGEKTIWL
11319	25220	A	11417	79	253	KIFNFQFSNMLENNSHTRINNYFPGRE RWLTPVIPPLWEAKAGRSLEVR*RPSC P
11320	25221	A	11418	180	4	EVGFMPKGLCGVFLEAGSHSVALTIVQW CDLGSPQHPPLGSRDPPP*ALQIVGNTR RVP
11321	25222	A	11419	154	3	STLKDKENQKLSIQPDTMAHVCNPSTLG GRGGWIT*VQEFETSLNNMVKP
11322	25223	A	11420	436	478	AIPLPH*RKKILHAALFFFLKGSFVLS PRLECSTKIWAHCSLPPNINSPASSS QEGGTT
11323	25224	A	11421	143	398	AAFGFWFVLIRFLRQLALSPRLDCFFA KSASCQPRPP*FKRVCWLSLPKSWDYRF DLLCAAGLVVYLSVSRHLHINEKNQPPP P
11324	25225	A	11422	1	138	MVFHRVQDGLDLLTS*SAHLGLPKCWD YRHEPPRPAHSYFLLHK
11325	25226	A	11423	2	390	LELPILLNTLILFLFLILYIYLVFSPN AFRILFITIVLESFSFILLVPSKPWKYS LILSNAFVLCMMISSPPFPLFSLSTTRI NKKLDFWLGAHAHYNPSTLGSQGGWII *GQEFETSLTNMAKPHL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11326	25227	A	11424	267	414	VFQITFCIKNFWPQGVVAHACSPSTLGG* GGRIT*AQEFETSLGNMVKPC
11327	25228	A	11425	189	73	HQDGLDLLTS*STRGLPKCWDYRHKPP RSARPNWVAP
11328	25229	A	11426	318	33	KKTISSHARGRKLGSFKTAAPFFFFF*T GSCSLAQAGVKWCSHSSMQPRPGLK*F SASGSAGIIGMSHHTRPPIAGFLLAKLKK KSNSTGYGGAHV
11329	25230	A	11427	291	393	DRVSLCLPGWSAVLPS*LTAAQISWAQV IFLPQP
11330	25231	A	11428	51	399	KRVARQNPPNGQGFQWCSFPIYQSR AQGENIYKLLGSGEWPQGLIIDVEREQL EDWRQGD LGRGMWMTKARVHKGPGLVAG TCNPSTLGGGRWIT*GQEFENSLANMV KPCF
11331	25232	A	11429	242	420	VKKKKRGGRFKGSKFTSACLQGISFFKG APKLN SRAGF*QRWEGKNLGV PQFNRF AHP
11332	25233	A	11430	77	405	TKRGDSSFCLYRIWIIDSVMKWNQSKAA AAAAFFFFLGRGTLFLFRLKGVGASVI *NFCLRGWGGSPASPSKEVGMGACHNS GLFFVFLEKRRFPLVGQEFKTTTRAN
11333	25234	A	11431	121	439	LPLPTSGPEDPLALSFKPTFPSTLSGM IYTGHPSP EHTSHLMPAPPVNNKACRF FKT*KKKKKKKKKKKKKKKKKKGGPL KKKKIFAPPGGEIFFFWGPKK
11334	25235	A	11432	109	283	LTPWNLDSRCEIKGNKGPQENHNLGGG GCSEPKSHHCTPAREKRQNSVSKK*INK IK
11335	25236	A	11433	296	1	FLKKPSKGFSLPHLPQNLNLFPPK*K CPRAKKDIPPPSF*KISSLFGE*GFTG SRPPSLNLENPPKRIFFFFFLDRVSHC RPGWSAMASSCPRV
11336	25237	A	11434	385	418	QSETLSQKQTK*E*SWLGAVAHACNPS TSGGRGGWIT*GWEFENSLTNMVKPCL
11337	25238	A	11435	3	405	LLHQGRMLGQWGNRTKTLMLRENVGK FPAEPSCSALGVWLQALACYPGLVRRQ* ANHWEKKKKKKKKKKKKKKKKKSGG G
11338	25239	A	11436	221	3	KHEFQTIQMESMK*NTSIKICIYAS*IQ DCLRYQWRPAAVAQAITEHFGRRQAD HLRSGVSDQPGHGET
11339	25240	A	11437	288	366	KMFFSWA*WLMPIIPELWEAKAGGSL
11340	25241	A	11438	160	370	LWYHYFPVRDGLTILVTYQLKAI RLLT LKSRSGAVAHTCNLNTLGGRGWIT*GR EFETSLANMEKPHL
11341	25242	A	11439	230	404	MQHGQVGIYSQGGGWRPVDKKNSQLGTV AHTCNLITLGGRGWIT*GQEFKTSLTN MV
11342	25243	A	11440	302	54	LSGVWFLTPPPKGGGFPT*NGGAPGFF PPPPFKNPPPEGKLGPKKKKNFPPGG EKLVLKGAPPPPPPPPPPPPPPPFL
11343	25244	A	11441	271	416	KRTLSTELQYMCCLLIKSKSIFK*KKKK KKKKKKKKKKKKKKKNPPSLP
11344	25245	A	11442	254	392	SVTGMTIMTSSCCYKIQCKTIQKLARH GGTCL*SQLLRRLRQENS
11345	25246	A	11443	390	150	LLKNQKTLGGPARNPPLGGPENGVPKA GNWGP PPGPGGT PFFPKNQKITPGGGG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						P*FPPLRGGGPGNPLYPGGQGCH
11346	25247	A	11444	122	1	PAPLFFFFFFFETQSCSVA*AGVQWRNLGSLQPPPPDDGTRL
11347	25248	A	11445	272	403	RPKVDKTTKMGRNQSRKAENSKNQSASSPPKDHNSSPAME*SWM
11348	25249	A	11446	70	397	LCHCAPAWATERDPVLGEKKRTMMSYCHPPMRMVEKKIVGDIKC**GYGETGFLTHC*WECKMVQIL*NIV*QCLKNLVHSPYELAIVLLGIYPREMKTYIFTKKTSM
11349	25250	A	11447	3	401	HASAHASAHASAYYRLCAYPKSSFLYPSFLLLVVSNFPLNILDITIGPKATETLFIKHMHDVISMQLKSKTFYNYFFLLSLNVFYFVLSCKRRKRKSQLGMVSHICNPSTLGGGRWIT*GQEFETSLANMA
11350	25251	A	11448	333	1	KSGCIPPKGQVVLFFLQKTAKIGSPKPVSPPRGKGQFFPQGLRGFY*FLPPPPGVP EIFFFFFF*DSSHVTLSPRLEYSGMNTAHCSSLHLPSSSNPASDSHIAGSTGTCHH
11351	25252	A	11449	104	402	VVCRPLLGGVSQLGYMGVMDPFKEAVCLFSELKHCAGRTTALFRAVRQGCLSLKNFLLPFFQLCPAHRGGVL*RQ*ALLSCGGLHPVRASRPLCLPTQA
11352	25253	A	11450	198	2	KYKFMAGLGGSC*SHHFARPRQDGLSPGV*NQPGQHGETPSLQKQVSWAWHASVEAEAGEQP
11353	25254	A	11451	171	3	TPPPRATSLFFFF*TESHSVSQECNGTISAHCNLCPLPGSSDSPASASRVAGITGA
11354	25255	A	11452	177	461	PMTGGKYISNSTCSKPNLSPLPLKTQTKNMEHFGRLTRGDCLSPGV*DQPGQRGKTL LLQKISQALWDVTAHAWVVPGLPTRERRRSLSFPTG
11355	25256	A	11453	247	3	EGECCGIESR*ILHLKGRICWHINYLKTKIKN*VILKKMYKQLRPGAVAHAYNP SALGG*GGRIARAQELTRLGNIVR
11356	25257	A	11454	328	57	EVHSNICATLSTHQMILTKGTRHQHIS*GFF*EGEVTLTSTKLECSGVIMAHCNLNLGGSSDPLALVSQVAETRGASYLLLAICPKVKN
11357	25258	A	11455	70	435	ATRAKLHLKKKKEGRKKEFFPHWQGOPTPALVFPQPRTHFIFKVSIFSLKKNREQLPYTVQTQSLLPLNSHWGQVA*AGVQWRNLRFSCLSLPSSWDY
11358	25259	A	11456	112	401	KCWDYRRERPCPAPNICIF*LTFFFLGLKLNQSFFFFFFLKGSLVLPRLKGGGAF LFN*NLTLOQKNNSPASPS*RAETLGLGPHAKLWFVFLKK
11359	25260	A	11457	198	3	EKTSVKQSGDSNKKAWLEMTNKKSLKR*GVVAHCNPSTLGGRGGWIS*GREFETSWTNMEKP
11360	25261	A	11458	179	1	FFHMYNHIVCEYTTITLSVNNINSQGPGR AHAYNPSTSEDRWIP*AQEFKTSANMVKPH
11361	25262	A	11459	210	5	RLIHYFFKNNLPSSGGGSTA*GQFEIIRLDNTVRPHFLKK*KISQVWVCMVVVSATQ EVEVGNGLSPGV
11362	25263	A	11460	139	2	RILALSKLFFFFFFKQESHFFLPMLECSGVISAHCNL*LLGSSDLS
11363	25264	A	11461	388	272	S*KKKRGGRFKGSMFLSPAGQGNPFFM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GPLKSI SLAVV*QRREGKNLGAPHITRL GAHPLFAGWHKTQGAEF
11364	25265	A	11462	2	387	CVWKSNNKKAPPCVAALRFRWKDDMDDEM APGKHWGGLTSKVQSGGLMGRYTGPLTK TENSILLKNPYFEAGHSGSRL*HQHLGR PRWEDYLRPGGQCSEL*SSHCTFT*VT EGDPVSKKLKRTIFGG
11365	25266	A	11463	325	398	SLPTWAVCAPRPSG*GSGTPELKTMLAG VILEDYLDIKNFGAKVVGLSCTLATGST LFLGKVGPPFVHLSVMIAAYLGRVTTTTI GEPENKSKQNEM
11366	25267	A	11464	174	2	YLEILFFFETGSRSTIQAGVQWSHPGSL QTTPPCPSNSPASA*VAHASADAWADA W
11367	25268	A	11465	105	411	TDVELLLMDE*RKWFLELETTPEGEDDVN IVKMTTKDFGYSINLVDAVSEFKRIHS YFERGSAVGKVLSHSIVC*GEIFHERKS PLMQQISLLTFILFYFSE
11368	25269	A	11466	291	404	SQEGVKIKRQGTVAHTCDPSTLGG*GGR IT*GQEFKTS
11369	25270	A	11467	64	236	THASGLDLLTS*SSCLGLPKCWDYRHEP PRPARFSSFYSGSLNLYLAKIIKRDAFC I
11370	25271	A	11468	278	416	NPQISCLKQHVWGAHAHCNPSTSGG*G GRIT*GQELKTILVNMVK
11371	25272	A	11469	178	325	RPEVKDQGASCRDQPHRVGGLLPVCSDE RVPOKXXXXXXXXXXXXXXXXXXXXX KKASSGGARF*XXXXXXXXXXXXXXXXXXXX
11372	25273	A	11470	264	60	DINHQSWSLGRWTPLSWVSISQREDRR GFSASIYIYIYIYIYIYIYIYIYIYIHT YT*SYHFNQNT
11373	25274	A	11471	95	399	DFPHLLFLPLSQFCTACCPVPENRCFM YFFLI FSALCWEMNSRISHSNTARVEQC CKVFILQMKSVLGQVQWLTPVIPALWE AEAS*LPEIRSRNQPGQ
11374	25275	A	11472	139	2	NHVSTEKLSLHTMAHTCNPSTAGGQGGQ IT*GQEFKTSLATMAKP
11375	25276	A	11473	179	3	RARWNPQVFC*GFLPVFPKILPTWPLRK GVFPFPNFFFFLRLVSLCHPHWSAVARS RL
11376	25277	A	11474	282	12	KYIRNE*IVLFVIYFCRNRI SWCCPGWS *TPELKRSSCLCLPSCWDYRHEPLCPAE MNKLDRLNKMDDTKWIIQKKKNHRTQRQ DNKII
11377	25278	A	11475	145	3	VCMQLRTDFQPGAVAHACNPSTLRC*GG WIT*GREFKTGLNNMEQPC
11378	25279	A	11476	61	397	PQTPRLKQSYHVS LPSWDYSWIYHERL VNPGETDWATCYSGGNIQLQENKLNT TDSTLWVSLCCPRLECSAIPADCSLNL PG*SDPPTSTSHVAETT GACHYAQLIFG
11379	25280	A	11477	156	3	FIFLKSSQNSYI*KCWPGAVAHACNLDT LGG*GGWIT*GHRFKPTRRPRV
11380	25281	A	11478	224	383	CWVCLIHRAFLAPRPVLGCQ*QKKKKKK KNKKKKKKKKKKDSRGGG
11381	25282	A	11479	339	58	NFKNKLFCASGYLDSKDSQHYIIFIR WSLALLPRLRWEDCLNPGGGGCSEPRSY HRTPAWVIE*DPVSKK*IK*NKIK*KQQ DWLRLHDKIF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11382	25283	A	11480	244	407	SFGKKIGFLFGPKKFNNGSSYGNYYKINR RFFFPILGEGFSPHVYF*NLETRTTGGG LLETTKTTTFNLLGRKLGSLGPRSLTAA PTGTTIKLTGGFFQFWGKVFPRMYIFW KDEWKKGF
11383	25284	A	11482	308	30	SPQKNPPTYSGFKNLSASPGQKAKPRF FLKNQFLPGIMGGGRQFPLLRVRPPNC FNFGGKRCN*QKLGPCPPGGPKETVSKK KKKRERQQ
11384	25285	A	11483	226	407	NHWKK*FWPKVAHTYNLSALGGQGRI T*GQEFETSPSNMRPHAS
11385	25286	A	11484	10	411	QPFIYFLSLRISLFWVFHINGIIQYVAI CVWLVSCHNFSRFICVAACDQDFIVFLW LNNIPLCGYNILCIHSICPNWRTTGLFP LLAI I I K L * T F V K K K K K K K K K K K K K K K R
11386	25287	A	11485	184	1	TDEELLPMDEQRKWFLEKKPTSGEDAVN IFEMTRKDIECYVH*VDKAAAMYERIDS NFLSN
11387	25288	A	11486	435	222	AKNLNRHFSKKVI*MASRHIKRCSISLT IRET*IKSIR*HVIPGQMTFIQKTGDM FGSVSPLKSHHLKL
11388	25289	A	11487	317	408	FRPGTVAHACNPSTLGGQGGWIT*GKEF KT
11389	25290	A	11488	340	469	GKGDTKCHLWLGTVVHACDPNTLGGQGR RIA*GQEFKTSLSNM
11390	25291	A	11489	38	389	KRPTSLKKSNFCSLQGGFFFGLSQKPGK SNRSPGKKKNPFFSGGKAP*KG*KIPL SPGLGGSPQKPHLLGGLGEKNYLTLEKG GCRDPK*CPCFPPWAGECNPFSSKKKQK PFFFG
11391	25292	A	11490	235	2	FVLMWLMPKLHIPPVTEFRRILFAPEFL* FLFCFVLSYFVLLETGSHYVTYAECSGA ISVHCSSLNLPSSDPPTSVLV
11392	25293	A	11491	25	417	GTLCRLRIGFINISHHCMLKENSLEFFF WETKFYFAPQADGRGNLG*WNPPSPG* RGSPGPTSRKRNGGGGPPGPVIFGFLR KNGVPPGGLKGPKSLAPGIGPPGPPKDR GLRGGPPAPGLLKKNPKW
11393	25294	A	11492	234	438	MVVI I AQQCDCTECHY*LKMAKMINFML FIFYHTHTHTHTHTHTHTTRERGPSYI YGVVSFKLTHL
11394	25295	A	11493	344	477	CFTMFIS*IKT*KFNISQLVAHTCNPSI LGGQGGRIT*GQEFKT
11395	25296	A	11494	35	482	GIPGFHHVGNGLDLTS*SIHLGLPKC WHYRPGPPRPAISITPST*AYLLGNQKI GVTHFLAILALFFSGTKAMISPKYVCII FYLLVEEHLGCFYFLAINTATCVCVYKL FDTYMYQVESATHETISYFFKILCSL SIRLYAVLL
11396	25297	A	11495	307	484	LSPSERHELKCVLWPGAVAHAYNQSTVG GRGRQIT*GPEF
11397	25298	A	11496	487	349	FLIKTEFHPIGQEGDFLTL*FARLGLP KGWDYKGEPLRLAFWHPF
11398	25299	A	11497	224	417	ASGASALKVELCSFSRYKIYPRHKRRYA RTDGKVF*FLSAKCEGITFFLSFFFFFL EVLFCSPG
11399	25300	A	11498	17	411	KRLVFGGRGRTDRFISQYV*AEVVSINL

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						LI FLTKKKKKKKKKKKKKRGGALKKKKP WGGQNKTEGKKKNFFFLRGKKKPWGGDF KKKNFFWGGENWGKPPPKKKTTPWGKKKI FKGKGGKTPPYFCFLKMG
11400	25301	A	11499	117	370	VSESADLAWSLGICFFIEFPSDADVAGL ETAFFLGGWTGSCSVVQGV*WCNHSSL QPRPSGPRQSSCLSLPSSWDYKYMPPCL
11401	25302	A	11500	244	1	EELFECYSCSPTFSSDPLTTPLLIIT* LPLTIMASQRHLSSEPLSRKKLYLSIL ISLQISLIITFTATELIIFYIFET
11402	25303	A	11501	130	55	RFVCSTIKVLRDLSSDRSNPGRFLSTSN SSLKKKKKKGRPF*RDNSAILF
11403	25304	A	11502	186	421	SERLKIAGTIGVHHCTWLVLILNLVLL K*ITFALKIMMFSKYSDIGQAQGLMPVI PALWEADAGSLQPRSLSLGNK
11404	25305	A	11503	1	213	GELLFLYIFA*WLFLLPKLLKFVIVCLC ELQFNERFIMVLCIIILGVGGFFLFCF LL*FCFDFFFFFFWRG
11405	25306	A	11504	82	6	AGVQWPRSWLRPL*LFFTQVLMIFPPPF YHQNFFFP*KGFFFLGGLSHFFPPPNKG FFFNYPQGFFFSPLKKKFFFSPIFL APPGIFL*GPPRFFFFFFFF*EGVSL CHLGWSAVAAILAPPAGFTPSSCLSLPS S
11406	25307	A	11505	245	440	WAPCIG*QLLKDPQVLFAGYKVPHPLEH KIIIRVQTPDYSPQEAFTNAITDLISE LSLLEERFR
11407	25308	A	11506	256	370	GKLM*GHHVGGAGLKLTLSSDPPALASR SAGITGVNRHAPPRLNVTLYTKGQTIL YHNQYNQ
11408	25309	A	11507	1	149	GCMWPRTVLFAFQHKFVNFLKTLGDFGQ VQWLMRVI PALWEAEAGKLPEARWRPP *PRTVLFAFQHKFVNFLKTLGDFGQVQW LMRVI PALWEAEAGKLPE
11409	25310	A	11508	316	420	YTYIYEPG*VQWLTPVIPALWEAKAGGS LEVRSRLR
11410	25311	A	11509	136	2	LDNRLWPGAVAHACNSRTLGDQSGWIT* GQEFETSLANMMKPHL
11411	25312	A	11510	167	420	PTPRSGNTALQPPHHTHTHTHTHTHR HTHTHTHTHTTRACI*KVRVRALFSPKKK PLFCLSVSQIYVGRCLLKRLLFIPLYRH
11412	25313	A	11511	124	415	IYISVANTILIFIAIHVLAISFFFFKK EVLFLPPRREGGAF*VN*NLCFWG*GN FPA*PSLKKGITGALYTPGLFFVFLKKT GFRHVGQAWLDFL
11413	25314	A	11512	121	1	PPVKFWAPFFFFFF*IGSPSVAQAGVQWN NLSSLQSPPSCL
11414	25315	A	11513	245	13	VLFILSGFFGPINYPTSPFPQLPFPASG NHPSTLYLHEFNCFYFYFLFIYFF*DRV SLCRPGWSAVARSQLLVPSDS
11415	25316	A	11514	434	2	RPPFFPVWGSPPPPFFFGEGIWQEER KGASSPPVVRGILRGGGPFGGGAPPT PLKKPPLFFFLAPPFLGVFPFFFSFPTV FPLPFFVCPKKREALLGVPKGRPFFFR SFLFFFSGD*VSLCRPGWSAVARSQLTE SLAS
11416	25317	A	11515	247	390	QGLRIYSQDFFFFFFLETKSRFVAQAGEQG GNLG*LEPPPPS*SDFMASP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11417	25318	A	11516	269	368	FFFERESCSVTRAGVQWHRLLSSL*PLPPAFRRF
11418	25319	A	11517	256	404	NILKIFYLRI*KKKNQLGVVAHACNLRTLGGRGGWITRGQ*FKTSKEKMKVK
11419	25320	A	11518	211	404	YLCFTRCSVHSHLK*VFLHKCVI*MYRPH*HT*GTL*CMQVHTHTHTHAHTHTHTPLSQGGDCI
11420	25321	A	11519	41	232	ESVEPRRRRVPRQAQITPLHCSLGDRARPCL*SQLLKRRLRHENLLNPGGAGCREPRS HHCTAAWATEQDPV*KKKSLNFKTVRA INLKMLGALISFHLFLWGIWF
11421	25322	A	11520	146	2	LIDQQGVNQLPRMECSGAIHAHCCLELPGSSDPLTSAS*VAGRPPTRP
11422	25323	A	11521	297	437	TDHFWNRILSSCGDTFRDTWLGVPVPHAYNPSTLGGRARRIT*AQEFE
11423	25324	A	11522	244	460	NCATITTNSTRIFLQLQKHCTKWLSLSISWQSLISF**ICFVLFFETNLAVSLRLECSGAILAHCNLCCLSS
11424	25325	A	11523	222	1	ESKDLDFRCQLAPRNSSCFVLFCFVFPLEIGSCSVAQAGAQWCNHSLSLQPPPIASAS*VAGTTNVRHYVQLF
11425	25326	A	11524	308	424	ITFLTMFKIYLQFDPATPLLGIYPKDY*SCCYKDTCTRM
11426	25327	A	11525	98	2	NIGGRPGAVAHAYNPSTLGGRGGQIT*GQEFE
11427	25328	A	11526	113	399	LDRFLTLLPRLRREDCLSPGGQGCSEP*SHRCVPAWATE*DLLSKKKKGVLEKPLFPPPSVGKPPFPSPPERLFFFILRPPLGGVFPPPSKKIIS
11428	25329	A	11527	280	3	PKYCQI*VLQCIAQLFKLSIYNTYTHTHTHSLSLSLSLPPPKVKNWLMSSFTLTFKMYTFGPGRVTHTCNPSTLGG*GGWIT*GQEFETNL
11429	25330	A	11528	284	2	FWGPQKKNFSFPPPGKLGISFKRAPPPFFFFFFETKCSVTQAGVRWCDLGSLOPLAWATERD*LNK*IKGMSKKLHT*VCMFRT RGRTRGRTRG
11430	25331	A	11529	134	2	DTLLPRLECNGTITAHCSLKLPGSGDPPASAS*IAGTGMCSHA
11431	25332	A	11530	104	1	GRGFFFFFFFFF*EVESCSVAQAGVQWLNLGSIQ
11432	25333	A	11531	157	373	CVFYTYSTSQLRCYIFIGNTRSVFRCHEIYT*KNRFWASTVAHTCNFSTLGSRGKWWII*G*EFMTSLANVVR
11433	25334	A	11532	237	389	ICKCKSTGFG*DFQEFETSLGNIVRPCFYRKIKASQV*WHAPITVATWEAE
11434	25335	A	11533	259	122	HISPSVQRHFFLFYF*TKPHLVAAQAGVQWCNLSLQSPPPGFKRF
11435	25336	A	11534	164	1	SSVVSQALILLFLKKTCFWPGAVAHACNPCTLGGRGERIT*GQKFETSLASINL
11436	25337	A	11535	106	310	GGDKGTVDWTLHFFDQKRLDHNKDHWM TIHAELPHELSA*CYAFKKECISGIGSI*AEKEYKIQFDG
11437	25338	A	11536	167	378	ASFFGTTITYKTILVYVYMFEEKFTIYIHYMYTF*RQGLVLSKLECSNVIIGHCNLKLH LGSSNLPTSASRVA
11438	25339	A	11537	101	396	VNNLKQRIGLSKRGEKLLVLISGFGGGFPGAGWIKKGKPPPGFPGGLGP*KRGGP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GKKGNFNKMGFNPKTLVFNQNFPGGA KPGTPGVRGELGDL
11439	25340	A	11538	18	361	QIGPRLY*DONGETPSLLKIQKKKIPGF GGGPLKSQLLGGLGWENH*NPGGGGCRD PK*PQGLPPWGTNQNPFVKKKEGGREKGT EGRKEGGEGKKKTLPGKIGALNLGGLLT SP
11440	25341	A	11539	134	365	PGFQNKKTGGGGPFRPKTKTNFKVF*KY LKICFGFWPKRPPPPGFFILETRSLFFI FFLGFFF*ETKRSVTRLECSGVILAH NRLVGSSHYP
11441	25342	A	11540	2	318	TTERFIYRITFGPKETEVDNLPGAPSEP VAALRLEARSFILKL*SFSLVDFDFFLP F*KTGSCLSPLRECRGEITIVHCSREL S*SHPPTSASQSSSGSGFHLG
11442	25343	A	11541	294	409	GTISFFRTCRGLGMAHTWNPSTLGGQGG *II*GQEFQT
11443	25344	A	11542	1	123	GKQRQEPALSYDHATVLLTS*SAHLGLP KCWDYRSDPPCLA
11444	25345	A	11543	69	350	VGAKHWHMDTKIETADPGNYYSGERGK RPRAEKLPCYYALYLNGIICNPKPPC CWKGHDFIYIVCGHIYIHIYICTHIYI YFF*DGGLLC
11445	25346	A	11544	103	340	LFCAFFLSPSKLDIFYHLSFYV*TLFLKD LISLAFFFLFWEAGSCSVTQAGVQGPNS THCNLCPLGSNNPSTASQAAGT
11446	25347	A	11545	256	354	PYPFGKPKRGDHWGLGV*NQPGQQGETP SLLKI
11447	25348	A	11546	196	335	EIVARLKRSVPVGRQWLPVIPALWKAK ESGSPEVRSS*VKKITCRPGTVAHACNP STLEGQGWIT*GQEFKTSANMVK
11448	25349	A	11547	202	377	TIHTKGMVGNFILVVFYQNFKTF* D KILGWARWMPPLIPAFWESEMGGLLEPK SL
11449	25350	A	11548	396	26	PPRIKKEKRSPNGAFYFPCWNF*KKKN LSLAKRFRDVSFFVSW*GSYLPPTFL QLLRWYVLTSHIAVSFKHLCEPHKNFTL QHSIPYLYIIEIEVYSYFINRNTIYKIN MDFSIVGFVFL
11450	25351	A	11549	232	371	REVPFENIKIGQVQWLTLIIPALWEVKA GGSLEARSL*KYQNWPGAVAHAYNPSTL GGQGGRIA*GQKFEISPANMAKP
11451	25352	A	11550	174	381	NRDEGFRYADRAEVQRLTGTILEHCGL QRPL*RSSCFTLPCGWDRH*SPSHVA GTTGISHTRLIKKAFFSQTGSSC
11452	25353	A	11551	262	359	DYSNLGLVWLTTVIPALWEAKAGRSSE VRSS*PALWEAKAGRSSEVRSS
11453	25354	A	11552	70	380	LHKCSFYIYNHCNNPIYGLISLYPKQLF SYENFKDFCNKI*P*IPNFELKTSTP*L EKL*NWAMARHGGSL*SQHFGRRRAD HMRSGVPGQPGQGESPT
11454	25355	A	11553	319	56	TFFLGPPGFF*KIFFSVGDPLIFFLPKK FIGEQKNAPGKNFFGFFLSFLFFFL TLSSALECSGAMSAHDNLCLPGSSNSPA SAF
11455	25356	A	11554	230	399	MMGEIINQANIISVCQIIRRLRHESHLI PGGRGYSELRSYHCTSTWVTE*DSCLKK
11456	25357	A	11555	376	396	F*IFWRDGVSPCCPGWSQILRLQOSTCL

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						GLPKCWDYRPPHPATAASCPYFYHYVLL KIWRYSFDLSCLWNLVVWGLAFG
11457	25358	A	11556	176	384	KAWPNVRNNYR*NFFFQCLNNFRKRLK CFRCGADKFGKTGFSCLYALKPTNWGR EQWLTVNPTNFGK
11458	25359	A	11557	295	391	PYKLLITHHTHTHTHTSRTHTI*HTTLS LYTF
11459	25360	A	11558	1210	1753	NTWCMERLAVAFGSFNRRNSPLRGWALWL TPIILALWEAEAGGPLEPQEFETCLGNM VKHCLYKNLKNVSGV*DLPGQHGETLSL QKFKKCVRRGGTCL*SQRLRRLSWEDCL SQGGQGCSEP*SHQCVPAWVTELDPSK KTKTKKFFGLPSPFLFVCFLTHIYVKE YAFVLAEEASGKTTSKLTMVTSRNLGK TKKFFGL
11460	25361	A	11559	172	3	KQKFFFPFPPSHQIKIFGGGAPEMPPFFF FFRKESRFVA*AGVQWRNLSSLHPPPHP
11461	25362	A	11560	143	1	GQAQWFMPVIPVLWEAKAG*SLEARSSR PVCATATPPQLIPK*YEGL
11462	25363	A	11561	84	2	KPLDTLGGQGGCIT*GQEFETSLANMV
11463	25364	A	11562	12	387	QGILLPCFMSSEERGRIYSNTFSFFFF FGKGGQINPQGGGQATEPRLREPSPSGL TLQGPNGGPPPPPGQNFFFKKGGYPG GAGGVLPNPGPKGNTPPGPPKARKKRGGP PGPGQKFL*NPKG
11464	25365	A	11563	230	375	RAKGKLLSESLLSIQSFKKPSVHTCNPS TLGG*GRWIT*GLETTSLA
11465	25366	A	11564	287	55	PEDGRVQWLTVPVPGWLWEAKEGGSLSR SS*SQINPVGSVPYSLRVL
11466	25367	A	11565	115	411	FFFFFFFFLGENSFFSFRGGPRGGHIFW NFPFPG*GVFPPPPPPGGGNKGGAPPPG FFFFFFP*KTGFPPPLPGGPPPPPLFGPPP FPPPKGYNFRDPPP
11467	25368	A	11566	139	356	CLLIGWYNTGCITQGSTRKIGTTFFLRQ SSSVAQAGVKCSGMILCYRNLRLPGSSN LPDSAS*VAGTTATYP
11468	25369	A	11567	101	410	FLFFFFFFFFLKKIFFFPPRGGGGGN*K KQTPPLGGKKNFPPPPKRGGGGTTPPP PLLFLVF*GEGGFPGGAGGGKKTPKGNP PPPPKGGEMGRGPPPRGG
11469	25370	A	11568	417	56	EDCLRTGVRDLLPNPHNLQIAGRDGAR L*SQLQEHHLSPGFRGYSEL*SCHCSA WATE*AYRKQNKTKQNYRSSALLHLYTP MATAWIKIAFLRAGDIFLSVLSFLPNSY PLFSHPSQ
11470	25371	A	11569	301	443	EDTTFVCFEVESCSVAQATDSPASAS*I AGIIGVCHHARLIFVFLVE
11471	25372	A	11570	44	408	RGRGHGPHSPWRRRRRLRVVEGRKATES KRRAYKYPPLALLCSHQWKPNWELDSQI KIPTGL*LK*PSFIFIFIYLFWKQGLS LAPMLECRGAVLAH*HLRLPRSSLSHAS ASQVAVTTG
11472	25373	A	11571	201	1	AERPVTGPPVYAEPGLQGRQG*KNMFKN MQHPRWADHLRSGVQDQPGQYGETPVST KNTKITQAQCI
11473	25374	A	11572	343	1	FGLLFAFTLEYKLYESINHFHACCVCRF SSGTLHVVCNRRHPNKLDEWNSGGGGRQ DLTLTPRLGCSGVIMAHCNLVLLGLSNP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VSAS*VAGTTGAHSHAWIDKLFVKTGPLY
11474	25375	A	11573	209	3	VGPPPKSLPGGFPPFFFCPKCFPRLLKKKKKPKPGLVAYTCNLNTSGVRGKKIT*AQEFKKSPSNIVKPMY
11475	25376	A	11574	312	430	QRYARPGPVVHCYNSSSTVGGRSRGIV*AQEFATSLCNMT
11476	25377	A	11575	125	3	NSLGPVVHACNPRSLGG*GGRITSAQEFETSLGKIRRPPLY
11477	25378	A	11576	190	362	CVNNYID*EKKKKKKKKREREKKKKKKKKKKKKKKK*GGGAPKKKKKFTPGGGKNEFFL
11478	25379	A	11577	231	340	KRITRVNQDGLDLLTS*SAPLGLPECWDYTMKPCLY
11479	25380	A	11578	60	3	RMQVSV*ITFPMSLQAYLIYSSSVAAGAQSGIEECKYQFAWDRWNCPERALQ
11480	25381	A	11579	285	406	KKGNWPGAMAHTCNPSTLRGRGGWIA*GQEFETNVGDMAK
11481	25382	A	11580	121	1	NLNCPPGVAHASNPNTTGG*CRPIV*GQEFYTRIANTVKP
11482	25383	A	11581	199	384	KKTPPGGIFFCPEAGPAPPL*TPFC*TPLFFSPAPFKPKRALKFPLKPKRGFFQIPFFFF*DGVSLLCHPGWSTVARSCPRV
11483	25384	A	11582	677	934	YGSRHCI CFLQAISEILFLKNPARHGGSQVQDQPGQSKTLTLRKKSK*ARHNGSCLSSQNFGRLRQEGHLSPGG*GCSEL*PRHC
11484	25385	A	11583	104	2	KKIGGGPPLFFFFETESCSVARLE*SGAISAHCN
11485	25386	A	11584	349	9	GGRSLGPRKTRVQWGIPFPPPLHLGGKAKPCFPKPKKKKKVKGLNKHYSKEDIQMVNRYMKKCSSTSLPRERKIKTIMRYHFPISIRMAIRKIKDKPDQ*GCIEKGGSVVRPMYL
11486	25387	A	11585	163	1	TAVRIKHNSYTLTPCLRHSRYLINVTCWPGPVAHACNPSTLGGGRGWIT*GQEF
11487	25388	A	11586	192	41	SKSKYHIYGDALQKSTVYKWIHFKKG*DDVKDKAHSTRLSMSICEEKE
11488	25389	A	11587	30	374	GWSPEDLFPGLSLPPALKGFSGEGG*PFLPFQKKRGGGGSSPPFVLKVRPENRLYPGGGGFR*PKQGCPSPAWEAEPDSLKSKKKKGFGQKKKKKKVLKEKT
11489	25390	A	11588	66	245	SLCFFVFFVFF*TESCSVTQGV*WYNLGSLLQPPPPKKNKIKKQKKKINWGRGFKRRL
11490	25391	A	11589	243	402	FLHLKKKKKKKKKKKKKKKK*RDAG
11491	25392	A	11590	205	3	IRLLGIIKNPTPAHCQ*K*KTGEPLW*VW*FFRRLHTELSYDPAIPLLCINSTEVLAPGI PRFR
11492	25393	A	11591	404	152	MGFHVSQDGLDLLTS*STLLSLPKCWD*CWDTREPLCPGHFAISFNKVVLTNTTVVLYFYLIILHICIYCPYKLLFLFFFYIY
11493	25394	A	11592	311	386	TVYPPLAGNLAHAGA*AGIVGTALSILIRAEKGQPGALLGDDQIYNVIVTAHAFVIFFFIAIPIIIGGFGN*LVPLIIGAPDIAFPRINNISF*LLPPSFLLLASSIVEAGAGTG*TVYPPLAGNLAHAGASVDLTIFFLH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11494	25395	A	11593	39	397	EGCPLFFVFVFFVFFFGGKKIFFPPPRG GGGAPHKIPGPPPPGGNFFPPPPPLRG GKRGPPPPPGFFFF*KKGGVSLFPRGG VFFFSFWRGGRGGFPPPPQKKIFLKGP PPFYKKK
11495	25396	A	11594	243	46	GILSCCFHDSLSLSLNSL*CD*VWISLCLS YLVSIELLGQCGLIFFIKRESFWLLLLK MYLQPLSFLS
11496	25397	A	11595	327	2	PRAILRIQFLWPMRPYVWMSQPCSLCF CHTAKTVPTSRPLLLGFFSLPGIAHISM WLVLSYGLGFSSKVTWPGVVAHVCNPS TLGG*GGWIT*GWEFKTSLANMVK
11497	25398	A	11596	292	384	LGTVAHTCNPSTLGGQDGWIT*IQEFET SLR
11498	25399	A	11598	125	2	PFOGQSGGTRGPGAVAHTYNPSTLEG* GGRIT*GQEFETS
11499	25400	A	11599	302	408	TGGWLGVAHACNPSILGGRGRQIT*GQ ELETRLA
11500	25401	A	11600	409	131	GRSGGVPKSGVLKPPGPPGGTFFFKKP KITRGGGQPLFPLLRVRPENCLSLGS GGCH*TKLPPCPSTWGAQ*KLVSKKKKC EGGGRIYS
11501	25402	A	11601	196	330	HHCMLAWVTGRPYLNIYICIVADIYIHT YICIVYTHTRVYIYLAI*YIYVYMR YIYIYIYVYIYTHTHGYIYIY
11502	25403	A	11602	41	252	TPGRARGQLGHSSSTGLDLLTS*SACLS LPKCWDYRREPPRAEDIKFMF*AILSE TILVRGVRSRATPS
11503	25404	A	11603	271	440	KKKKRGGRFKESKFTSAGLQGNIFFIGP PKLIPRAAV*QRGDWKNLGVTLNRLCH
11504	25405	A	11604	429	2	FSSFFAEKGCHCVSQAGFKLLSSRDLP SAPHLGIRLLGRLRQEDPPSPGV*GCSE LQSRCLCTPAWITKRDPVS*KFKKQKTKT HTH*RKPTKGQDHQYHCLPPPHVMPKV FRGSNVHGAVRTGRSGRSIPELSHAVPH AP
11505	25406	A	11605	113	2	TEATHLVCTYKN*KLGWAWWIMPVIPAL WEAEVGRLL
11506	25407	A	11606	301	3	WVMVCSVKNIALGHACGKFHYEGRGKPA EHPSWVLLVLESLQKKLFLSYFL*FTLL QPPSPRLT*PVFRFFFRDRIMLCCPGW SAVVPERVGRAGNSE
11507	25408	A	11607	117	431	SCDFCLSFSLSLFFFFFRKGIFFLGPRG ENKGGNKIKWTLPGGKGNRSRPPKGG GKRGGPPPGANLDF*KKTGFPGGGRGGE KPPPPGGRAGGAPQRGKPAAG
11508	25409	A	11608	277	88	RRTTSSWLARNCIQGPAGYHTGS*TPDL KGSACLSFPKCWDYRWRLDL
11509	25410	A	11609	200	27	VRLKPGDSRDPDMQWYI*ENRPARCGG SLL*S*HFGRKRKADHLRLGVQDTRSSA R
11510	25411	A	11610	17	414	TVWLVMQDPENEWIVSGWGGKEEPRYF MCEARSSMDRVFFFF*KKTLLFFPPGGG GGAKIWNIGIPPPQGSPLSVAYPLGVWE KKGPPPHPKKRVPPV*PGGVLFSEPGN PPPGPPKGVGKRSSPPSPVL
11511	25412	A	11611	296	428	RIYENWRGTVAHACNPSTLGGQGGWIT* GQSLKTSTGTVAKP

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11512	25413	A	11612	20	362	NFVRGVARGSRGGATRCCEWVGLRPVGMAYGRSPSWLL*VKPSAASHRPPLPRAADTPGTAPAPTPTPAPAAAPALTPSSGPGSALTLLEELQEAIRRAQRWGLTMLPRLASNS
11513	25414	A	11613	158	2	LMLSRTPQLQL*YTLLELELPRLIAPDL LSNGLSLKDLKWTHTSNYRASKETK
11514	25415	A	11614	3	410	RSEVYGLVLTWYQVNRVPWTHKAARFTRVSRWARPRSKI ESECYWLPQAHRTKS*PLVRTLSGLCSLLGFHPLFLSLLATDLVPLPSFALLLLELFFLPMPKLPAP*SPTKRSFSFYFFRDRVLLCCPGWSQTP
11515	25416	A	11615	189	397	YKVLFLVEKNGFFFLFFFTKPCCVAPTGVQGNFNG* LQAPPPGLPLFSALAAPEVGTNGTPPPPPRFFF
11516	25417	A	11616	158	1	KGKPTPKTFFCQKQIFFLVFFF*TESHSVARAGVQWRDLDSLQAPPPGFTPR
11517	25418	A	11617	319	425	KVWLYSQAV*KVWLYSQAVAHYTNPNLTGGQGWRIA*AYEFKTSL
11518	25419	A	11618	94	2	CLTISWLGTVAHVCNPNSTLGG*GGHITRSR
11519	25420	A	11619	381	9	FFPLPLPLPTVSLFPRSPSDAEPKLDCTAAISAHCNLP*FSCSLPSACNCRRAPRLTASASRGAGIADGVSTQCSMVPRL ECGVISAHYNLHLPATSLGLPKCRDCSLCPDEIVDPRI
11520	25421	A	11620	144	431	IVNVIVGKGEKGRKIPE*LIRCNGWN*SWDRWVAEDHVLREPSNRRRLARVCLTPVSQHFGRRRRLDHEVRSRIPACATWRNSVSTYNTKSGWAC
11521	25422	A	11621	174	449	VFSLPLLGGASQLGYLEVDPLEEA VCPFSDLKPHAGRTTTLFKAIRQGHLSLQRFLLPFVWLCPAPRGGVYRGRQASLS*GGLHPVRASRP
11522	25423	A	11622	316	412	GGPSAVAHACNPSALGGRGGRIS*GQEFKTSL
11523	25424	A	11623	183	2	PKQVYLRNGLLSHSHKCNKIHHINRLKREKIOPGVVAHAYNANTLGGQGRWIT*GQEFENE
11524	25425	A	11624	355	168	DLIVCYDPNAINL*SLLLRRLKWEDCLSPGG*GYSEPRSCHCSPA WAAEPDPVSKKDRNVEFIYCC
11525	25426	A	11625	154	3	TADVLFLLGQAGRGNFVVMKKNCPRGTVAHACNPSTLGGRGG*ITRGLEFK
11526	25427	A	11626	412	3	IFFPPPKKDKRTRGGQKKNIPPAPPRNFLGRGGNFPPQKPFPPPLF*IFPRPP*C KGSIPPFLPLCFQKKKTPSFFFLPNGSPPICEKIFLFPKKGFLKFKPRFLKKKG PFFFFFGNAVLLCQPGWSAVAQSQ
11527	25428	A	11627	290	423	VFEYFFKFFKKNNSWPGVVAHTYNPSSLGGQGGWIT*SQVLRPP
11528	25429	A	11628	213	3	LSGIYSGNRRLLVRYSKSVSVIHHINRLKKNHIIISIDGKPLEQIQNSFMT*KRNKLKWDHLRPADA
11529	25430	A	11629	152	2	FQKNRDLPSKAGWPGMVAHACNPSTLGARGGQIT*GQEFETSMVMNVKP
11530	25431	A	11630	422	189	PLSGFCPSTWGAQRALSKKKRSEAGHSGSCL*SQYLGRLKQKDHPSPGGRGFSE

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						LLNCTPAWVAKQDPVPPKKRLK
11531	25432	A	11631	239	424	KEDNNRVFVIGPLGGLNELAHDKAFKTO NHHWLGVGHAACNPSTLGGQGRWTT*GQ EFTTSL
11532	25433	A	11632	343	401	AREHEKSAACQ*GMERSVIKCHVATE *EREQKRERQKERASEKERQESERDSK RERARESERERESTRAQLVRKIVNQIS
11533	25434	A	11633	125	371	FQGCACIKLTNTLLPYAHGYLIWREDGK GCHCKMTAKI IHSCKLSPDAL*SQLGVP L*THTHTHTHTHTHTHTFSEKKGLVP
11534	25435	A	11634	235	433	AALTSFSGPFSFCSYLINTLGKNFNPHE ISTT*FTLQRL*KIIFWPGMVAHACNPS TFGGQGRWIT
11535	25436	A	11635	93	385	FTLKSEERRKHSVPQGGKQNKIKLLSPDC KLENKRFGWARWLTVPVIPAL*EAKAGES PEGNGEREEATEPFGSIILGFFFTQIA HLHRSDYEPNEDS
11536	25437	A	11636	190	398	NTKKSQKAFKTKQKPPPLDPKKKASKK TKFFLPKKISTRKFRTGPWRGTNFSCLK AKKNLGKTRKKIFP*RPFFPSISLFWP FFFFLFF*KDKVPLCHRGWSAVVQSQLT ATSIISQMY
11537	25438	A	11637	190	380	TPKKWPKAFKTKGKPSFFHPRKKALRK TKFFLPQKFP*NPLSPLIPALFWPFFFF FFF*KDKVPLCHRGWSAVVQSQLTATSI SQMY
11538	25439	A	11638	261	91	EKTLWAGHGGTCL*SQLGLRLRWENHLN LGGRG*RSRHCTPAWVTERDSVSNK*IN K
11539	25440	A	11639	1	334	FRANRTVKDAHSIHGTNPQYLVERTI RT RIYESKYWKEECFGLTAEVLVDKAMELR FVGGVYGGNIKPTPFLCLTLKMLQIQPE KDIIVEFIKNEDFK*VQCSLANIRGMY
11540	25441	A	11640	193	457	DGILLCGPGWSAVAPSQLCSGTISAYCN LCLPGSSESPVSAP*YLGLOACAHAPLM FVFLVYTGTCLPLSAHHSRAANSSHFS YPLL
11541	25442	A	11641	257	373	NTISCFRSLRPVAHTCNPSTLGG*DGQI T*AQEFETCLG
11542	25443	A	11642	211	367	DTTSHPFEWL*FKKSRK*RVLDRIWGN* MLVHCWWEHKMVQLL*KTVWWLFK
11543	25444	A	11643	112	367	LQIKTIRYHHILTRMAKIQNTDTNKCQY ECGATGTLIHCWWEFKIIPVIPALWEAE VGGLLEVRSSRPAPWTRENPIFTKIIKN Y*KYKNTPYIIR*LQIKTIRYHHILTRM AKIQNTDTNKCQYECGATGTLIHCWWEF KIIPVIPALWEAEVGGLLEVRSSRPAPW TRENPIFTKIIKNY
11544	25445	A	11644	310	335	YHLIAGSLGDIERLSML*IGKAVCHNKY **GCGEFGFLHCWWEWMVQSL*KIVC QILQT
11545	25446	A	11645	143	455	KRKGPSLWLLGKSMGGIRFF*KKVFFSG FKSLWFFFWPLWKPLERLN*IKISFYPP AKKKGQKQAQFFFFFPFSFSLAGCSG SISAHCNLCLLGLSDSPTS
11546	25447	A	11646	182	458	SRGGIRFF*KRVFFSVIKSIWFFFWPLL KPLGRVN*IKISFNPPAKKRGWERKAQF FFFFLPRSFSLAGCSGISAHCNLCLLG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LSDSPTS
11547	25448	A	11647	319	3	RSTKYSPRGWEPSMWFLFLHVFSLPFRS ILGPPLLGTPLRGSPPPPPFFEGKGFIY GLTFFFF*EPPCEIFFFFFLDRVLLYCP GWSAVVQSAHCSLELKDVCVI
11548	25449	A	11648	165	2	DQSGRPRKILCAHTHTAHMHTSLGQT* QDPV*THHTHTHTHTPLAAAAQRIN
11549	25450	A	11649	290	3	SKQNTTHTWATLKSIIYPSQFWRLGSPSS RWQLDGLFVLRALFLVCRQPPSLRILTW EKTEERKREREREK*DRERERNEIERNERE RERERETQRMV
11550	25451	A	11650	220	2	TPTLPGTGLTALDRIPGRDPGPRRAGR PF*AGVAAENCPDPAEGGSTRPLGAPGR GSAPP*RHPGPAGGRR
11551	25452	A	11651	29	387	FLIFDVTIVIDLACHEPHSYKMAHLINV VCVLTAPPTSYPFPIISFLGPPYSLRHNDI EIRPINNPRTSQCSEKRSHTSLTLNQ KLEMTTLSKDGMSKAKTG*EPGL*C*TV SQAVNAK
11552	25453	A	11652	267	2	KFFFFVFSTSKLNFYPTFPPLFLFSFF FFFFFFFMREGFAVTWVPAGAVAPAVLA HCSLELVGSGKPPISAS*GAGTTGMHYH TRMY
11553	25454	A	11653	50	411	EAVAGGMEKSMNNLPKGPDTLCFDKDEF MNEDFDVDHFVSDCRNRGQLEELRDNPQ LYYKLLKTAMVELINKDYADFNLSDDL VGMEQALNQLSVPL*QLREEVLSL*SFV IERISPPS
11554	25455	A	11654	303	403	VRNMVEWLGVAHAACNPSTLGGQGEQIT *GQEF
11555	25456	A	11655	356	653	SVSPCFPPGPASTLSFLVADFRRRGVDV SQVAWQSKGDTTPSSCCIINNSGNRTIV LHDT*GPRASPCYNPPISWLNQFPHPSP WASQLPPSVASVYQK
11556	25457	A	11656	442	2	GRPILMRPAVL*SEPRTPACVDIQQQIM TIIDEVVKACAKVQTLAPINSASRMQS IRHVYIYLDSSARPAGKGAIGFIKVG YKKLFVLDDREAHNEVEPLCILDPIIHE SVQRHGHGRELFQYMLQKERVEPHQLAI DRPSLV
11557	25458	A	11657	109	474	DINMCGRVVLVAERM*KRKRDKYNIEET E*VL*KKVRHSQLOKENVAQNAPVVQNA AYIDQPSPAHVGGQGLSKLPSRPGDQGV EPQNLRTLQGRSVIRSATNTTLPMLMS QRVIAPNPAQLQGQGPCKHICRTTTP NMNPANV
11558	25459	A	11658	342	3	ENQLKNGEHSKSSQASAPPNDHNTSLAR A*KWAGAEAEIALLTEAGFRWVIMNFA ELKEHVVTQCKEAKVHDKTTQELIAGFE RNITYLM*LKITTREPHIAITSINSRMA
11559	25460	A	11659	204	17	STCTPLPTA*SQSRPHPPPTPTPPAPWR SSNGPLSRGSSSRNSTSSWSIALATGPW THRSEL
11560	25461	A	11660	505	514	GS*GNHFNPDGASHGGPDSDRTGPRGP CLPSPWGAQILRDWYPQEMGTGKQ
11561	25462	A	11661	80	374	FLFDIYNRCYLIFINIT*YLSNFD*IF IIYLVAIYRLCLGLFRAPRQCKHPRP QFSFNKIGTKR*AWPGAMAHTCNPNTLG